From Autopsy Donor to Stem Cell to Neuron (and Back Again):

Cell Line Cohorts, IPSC Proof-of-Principle Studies,

and Transcriptome Comparisons of *In Vitro* and *In Vivo* Neural Cells

by

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ABSTRACT

Induced pluripotent stem cells (iPSCs) are an intriguing approach for neurological disease modeling, because neural lineage-specific cell types that retain the donors' complex genetics can be established *in vitro*. The statistical power of these iPSC-based models, however, is dependent on accurate diagnoses of the somatic cell donors; unfortunately, many neurodegenerative diseases are commonly misdiagnosed in live human subjects. Postmortem histopathological examination of a donor's brain, combined with premortem clinical criteria, is often the most robust approach to correctly classify an individual as a disease-specific case or unaffected control. We describe the establishment of primary dermal fibroblasts cells lines from 28 autopsy donors. These fibroblasts were used to examine the proliferative effects of establishment protocol, tissue amount, biopsy site, and donor age. As proof-of-principle, iPSCs were generated from fibroblasts from a 75-year-old male, whole body donor, defined as an unaffected neurological control by both clinical and histopathological criteria. To our knowledge, this is the first study describing autopsy donor-derived somatic cells being used for iPSC generation and subsequent neural differentiation. This unique approach also enables us to compare iPSC-derived cell cultures to endogenous tissues from the same donor. We utilized RNA sequencing (RNA-Seq) to evaluate the transcriptional progression of *in vitro*-differentiated neural cells (over a timecourse of 0, 35, 70, 105 and 140 days), and compared this with donor-identical temporal lobe tissue. We observed *in vitro* progression towards the reference brain tissue, supported by (i) a significant increasing monotonic correlation between the days of our timecourse and the number of actively transcribed protein-coding genes and long intergenic non-coding RNAs (lincRNAs) ($P < 0.05$), consistent with the transcriptional complexity of the brain, (ii) an increase in CpG methylation after neural differentiation that resembled the epigenomic signature of the endogenous tissue, and (iii) a significant decreasing monotonic correlation between the days of our timecourse and the percent of *in vitro* to brain-tissue differences ($P < 0.05$) for tissue-specific protein-coding genes and all putative lincRNAs. These studies support the utility of autopsy donors' somatic cells for iPSC-based neurological disease models, and provide evidence that *in vitro* neural differentiation can result in physiologically progression.

DEDICATION

This dissertation is dedicated to the three amazing women I have lost during graduate school:

My grandmother, Eunice Hjelm

My mother, Nancy Bjorge Hjelm

My dear friend, Jennifer Poels

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LIST OF GENE SYMBOLS / HUGO NOMENCLATURE

Symbol	Gene Name
ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1
ANG	angiogenin, ribonuclease, RNase A family, 5
APOE	apolipoprotein E
APP	amyloid beta (A4) precursor protein
AQP4	aquaporin 4
BACE1	beta-site APP-cleaving enzyme 1
BACE2	beta-site APP-cleaving enzyme 2
BDNF	brain-derived neurotrophic factor
BIN1	bridging integrator 1
C9orf72	chromosome 9 open reading frame 72
CACNA1A	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit
CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit
CALHM1	calcium homeostasis modulator 1
CLCN2	chloride channel, voltage-sensitive 2
CLU	clusterin
CNTNAP2	contactin associated protein-like 2
CPA6	carboxypeptidase A6
DCTN1	dynactin 1
DLG4	discs, large homolog 4 (Drosophila)
FIG4	FIG4 homolog, SAC1 lipid phosphatase domain containing (S. cerevisiae)
FOXG1	forkhead box G1
FUS	fused in sarcoma
GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1
GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2
GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2

GAD1	glutamate decarboxylase 1 (brain, 67kDa)
GBA	glucosidase, beta, acid
GFAP	glial fibrillary acidic protein
GSX2	GS homeobox 2
HD	huntingtin
HTR1B	5-hydroxytryptamine (serotonin) receptor 1B, G protein-coupled
IL1A	interleukin 1, alpha
KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
KLF4	Kruppel-like factor 4 (gut)
LDLR	low density lipoprotein receptor
LGI1	leucine-rich, glioma inactivated 1
LIN28	lin-28 homolog A (C. elegans)
LRP1	low density lipoprotein receptor-related protein 1
LRP1B	low density lipoprotein receptor-related protein 1B
LRRK2	leucine-rich repeat kinase 2
MAP2	microtubule-associated protein 2
MAPT	microtubule-associated protein tau
MBP	myelin basic protein
MECP2	methyl CpG binding protein 2 (Rett syndrome)
MOG	myelin oligodendrocyte glycoprotein
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)
NANOG	Nanog homeobox
NGF	nerve growth factor (beta polypeptide)
NKX2-1	NK2 homeobox
OLIG2	oligodendrocyte lineage transcription factor 2
OTX1	orthodenticle homeobox 1
OTX2	orthodenticle homeobox 2

PARK2	parkinson protein 2, E3 ubiquitin protein ligase (parkin)
PAX6	paired box 6
PDYN	prodynorphin
PGRN	granulin
PICALM	phosphatidylinositol binding clathrin assembly protein
PINK1	PTEN induced putative kinase 1
PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)
POU5F1	POU class 5 homeobox 1 (Synonym: Oct3/4)
PRNP	prion protein
PSEN1	presenilin 1
PSEN2	presenilin 2 (Alzheimer disease 4)
S100B	S100 calcium binding protein B
SCN1A	sodium channel, voltage-gated, type I, alpha subunit
SCN1B	sodium channel, voltage-gated, type I, beta subunit
SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3
SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
SNCA	synuclein, alpha (non A4 component of amyloid precursor)
SOD1	superoxide dismutase 1, soluble
SOX2	SRY (sex determining region Y)-box 2
SYN1	synapsin I
TARDBP	TAR DNA binding protein (Synonym: TDP-43)
TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)
TUBB3	tubulin, beta 3 class III
VLDLR	very low density lipoprotein receptor
WWC1	WW and C2 domain containing 1

CHAPTER 1

ESTABLISHMENT AND BANKING OF PRIMARY DERMAL FIBROBLAST CELL LINES FROM NEUROPATHOLOGICALLY-EXAMINED AUTOPSY DONORS

Introduction

Human dermal fibroblasts (HDFs) are a valuable resource for both primary cell research and stem cell-based, *in vitro* disease modeling because fibroblasts are typically easy to establish in cell culture and exhibit robust *in vitro* proliferation (Mansbridge). Moreover, these primary cells are permissive to a variety of reprogramming techniques, including nuclear transfer, cell fusion and transcription factor transduction (i.e., induced pluripotent stem cells) (Yamanaka and Blau). Because of these advantages, HDFs have become the most widely used somatic cell type for the generation of human induced pluripotent stem cells (iPSCs) (Lowry and Quan). In fact, the first human iPSCs described in the scientific literature were generated by lentiviral integration of the Yamanaka (*POU5F1*, *SOX2*, *KLF4*, *MYC*) or Thomson (*POU5F1*, *SOX2*, *NANOG*, *LIN28*) factors using HDFs as the somatic (or genetic) donor (Takahashi et al.; Yu et al.).

It has been hypothesized, however, that fibroblasts may not be the optimal somatic cell type for the generation of clinical-grade pluripotent stem cells and their derivatives (Lowry and Quan). Fibroblast-derived iPSCs exhibit epigenetic modifications slightly dissimilar to human embryonic stem cells (hESCs) and elegant studies with murine iPSCs suggest those derived from tail-tip fibroblasts are significantly more likely to produce tumors following neurosphere engraftment (Miura et al.; Kim et al.). For these reasons, much of the reprogramming field is shifting towards using primary cells derived from whole blood for generating iPSCs from living donors (Mack et al.; Rajesh et al.; Brown et al.). Despite the disadvantages fibroblast-derived iPSCs may have for use in regenerative medicine, these cells still retain immense value for creating donor-specific, *in vitro* disease/toxicity/genetic models, many examples having already been published (Dimos et al.; Park et al.; Ebert et al.; Ghodsizadeh et al.; Somers et al.; Raya et al.; Lee et al.).

Studies that aim to use primary human cells lines for genetic disease models of both rare diseases, and diseases that have either late-onset or complex genetic etiology, will likely continue to use HDFs as the somatic cell source; living donors may either be difficult to obtain, or it may be beneficial to obtain cell lines from a biobank that has additional genetic information about the donors' disease, respectively. One primary example of a biobank that stores primary HDFs from individuals with a variety of genetic disorders is the Coriell Cell Repository, a part of the Coriell Institute for Medical Research. This biobank includes HDFs from diseases such as amyotrophic lateral sclerosis (ALS; mutations or repeats: *SOD1*, *FUS*, *TARDBP* (TDP-43), *ANG*, *FIG4* and *C9orf72*), familial early-onset Alzheimer's disease (AD; mutation *PSEN1*), frontotemporal dementia (FTD; mutations *MAPT* and *PGRN*), Huntington's disease (HD; repeats HD (CAG)), Parkinson's disease (PD; mutations or repeats *LRRK2*, *PARK2*, *GBA*, *MAPT*, *CACNA1A*, *DCTN1*, *PINK1*, *PLA2G6*, *C9orf72*, and *SNCA*), as well as countless rare disorders with and without clear Mendelian inheritance (http://ccr.coriell.org/). However, many of the neurodegenerative diseases mentioned are dominated by sporadic cases where no known causal mutation or repeat has been identified, and many of these diseases are not mutually exclusive (i.e., an affected individual may actually have pathological features of multiple disorders). Due to these complications in both sensitivity and specificity, robust classification of an individual as a specific disease case or unaffected neurological control is often strengthen by the additional information obtained from a postmortem neuropathological exam (Beach, Monsell, et al.; Beach, Sue, et al.; Corneveaux et al.; Hamilton; Joseph et al.; Nelson et al.; Piguet et al.; Tolosa, Wenning and Poewe).

We aimed to establish a cell line cohort of primary dermal fibroblasts from autopsy donors that had been clinically diagnosed with a neurodegenerative disorder and were further evaluated by a postmortem neuropathological examination. Likewise, we aimed to establish HDFs from autopsy donors with no known neurological impairments, but upon postmortem examination may or may not show neuropathological features of disease (e.g., beta amyloid plaques). Meske et al. have demonstrated that HDFs can be established in cell culture from autopsy donors up to 48h postmortem and from individuals up to 99-years-old (Meske et al.). These studies additionally demonstrated that (in a rat model) fibroblast viability/proliferation was negatively affected by longer post mortem intervals (PMIs).

We collaborated with Dr. Thomas Beach and Lucia Sue of the Brain and Body Donation Program at Banner Sun Health Research Institute (BSHRI) to obtain skin biopsies for the purposes of fibroblast cell line establishment and protocol optimization.

> "The Brain and Body Donation Program (BBDP) is an autopsy-based, research-devoted brain bank, biobank and biospecimen bank that derives its human donors from the Arizona Study of Aging and Neurodegenerative Disease (AZSAND), a longitudinal clinicopathological study of the health and diseases of elderly volunteers living in Maricopa county and metropolitan Phoenix, Arizona" (https://www.brainandbodydonationprogram.org/).

Donors enrolled in this study are usually evaluated by autopsy and have their brain removed after a short postmortem interval (< 3h), thereby preserving sensitive molecules like RNA that are subject to rapid degradation following death (Beach, Sue, et al.; Birdsill et al.). Here, we describe the establishment of over 200 low-passage, primary HDF cell lines from 28 autopsy donors enrolled in the Brain and Body Donation Program at BSHRI.

Materials and Methods

Whole Body Donation

Tissue was collected after a postmortem interval (PMI) of approximately three to seven hours during the rapid autopsies of 33 whole-body donors (ages 44-97). Although 33 autopsies were attended and biopsied, 5 donors had positive test results for Hepatitis B or C antibodies; these cell lines were not established due to safety concerns, resulting in successful cell line establishment for 28 autopsy donors. The subjects were enrolled as whole body donors in the Banner Sun Health Research Institute (BSHRI) Brain and Body Donation Program and had previously signed informed consent approved by the BSHRI Institutional Review Board (IRB) (Beach, Sue, et al.). Most fibroblast cell lines were established as previously described by Villegas and McPhaul, with minor modifications (Villegas and McPhaul). Fibroblast cell lines established by explant protocol were generated as previously described by Keira et al. (Keira).

Skin Biopsies and Fibroblast Cell Line Establishment

A small area (~ $20cm^2$) of the anterior side of the forearm, leg, and/or torso was sterilized with Betadine (Purdue Pharma L.P., Stamford, CT, USA) and rinsed with sterile Dulbecco's Phosphate Buffered Saline (DPBS; Invitrogen, Carlsbad, CA, USA). 3mm and 5mm punch biopsies (Acuderm, Ft. Lauderdale, FL, USA) were dissected from these areas and placed into 50ml conical tubes containing 25ml ice-cold Primary Fibroblast Media (PFM; Minimal Essential Media (MEM; Invitrogen), 18% Fetal Bovine Serum (FBS; ATCC, Manassas, VA, USA), 100units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich, St. Louis, MO, USA), 0.25ug/ml amphotericin (Sigma Aldrich), and 5µg/ml Plasmocin prophylactic (Invivogen, San Diego, CA, USA). Skin biopsies were dissected into pieces, distributing approximately 0.7cm^2 to 1.9cm^2 dermal tissue per 25cm^2 flask (BD Biosciences, Bedford, MA, USA). Any adipose tissue identified was removed with dissecting scissors prior to cell culture establishment. <u>Dissociation Protocol</u>: tissue pieces in 1ml cold PFM were dissociated into pinhead-sized pieces with a scalpel and were further frayed by pressure with the blunt-end of a 1ml tuberculin syringe (BD Biosciences, San Jose, CA, USA). Mechanically dissociated tissue and media were introduced into a BD Primaria 25cm^2 flask with a 1ml tuberculin syringe (BD Biosciences) and were then evenly distributed. <u>Explant Protocol</u>: tissue pieces in 1ml cold PFM were placed into flask with non-dermal side of tissue pieces facing the flask's adherent surface. For both protocols, flasks were placed at room temperature in a vertical laminar flow hood for 2 hours to allow for tissue adherence, then 10ml warm PFM was introduced into the flask prior to its placement in a 37°C 5% CO_2 cell culture incubator. Media was exchanged every five days until the first passage (Day 18), at which time the cells were counted manually with a hemocytometer and these numbers were recorded. Autopsy donor-derived fibroblast cell lines were banked in freezing media (PFM with 10% dimethyl sulfoxide (DMSO; Sigma Aldrich) at passage 3 (P:3) and were stored in a -130°C liquid nitrogen freezer.

Statistical Analysis

A One-way Analysis of Variance (ANOVA) and Tukey's HSD Post-hoc test was performed on the cell counts at passage 1 (P:1) from 30 primary fibroblast cell lines established from 3 autopsy donors to determine the effect of biopsy site. A One-way ANOVA was performed on the cell counts from 34 primary fibroblast cell lines (all obtained from the same biopsy site (arm)) established from 18 autopsy donors to determine the effect of age (binned into 4-year groups). Data sets met the parametric assumptions of normality and homogeneity of variances.

All statistics were performed using IBM SPSS Statistics, Version 19 software. Graphs were generated using Microsoft Excel 2008. In addition, one donor was used to evaluate the efficacy of the two protocols (Dissociation vs. Explant) and the amount of tissue needed; however, conclusions from these tests were based on gross observations and not statistics because the individual groups were not repeated and several of the cell lines started by Explant Protocol did not result in positive establishment (i.e., no viable cells at first passage).

Results

Primary dermal fibroblasts cell lines were successfully established from all 28 donors. An example of an autopsy donor-derived fibroblast cell line at the beginning of the establishment (i.e., 5 days after biopsy and cell seeding) and after two passages prior to cryopreservation are shown (Fig. 1).

The cohort of 28 autopsy donors included several neurodegenerative disorders and unaffected neurological controls. Details regarding the diseases and relevant, non-identifying information about the autopsy donors are listed (Table 1). Also shown are the donor(s) used to test variables for protocol optimization (Table 1). A summary of how many cell lines were established and cryopreserved for each donor is also shown (Table 2).

Although it was not tested by statistical analysis, it was apparent by gross observations that fibroblast cell line establishment was more successful using the dissociation protocol than the explant protocol (Fig. 2). Eight cell lines were started with each protocol, both using different biopsy sites and using different amounts of tissue. All eight cell lines started with the dissociation protocol resulted in cell proliferation and viable cells by the first passage (Day 18). In addition, 75% of these cell lines (6/8) contained > 4×10^5 cells, suggesting the established lines had robust cell proliferation. Conversely, only five cell lines started with the explant protocol resulted in viable cells at the first passage (Day 18). None of the cell lines established by explant protocol (0/8) had > 4×10^5 cells, suggesting their proliferative potential was poorer than cells established by dissociation (Fig. 2).

Table 1.

Autopsy Donors and Variables Tested for Proliferation Effects.

				Variables Tested for Proliferation Effects		
TGen Donor ID	**Age**	**Sex**	**Disease**	**Protocol**	**Biopsy Site**	**Donor Age**
F01	≥ 90*	F	Control	Yes	Yes	Yes
F02	75	M	Control	No	Yes	Yes
F03	80	M	Control	No	Yes	Yes
F04	≤ 50*	M	ALS	No	No	No
F05	81	M	PD / AD	No	No	Yes
F06	79	F	AD + LB	No	No	Yes
F07	≥ 90*	F	Control	No	No	Yes
F08	86	F	Control / MCI	No	No	Yes
F09	80	M	AD + LB	No	No	Yes
F10	67	M	FTLD	No	No	Yes
F11	73	M	PD / AD	No	No	Yes
F12	78	M	PD + dem	No	No	Yes
F13	84	F	Control / MCI	No	No	Yes
F14	≤ 50*	M	Control	No	No	No
F15	≥ 90*	M	Control	No	No	Yes
F16	89	M	FTLD / AD	No	No	Yes
F18	≥ 90*	M	Control / MCI	No	No	Yes
F19	89	M	AD + VD	No	No	Yes
F20	78	M	AD	No	No	Yes
F21	74	M	Control	No	No	Yes
F22	88	F	AD + LB	No	No	Yes
F23	79	M	Control / MCI	No	No	No
F24	85	M	PD	No	No	No
F25	79	F	PD / AD	No	No	No
F26	≥ 90*	M	Control / MCI	No	No	No
F30	88	F	AD	No	No	No
F31	83	M	AD + LB	No	No	No
F32	83	F	PD / AD	No	No	No

ID: F = Fibroblast; Age: * = exact age not shown so donor cannot be identified; Sex: M = Male, F = Female;
Disease: AD = Alzheimer's disease; PD = Parkinson's disease; ALS = amyotrophic lateral sclerosis;
FTLD = frontotemporal lobar dementia; LB = Lewy bodies; dem = dementia; VD = vascular dementia;
MCI = mild cognitive impairment

Table 2.

Summary of Fibroblast Cell Lines Cryo-Banked from 28 Autopsy Donors.

TGen Donor ID	# Cell Lines Started	# Cell Lines Established	% Success
F01	28	23	82.1%
F02	16	14	87.5%
F03	16	11	68.8%
F04	8	8	100%
F05	8	8	100%
F06	8	8	100%
F07	8	8	100%
F08	8	5	62.5%
F09	8	8	100%
F10	8	5	62.5%
F11	8	6	75.0%
F12	8	7	87.5%
F13	8	8	100%
F14	8	8	100%
F15	8	5	62.5%
F16	8	8	100%
F18	8	5	62.5%
F19	8	8	100%
F20	8	7	87.5%
F21	8	7	87.5%
F22	8	8	100%
F23	8	6	75.0%
F24	8	7	87.5%
F25	8	8	100%
F26	8	8	100%
F30	8	5	62.5%
F31	8	6	75.0%
F32	8	8	100%
TOTAL (28 Donors)	**260**	**223**	**85.8%**

The primary dermal fibroblast cell counts were analyzed to determine if biopsy site or age affected proliferation. Three biopsy sites (arm, leg, and torso) were evaluated, from which all cell lines were established using the same amount of tissue and procedures. A One-Way ANOVA demonstrated a significant difference in fibroblast proliferation between biopsy sites (ANOVA: F= 9.616, v_1=2, v_2=27, P=0.001). A Tukey's HSD Post-hoc test subsequently revealed the arm biopsy site had statistically greater fibroblast proliferation than either the leg (P=0.003) or torso (P=0.004) sites, while there was no significant difference between the leg and torso (P=0.998) (Fig. 3). Donor age (age range 72-97) was also analyzed statistically and the One-Way ANOVA showed there was no significant difference in fibroblast proliferation based on donor age (within an elderly cohort) (ANOVA: F=1.756, v_1=5, v_2=28, P=0.155) (Fig. 4).

Discussion

This study aimed to establish primary dermal fibroblast cell lines from autopsy donors diagnosed with and without neurodegenerative disorders. In addition, we aimed to evaluate several variables involved in the cell line establishment process. Many of these tests have likely not been performed as most fibroblast cell lines are generated from living donors, and protocol optimization is not a justifiable reason for the procurement of additional skin biopsies. In addition, we wanted to create a cell line cohort for potential use in iPSC reprogramming, so it was important that these cell lines were established under optimal conditions, thereby increasing our chances of cryobanking a large number (~40 cryovials) of low-passage (P:3) fibroblasts. We were able to successfully establish primary dermal fibroblast cell lines for all 28 autopsy donors.

We concluded that the Dissociation protocol was more successful than the Explant protocol. We hypothesize that this may be due to an increase in tissue-to-flask surface contact created after the tissue is minced, or that dissociated tissue may allow more cells to easily access the available nutrients provided in the cell culture media.

We additionally evaluated the effects of biopsy site and autopsy donor age on fibroblast proliferation and cell line establishment. Interestingly, the results showed a significantly greater number of viable cells by the first passage (Day 18) when using the arm biopsy site, compared to the leg or torso. It is important to note that while the same site and tissue amounts were used for

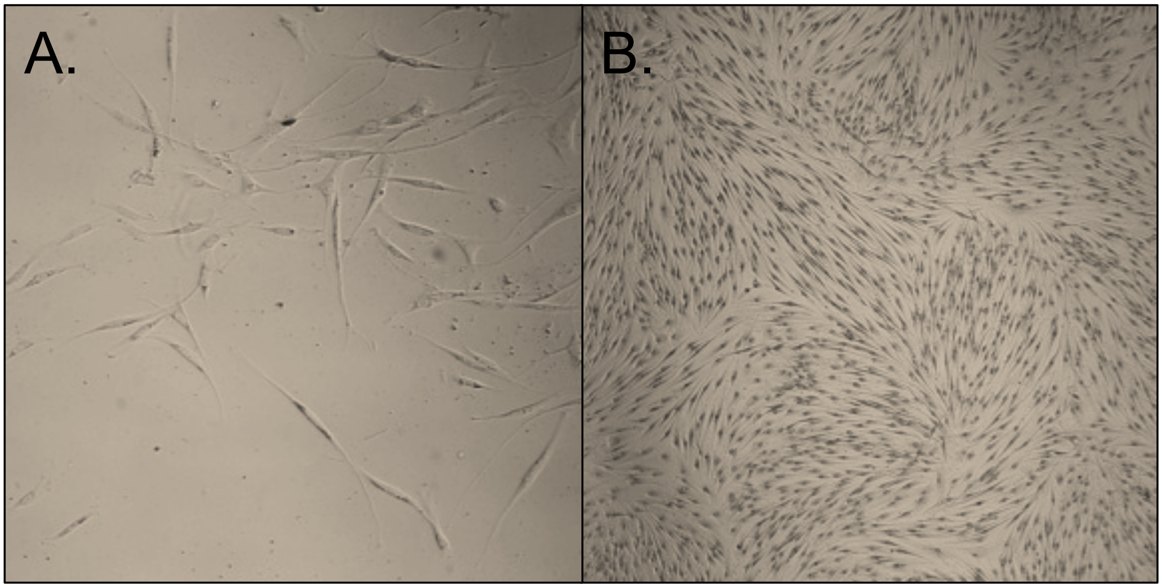

Figure 1.

Brightfield Images of Primary Dermal Fibroblasts During Cell Line Establishment. (A) Primary dermal fibroblasts adhering to BD Primaria tissue culture-treated flask five days after tissue dissociation and seeding. (B) Primary dermal fibroblasts (Wright-Giemsa stain for contrast) after two passages, prior to cryopreservation and cell line banking.

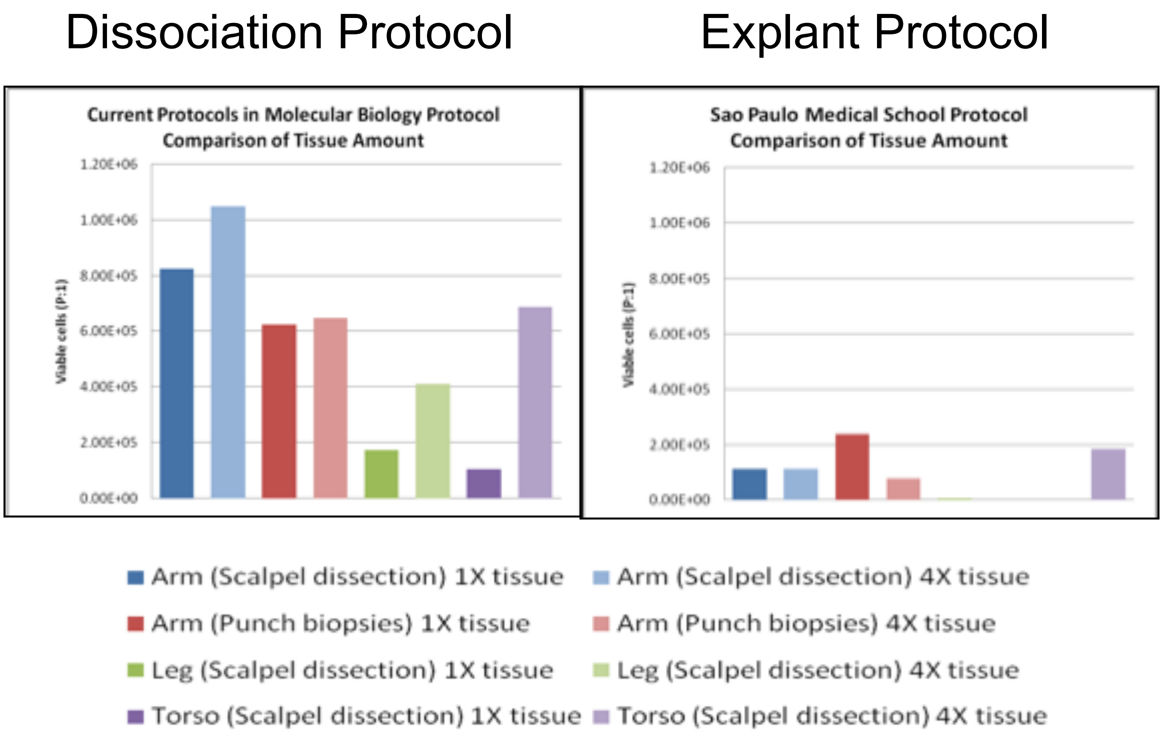

Figure 2.

Fibroblast Cell Line Establishment is More Successful using Dissociation Protocol. Number of viable cells (y-axis) was recorded 18 days post biopsy (Passage 1).

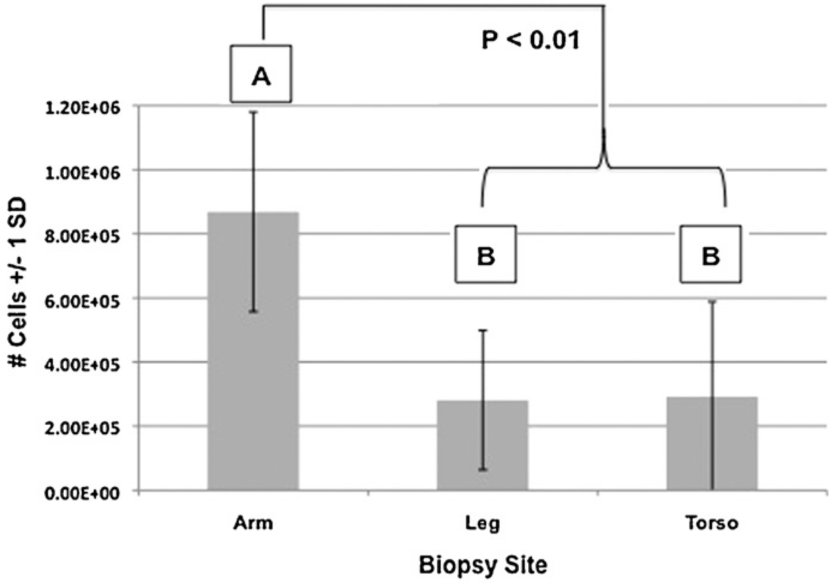

Figure 3.

Fibroblast Proliferation is Significantly Effected by Biopsy Site. Number of viable cells (y-axis) was recorded 18 days post biopsy (Passage 1). Graph represents results of One-Way ANOVA and Tukey's HSD Post-hoc test results, demonstrating biopsies obtained from the arm result in a significant increase in fibroblast proliferation as compared to biopsies obtained from the leg or torso (Hjelm, Rosenberg, et al.).

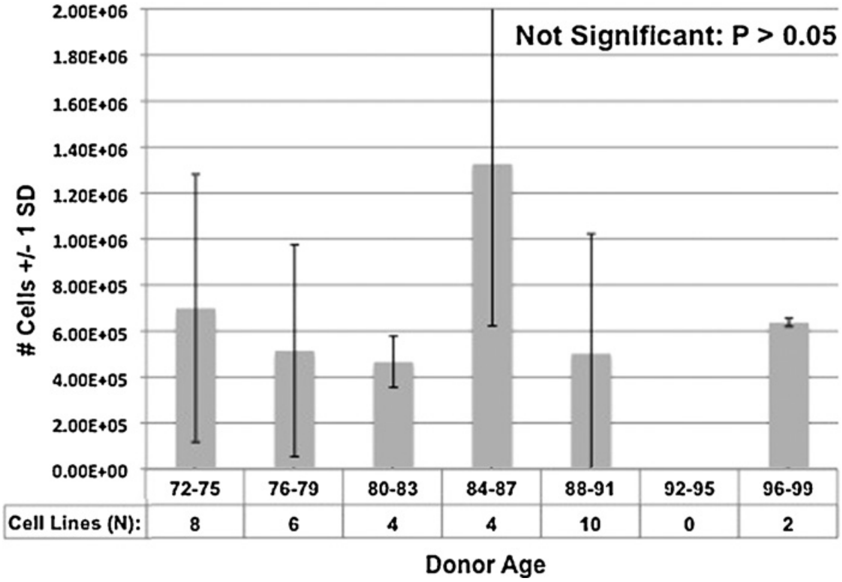

Figure 4.

Fibroblast Proliferation is Not Significantly Effected by Donor Age (within an Elderly Cohort). Number of viable cells (y-axis) was recorded 18 days post biopsy (Passage 1). Graph represents results of One-Way ANOVA and Tukey's HSD Post-hoc test results, demonstrating fibroblast proliferation is not significantly affected by autopsy donor age (within an elderly cohort) (Hjelm, Rosenberg, et al.).

all comparisons, only one specific site was tested per body region and it is possible that other areas of the arm, leg, or torso may exhibit effects that are more/less pronounced.

Another important issue is that we did not test the biopsied tissue (or original ‘starting material’) for the number of viable cells. As such, we do not know if the difference in fibroblast proliferation per biopsy site is because the cells from these regions are healthier, demonstrate greater postmortem viability, exist at a greater density *in vivo*, or really are just different (beyond a level that can be identified morphologically). Another possibility is that the leg and torso areas contain more adipose tissue, and fat cells appear to inhibit fibroblast proliferation when co-introduced in cell culture (observation during cohort establishment, data not shown). Lastly, it was observed that the arm biopsies often resulted in blood loss at the site, while this did not occur for the leg or torso biopsy sites. While these biopsies were collected postmortem, it is not surprising that there may be blood loss given that these are warm-body autopsies occurring after a short postmortem interval. However, perhaps the site-specific blood loss is also indicative of the proximity the fibroblast cells are to larger capillaries or nutrient sources, thereby prolonging their life *in vivo*, premortem and/or postmortem.

Finally, we found that donor age (within an elderly cohort) did not significantly affect fibroblast proliferation and cell line establishment. This is encouraging for future studies aiming to create fibroblast cell line cohorts from donation programs specific to diseases of late-onset. It should be noted, however, that our results can only be concluded for a cohort of elderly donors, and there may be (and likely would be) a difference in fibroblast proliferation if testing samples from a larger developmental range (e.g., fetal through adult tissues).

CHAPTER 2

INDUCTION OF PLURIPOTENT STEM CELLS FROM AUTOPSY DONOR-DERIVED SOMATIC CELLS

Introduction

Traditional *in vitro* disease modeling approaches rely on primary or immortalized somatic cells that are either obtained from a diseased individual, or are genetically modified to exhibit a disease phenotype *in vitro* (Li and Zhou). Unfortunately, these models require a physiologically relevant cell line, which may not be easily available, and genetic modification may not recapitulate the etiology of complex diseases. Human induced pluripotent stem cells (iPSCs) can overcome these shortcomings, because genetically identical, tissue-specific cell types that are disease-applicable can be generated *in vitro* (Li and Zhou; Marchetto, Winner and Gage; Takahashi et al.; Yu et al.). Donor-specific iPSC models are particularly intriguing for the study of neurological and neurodegenerative diseases, because unlike other tissues of the human body, live brain tissue often cannot be obtained from living subjects without undue risk of cognitive or functional impairment (Fitzgerald).

Previous studies have demonstrated that neural progenitor cells can be successfully isolated, cultured and differentiated from adult postmortem brain tissue (Palmer et al.). However, these adult stem cell populations can only be expanded *in vitro* through a limited number of population doublings before undergoing cellular senescence, unlike hESCs or iPSCs, which can theoretically be cultured indefinitely (Palmer et al.; Zeng and Rao; Carpenter, Rosler and Rao).

The statistical power of iPSC-based neurological models is dependent on the diagnostic accuracy of the diseased (case) and unaffected (control) somatic cell donors. For many neurological diseases, premortem clinical criteria do not provide sufficient information for the subject to be given a definite diagnosis, but rather a possible or probable diagnosis (Beach, Sue, et al.; Corneveaux et al.; Gelpi et al.; Hamilton; Joseph et al.; Mueller et al.; Nelson et al.; Piguet et al.; Tolosa, Wenning and Poewe). For example, Alzheimer’s disease can be identified through clinical evaluations as the possible or probable cause of dementia; however, the definite diagnosis of this pathology cannot currently be confirmed until clinical criteria are combined with postmortem histopathological observations of the subject's brain (Beach, Sue, et al.; Corneveaux et al.; Joseph et al.; Mueller et al.). Because clinical phenotypes like dementia can be shared by multiple neuropathies, postmortem brain banking programs have become an exceptional resource for providing neuropathy-associated brain tissue that has been subjected to the most robust diagnostic methods. In fact, much of what is known about many neurological and neurodegenerative diseases has been from analyses (histological, biochemical, molecular, etc.) on autopsy donor-derived brain tissue (Beach, Sue, et al.; Gelpi et al.; Hamilton; Joseph et al.; Marchetto, Winner and Gage; Nelson et al.; Piguet et al.).

Meske et al. have demonstrated that human dermal fibroblasts (HDFs) can be established in cell culture from autopsy donors up to 48 hours postmortem and from individuals up to 99-years-old (Meske, Albert and Ohm). To our knowledge, however, there are no published reports of autopsy donor-derived somatic cells being used for human iPSC generation. Because somatic cell senescence has been identified as a potential barrier in iPSC reprogramming, our group sought to investigate whether autopsy donor-derived fibroblasts could be induced to a pluripotent state (Banito et al.; Utikal et al.; Chan et al.; Liu et al.). In addition, we chose to examine if these iPSCs could be differentiated *in vitro* into derivatives of the neural lineage, since this approach may be particularly valuable for neurological disease research.

Materials and Methods

Lentiviral Transduction and Feeder-Free iPSC Generation/Maintenance

IPSCs were generated from one autopsy donor, a 75-year-old male identified by clinical studies and histopathological examination as being suitable as a "control" subject as he was negative for major neurological and neuropathological conditions (non-demented, without clinical parkinsonism and without diagnostic levels of histopathology for any major neuropathological condition). Autopsy donor-derived fibroblast cell line F02AA1 was selected for induced pluripotency experiments.

Human iPSCs were generated in a feeder-free culture system by lentiviral transduction of the Yamanaka factors (Takahashi et al.; Chan et al.). Autopsy donor-derived fibroblasts (F02AA1) were seeded in 6-well tissue culture-treated plates (BD Biosciences, San Jose, CA, USA) at 1.5x10^5 cells/well. Cells were infected at a multiplicity of infection (MOI) of 20 with prepackaged lentiviral particles, premixed with the reprogramming factors Oct3/4, Sox2, Klf4, c-Myc on individual vectors (Human OSKM Set; Allele Biotech, San Diego, CA, USA). To increase transduction efficiency, the Viraductin Lentivirus Transduction Kit was used according to the manufacturer's instructions (Cell Biolabs Inc., San Diego, CA, USA), and the virus complex was removed from the cells after 24 hours. Seven days post transduction, the 5x10^4 infected fibroblasts were transferred to a single well of a 6-well tissue culture-treated plate pre-coated overnight at 37°C with 1ml/well of BD Matrigel hESC-qualified matrix (BD Biosciences), diluted one aliquot Matrigel per 20ml of DMEM/F12 (Invitrogen, Carlsbad, CA, USA) (Xu et al.; Nakahara et al.). One day following the transfer to Matrigel matrix, the PFM was replaced by hESC/iPSC media (mTeSR1; Stem Cell Tech., Vancouver, BC, Canada), supplemented with 100units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich, St. Louis, MO, USA), and 5µg/ml Plasmocin prophylactic (Invivogen, San Diego, CA, USA). Complete mTeSR1 media (2.5ml/well) was exchanged every other day until iPSC colony selection (days 25 and 32 post transduction) (Ludwig et al.). IPSC clones were selected based on morphology, and colonies were picked with a 23-gauge needle (BD Biosciences) and a 200µl pipette. IPSC lines were passaged once a week by pipette disruption and mild treatment with 1mg/ml collagenase IV (Sigma) in DMEM/F12 (Invitrogen) and cells were split 1:6 onto freshly coated Matrigel-coated plates. IPSC lines (through P:10) were frozen in cryopreservation media (mFreSrR; Stem Cell Tech.) and stored at -130°C prior to characterization and differentiation experiments, which were performed using iPSC clones 2-13 and 2-21 at passage 8 (P:8).

Embryoid Body Formation and Neural Differentiation

Embryoid Bodies (EBs), with approximately 400 cells per EB, were generated using Aggrewell 400 Plates (Stem Cell Tech) according to the manufacturer's instructions. EBs were transferred in suspension to low adherence, non-treated 6-well plates (BD Biosciences) with approximately 500 EBs per well.

Inductive loss of pluripotency (LOP) was performed as previously described with minor modifications (S. M. Kang et al.; Schwartz et al.). Briefly, EBs were cultured in suspension for 5 days in hESC media *without* basic fibroblast growth factor (bFGF) (DMEM/F12 (Invitrogen), 20% Knockout Serum Replacement (Invitrogen), 1mM L-Glutamine (Invitrogen), 0.1mM non-essential amino acids (NEAA; Invitrogen), 0.0007% 2-Mercaptoethanol (Sigma Aldrich), 100units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich), and 5µg/ml Plasmocin prophylactic (Invivogen San Diego, CA, USA)), and the media was exchanged every other day. The LOP media was then replaced with NeuroCult NS-A Proliferation media (Stem Cell Tech), supplemented with 20ng/ml recombinant human epidermal growth factor (rhEGF; Stem Cell Tech), 10ng/ml bFGF (Stemgent, Cambridge, MA, USA), 2µg/ml Heparin (Stem Cell Tech), 100units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich), and 5µg/ml Plasmocin prophylactic (Invivogen, San Diego, CA, USA), and the EBs were cultured in suspension for an additional 5 days. EBs were plated in complete NeuroCult NS-A Proliferation media onto 6-well tissue culture-treated plates (BD Biosciences) pre-coated with 1ml/well hESC-qualified Matrigel matrix (BD Biosciences), diluted 1 aliquot per 10ml DMEM/F12 (Invitrogen). EBs were allowed to collapse onto the matrix, and adherent cells were further cultured in complete NeuroCult NS-A Proliferation media for 14 days. Neural precursors were collected by bulk enzymatic passage with 1mg/ml Collagenase IV (Sigma Aldrich) in DMEM/F12 (Invitrogen) as previously described (Schwartz et al.). Cells were seeded for differentiation experiments at 5×10^3 cells/cm^2 on glass coverslips (VWR, West Chester, PA, USA) pre-coated with 1ml/coverslip of hESC-qualified Matrigel matrix (BD Biosciences), diluted 1:10 as described above.

Cells plated onto glass coverslips were maintained in NeuroCult NS-A Differentiation media supplemented with 100units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich), and 5µg/ml Plasmocin prophylactic (Invivogen), and the media was exchanged every other day. Cells were allowed to differentiate for 14, 21, 28 or 35 days, at which time the coverslips were fixed in 4% paraformaldehyde (Thermo Fisher Scientific, Waltham, MA, USA) in DPBS (Invitrogen) for 15 minutes at room temperature. The coverslips were then rinsed and stored in DPBS (Invitrogen) at 4°C for later use in immunocytochemistry (ICC) experiments (see below).

Immunocytochemistry and Microscopy

Cells cultured on Matrigel-coated glass coverslips and fixed with 4% paraformaldehyde were used for all ICC assays. Cells were permeabilized for 10 minutes with 0.1% Triton X-100 (Thermo Fisher Scientific, Waltham, MA, USA) in DPBS (Invitrogen), followed by a 30-minute incubation with blocking solution (2.5% bovine serum albumin (BSA) in DPBS with 0.1% Tween 20 (Sigma)). All primary antibodies were incubated overnight at 4°C and fluorophore-conjugated secondary antibodies were incubated for 2 hours at room temperature. The primary antibodies used for this study were directed against the following antigens: Oct3/4, 1:100 (Stemgent, Cambridge, MA, USA), SSEA4, 1:100 (Stemgent), TRA-1-60, 1:100 (Stemgent), Nanog, 1:100 (Santa Cruz Biotech, Santa Cruz, CA, USA), Neurexin IV (NRXN IV), 1:100 (Santa Cruz Biotech), Neuron-specific Beta III Tubulin (TUBB3), 1:2000 (Abcam, Cambridge, MA, USA), glial fibrillary acidic protein (GFAP), 1:500 (Abcam), and myelin/oligodendrocyte-specific protein (MOG), 1:500 (Millipore, Bedford, MA, USA). Alexa Fluor-conjugated secondary antibodies (1:2000, excitations 488, 594, and 647; Invitrogen) were used for all experiments. In addition, 0.1ug/ml 4'-6-Diamidino-2-phenylindole (DAPI) was used as a nuclear counterstain. All brightfield, phase contrast and fluorescence images were obtained using the Leica DM IL inverted microscope with the Leica DFC 290 digital camera and Leica Application Suite software (version 2.8.1). All confocal microscopy images were obtained using an Olympus Fluoview FV1000 confocal microscope and the Olympus FV10-ASW 1.7 imaging analysis software.

Protein Extractions and Western Blots

Total soluble protein (TSP) was extracted from autopsy donor-derived fibroblasts (F02AA1, P:4), and two iPSC clones (2-13 and 2-21, P:8) using ice-cold RIPA buffer supplemented with a protease inhibitor cocktail and EDTA as per the manufacturer's instructions (Thermo Fisher Scientific). Protein extracts were concentrated approximately 10-fold with Microcon Centrifugal Filter Devices (30,000 nominal molecular weight limit; Millipore, Billerica, MA, USA), and TSP was quantified using the Pierce BCA Protein Assay Kit (Thermo Fisher Scientific).

Approximately 25µg TSP/lane was separated using 4-12% Bis-Tris precast gels and NuPage electrophoresis system (Invitrogen). Protein was transferred onto Invitrolon PVDF membranes (Invitrogen) that were subsequently incubated in blocking solution consisting of 5% nonfat dry milk (Safeway, Pleasanton, CA, USA) in tris-buffered saline with 0.1% Tween (TBST; Thermo Fisher Scientific). All primary antibodies were incubated overnight at 4°C and horseradish peroxidase (HRP)-conjugated secondary antibodies were incubated for 1 hour at room temperature. The primary antibodies used for this study were directed against the following antigens: Oct3/4, 1:500 (Stemgent), Sox2, 1:150 (Invitrogen), Klf4, 1:100 (Stemgent), c-Myc, 1:100 (Stemgent), and GAPDH, 1:60,000 (Millipore). The HRP-conjugated secondary antibodies used were as follows: Goat anti-rabbit HRP, 1:5,000 (Upstate/Millipore), goat anti-mouse, 1:1000 (Millipore), and rabbit anti-chicken, 1:10,000 (Millipore). Western blots were developed using the Pierce ECL Western Blotting Substrate (Thermo Fisher Scientific) and the chemiluminescence was detected on x-ray film (Kodak, Rochester, NY, USA).

Single Nucleotide Polymorphism (SNP) Genotyping

Genomic DNA was extracted from fibroblast cell line F02AA1 and IPSC clone 2-21 using the Qiagen Blood & Cell Culture DNA Mini Kit as per the manufacturer’s instructions (Qiagen, Valencia, CA, USA). Concentration and purity of both DNA extracts were analyzed using a NanoDrop ND-1000 spectrophotometer (NanoDrop, Wilmington, DE, USA) and Quant-iT PicoGreen Kit (Invitrogen). DNA aliquots were prepared at a concentration of 50ng/µl in a total volume of 10µl for use in the Affymetrix Genome-Wide Human SNP Array 6.0, performed as per the manufacturer’s instructions (Affymetrix, Santa Clara, CA, USA). Array images were collected using the GeneChip Scanner 3000 (Affymetrix) and raw data image files were generated using the GeneChip Operating System (GCOS) software (Affymetrix), after which a .CEL file was produced from each image file. Contrast quality control (QC) and other QC metrics were analyzed using the Genotyping Console 2.1 software (Affymetrix). Genotyping calls were generated in the Genotyping Console using the Birdseed version 2 SNP genotyping algorithm. Genotyping calls for 909,622 SNPs were exported into Microsoft Excel 2008 for further review. SNPs that were not called from one or both samples (fibroblast and IPSC) were manually removed, reducing the total number of SNPs called to 900,680.

The number of matching and mismatching SNP calls between the two samples were extrapolated in Microsoft Excel 2008 and this was used to calculate the percent concordance. In addition, Affymetrix Genome-Wide Human SNP Array 6.0 results were used for copy number variation (CNVs) analysis. CNVs were initially detected for both the fibroblast and IPSC samples using the free software tool PennCNV (www.openbioinformatics.org/penncnv) (Wang et al.). The log R Ratio (LRR) and B Allele Frequency (BAF) plots were manually inspected using the visualize_cnv.pl program available in the PennCNV package, and any identified CNVs that appeared as potential false-positives were systematically removed.

Results

The primary aim of this study was to examine if autopsy donor-derived dermal fibroblasts could be reprogrammed to a pluripotent state, for potential use in iPSC-based disease modeling. A visual summary of the various cell types used and generated in this proof-of-principle study are illustrated (Fig.5). IPSC clones from several additional autopsy donors have been generated using the same procedures as described, demonstrating this approach to iPSC generation is reproducible (data not shown).

Efficient translation of the Yamanaka factor proteins in the described iPSCs was confirmed by western blot (Fig.6, A). All four factors were strongly expressed in the two iPSC clones evaluated as compared to the autopsy donor-derived fibroblasts. Expression of pluripotency markers was also evaluated by ICC (Fig.6, B). The Yamanaka factor Oct3/4 and the hESC antigens SSEA4, TRA-1-60, and NANOG were all expressed and appropriately localized in the iPSCs.

DNA extracted from fibroblast cell line F02AA1 and IPSC clone 2-21 was used for analyzing genotype concordance and CNVs (Table 3). A percent concordance of 99.9625% verified that the IPSC clone had originated from the autopsy donor cell line. In addition, no IPSC-specific CNVs spanned regions greater than 100 kilobases, suggesting that no large chromosomal segments or whole chromosomes had become aneuploid during the reprogramming process.

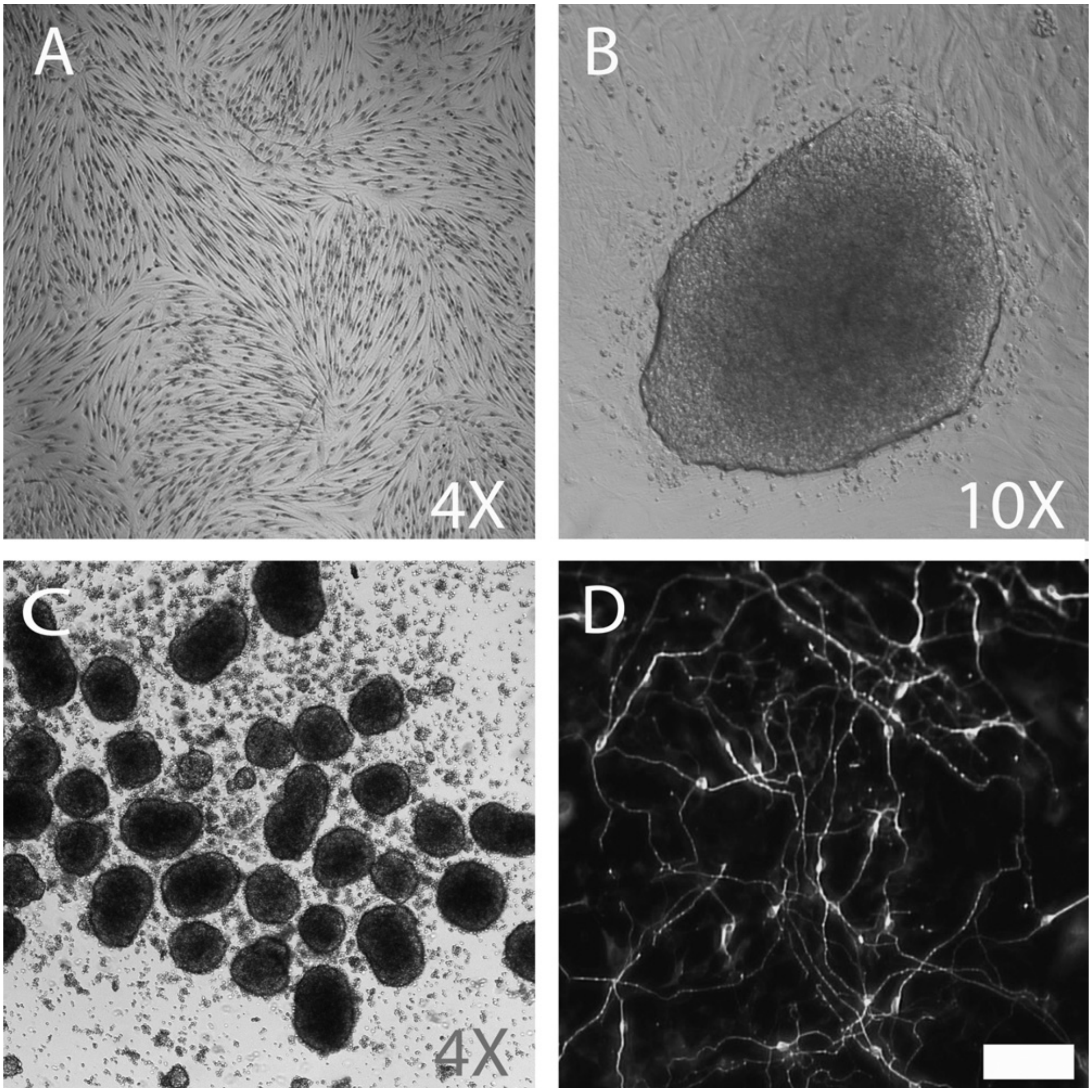

Figure 5.

IPSC Induction and Neural Differentiation from Autopsy Donor-Derived Fibroblasts. Brightfield, phase contrast, and immunofluorescence images of (A) autopsy donor-derived dermal fibroblasts (F02AA1; Wright-Giemsa contrast stain), (B) iPSC colony arising from feeder-free conditions 21 days post transduction, (C) EBs generated from iPSC clone 2-13, and (D) neurons after 14 days of *in vitro* differentiation (neuron-specific beta III tubulin antibody stained). Scalebar = 50μm (Hjelm, Rosenberg, et al.).

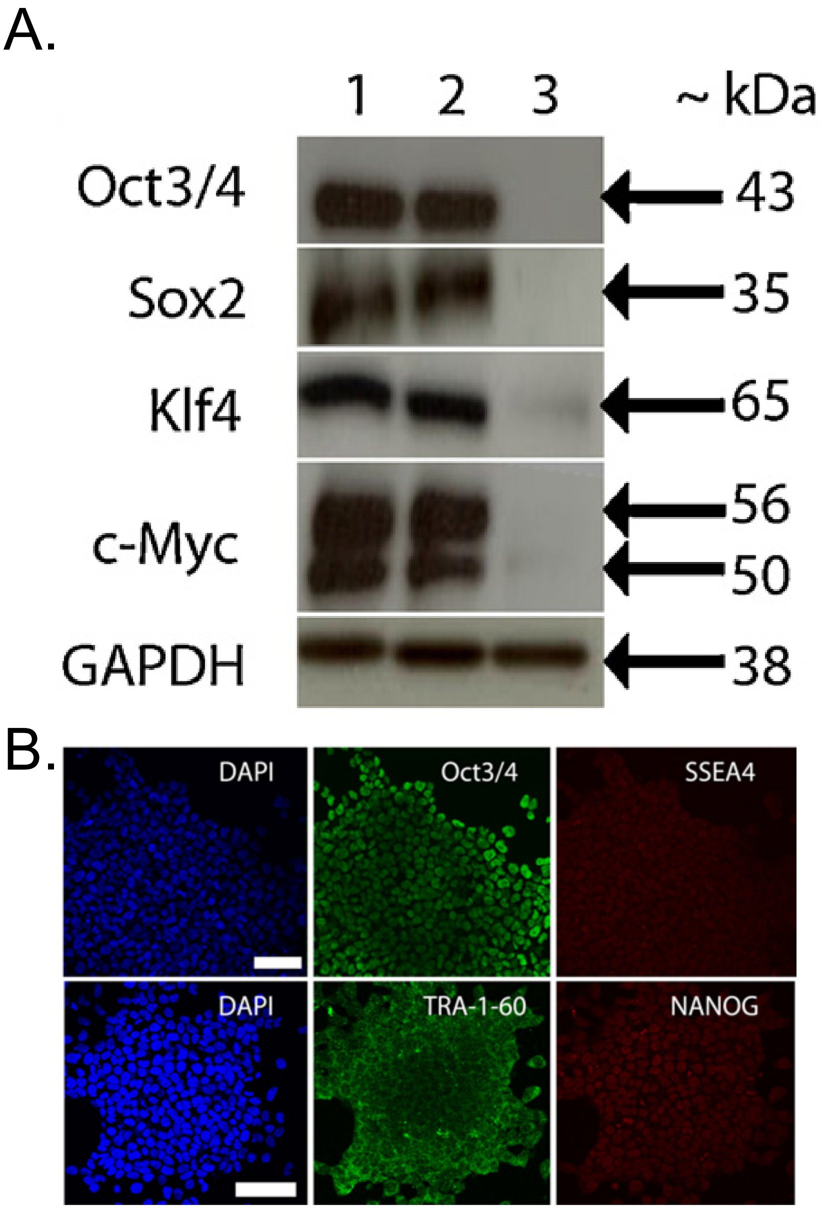

Figure 6.

Western Blot Analysis and Immunocytochemistry of Embryonic Stem Cell Markers. (A) IPSCs generated from autopsy donor fibroblasts express the Yamanka factor proteins. Lanes: (1) iPSC clone 2-13, (2) iPSC clone 2-21, and (3) autopsy donor-derived dermal fibroblast (F02AA1). (B) Confocal microscopy images of IPSCs show expression of nuclear and surface pluripotency antigens. Each row of images displays localization of DAPI and two hESC markers within the same field of view. Top panel: 1μm optical section; DAPI, Oct3/4, SSEA4. Bottom panel: 3D reconstruction of 16x 1μm optical sections through the Z-axis; DAPI, TRA-1-60, and NANOG. Scalebars = 50μm (Hjelm, Rosenberg, et al.).

Table 3.

Genome-Wide Human SNP Array: Percent Concordance and Copy Number Variation (Hjelm, Rosenberg, et al.).

Genotype Concordance	
Total SNPs called	900,680
# Matches [a]	900,342
# Mismatches [a]	338
% Concordance [a]	99.9625%

Copy Number Variants (CNVs)		
Total CNVs called	42	**% of CNVs**
Autopsy Donor-specific [b]	30	71.4%
IPSC-specific [c]	12	28.6%
Fibroblast-specific [d]	0	0.0%

[a] Fibroblast cell line (FO2AA1) vs. IPSC (clone 2-21)
[b] CNV called in both fibroblast and IPSC
[c] CNV called in IPSC, but not in fibroblast
[d] CNV called in fibroblast, but not in IPSC

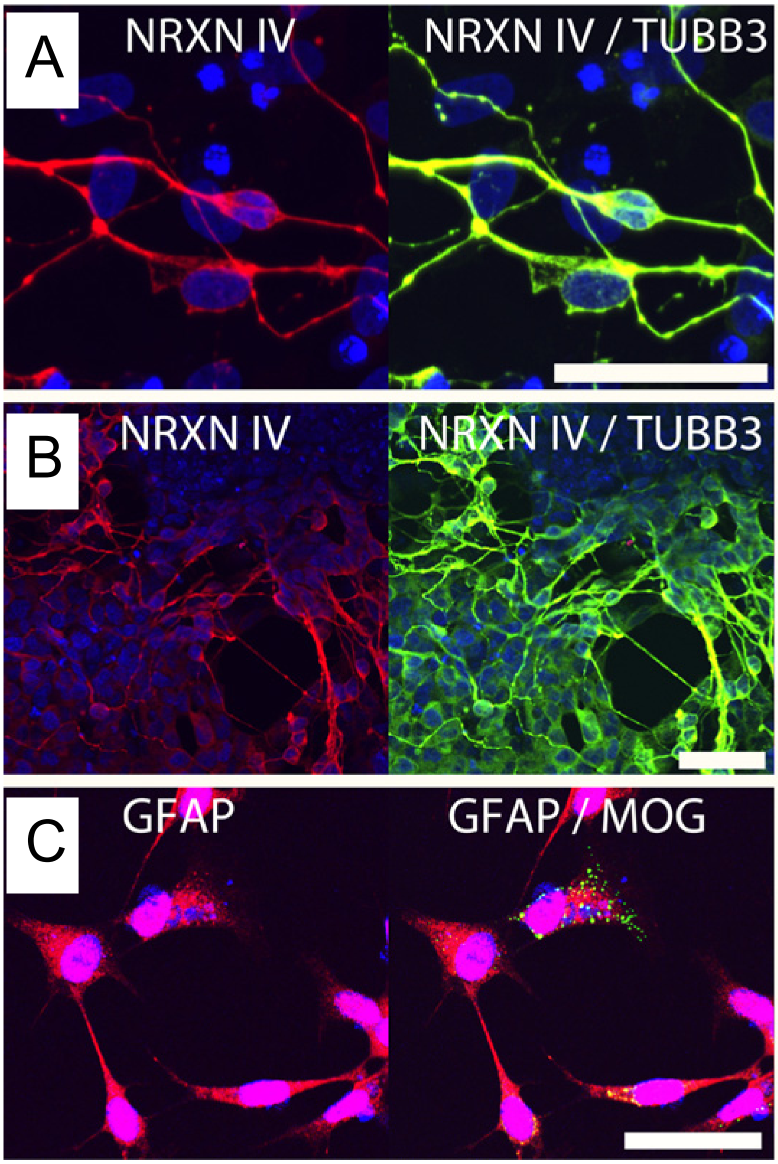

Figure 7.

IPSCs Generated from Autopsy Fibroblasts Can Be Differentiated into Neurons and Glia. Confocal microscopy images shown are from 1µm optical sections through the Z-axis of cells fixed after 14 (A), 28 (B) and 35 (C) days of differentiation. iPSC clone 2-13: (A, B) Neurexin IV (NRXN IV) (red), co-localization of Neurexin IV (NRXN IV) and neuron-specific beta III tubulin (TUBB3) (yellow), and the nuclear counterstain DAPI (blue). (C) Glial fibrillary acidic protein (GFAP) (red), myelin/oligodendrocyte-specific protein (MOG) (green), and the nuclear counterstain DAPI (blue). Scalebars = 50µm (Hjelm, Rosenberg, et al.).

The two iPSC clones (2-13 and 2-21) characterized in this study were differentiated into derivatives of the neural lineage. ICC assays identified neurons after 14 and 28 days of differentiation (Fig. 7). TUBB3 and NRXN IV were utilized as terminal neuronal markers; both antigens co-localized specifically to cells exhibiting a neuronal phenotype (Fig. 7). ICC assays also identified expression of glial markers, specific to both astrocytes and oligodendrocytes, after 35 days of differentiation (Fig. 7). GFAP was expressed in the majority of the differentiated, non-neuronal cells, while a small subset of this population expressed MOG (Fig. 7). This data suggests that the majority of the glia were astrocytic in nature, while a small minority was becoming oligodedrocytic.

Discussion

The is the first known published study to use autopsy donor-derived somatic cells for the generation of induced pluripotent stem cells (iPSCs). Since this publication, however, others have additionally shown that this platform can be employed successfully. Specifically, Bliss et al. demonstrated that autopsy donor-derived fibroblasts obtained from the scalp, in addition to human dura mater from autopsy-derived brain tissue, can both be successfully reprogrammed to a pluripotent state (Bliss et al.). These are additionally important avenues for future research, particularly for donation programs that only procure the brain (as opposed to whole-body donation).

One important technical note is that while we know autopsy donor-derived fibroblasts can be reprogrammed to a pluripotent state, we do not know if this process is as efficient as fibroblasts isolated from living donors. Future studies may include transduction experiments where fibroblasts derived from autopsy and living donors are tested for reprogramming efficiency side-by-side. In addition, we don’t know if elderly or autopsy donors are more likely to possess somatic cell mutations in their fibroblasts that could potentially be amplified in the cell population during iPSC clonal selection and cell line establishment.

These results provide evidence that postmortem human tissue can be successfully reprogrammed to a pluripotent state. This approach may be significantly useful for studies investigating diseases and/or drugs that may cause sudden death and for neurodegenerative disease research. The ability to combine both clinical diagnostic criteria and postmortem histopathological observations can greatly increase neurodegenerative diagnostic accuracy; this may subsequently increase the statistical power for donor-specific *in vitro* disease models. Human iPSC-based disease models generated from postmortem tissue may provide additional confidence for researchers investigating these conditions, and provides an avenue for comparing differentiated *in vitro* cell types to endogenous adult tissue from the same individual.

CHAPTER 3

IN VITRO-DIFFERENTIATED NEURAL CELL CULTURES PROGRESS TOWARDS DONOR-IDENTICAL BRAIN TISSUE

Introduction

Disease models for human genetic disorders exist in many forms, including transgenic animals (Chaible et al.; Pandey and Nichols), primary or immortalized human cell lines (Li and Zhou; Birney et al.), or the more recently described induced pluripotent stem cells (iPSCs) (Takahashi et al.; Yu et al.; Stadtfeld and Hochedlinger; Park et al.). IPSCs are particularly intriguing tools for modeling human genetic disorders, because tissue-specific and disease-applicable cell types that retain the donor's complex genetics can be generated *in vitro* (Takahashi et al.; Yu et al.; Stadtfeld and Hochedlinger; Park et al.). However, with any disease model system, there may be initial concerns about the physiological or pathological relevance of the model, and how subsequent drug screening or toxicity trials will correlate with clinical responses (Allen et al.; Marchetto, Winner and Gage; Han, Williams and Eggan; Murry and Keller; Hanna, Saha and Jaenisch; Wichterle and Przedborski; Stadtfeld and Hochedlinger; Patterson et al.). Potential challenges exist as to which iPSC-derived disease models will be able to produce a pathological phenotype, and how observed *in vitro* pathologies will correlate with *in vivo* disease onset, severity, progression and/or drug response (Wichterle and Przedborski; Marchetto, Winner and Gage; Han, Williams and Eggan; Hanna, Saha and Jaenisch; Stadtfeld and Hochedlinger; Patterson et al.).

Neurodegenerative disorders are commonly misdiagnosed in live human patients; often, a diagnosis can only be confirmed or refuted with the additional observations of a postmortem neuropathological exam (Hjelm, Rosenberg, et al.; Beach, Sue, et al.; Nelson et al.; Rohrer et al.; Beach, Monsell, et al.). Autopsy donors that have been subjected to these rigorous diagnostic criteria are especially useful for iPSC generation, because subsequent *in vitro* disease models can be produced with increased confidence that the donor was a neurological control (true negative; greater specificity) or possessed a specific neurological disease (true positive; greater sensitivity) (Hjelm, Rosenberg, et al.). In addition, this approach enables us to compare iPSC-derived cell cultures to endogenous tissues from the same donor.

In this study, we compared iPSC-derived neural cell cultures to donor-identical brain tissue. This particular donor was a 75-year-old male, defined by both clinical criteria and postmortem neuropathological observations as a neurological control. Data regarding the establishment of fibroblast cell lines, iPSC generation, and initial neural differentiation tests can be found in the Materials and Methods section of Chapter 2 (Hjelm, Rosenberg, et al.). For this study, we differentiated iPSC-derived neural precursor cells (NPC) over a timecourse of 0, 35, 70, 105, and 140 days (i.e., in 5-week intervals over a period of 20 weeks) and compared this to temporal lobe tissue from the same autopsy donor. The neural differentiation protocol used in these studies was specific to the development of forebrain, cortical neurons (and glia), or what is commonly referred to as the “default” neural differentiation pathway when no additional morphogens are included in culture (Zeng et al.; Brennand et al.; Shi, Kirwan and Livesey; Mariani et al.). As our endogenous tissue reference for these initial studies, we chose the temporal lobe because this brain region is part of the forebrain/cerebral cortex, and is pathologically relevant to multiple neurological conditions (including several late-onset diseases that are diagnostically aided by neuropathological confirmation) (Rohrer et al.; Beach, Sue, et al.; Nelson et al.; Scharfman; Whalley et al.). The brain tissue used in this study was collected and frozen after a short postmortem interval (3.33hrs), thereby preserving the RNA integrity (Beach, Sue, et al.; Birdsill et al.), and allowing us to use RNA sequencing (RNA-Seq) analyses for our *in vitro* to brain tissue comparisons.

RNA-Seq is a set of methods based upon next-generation sequencing technology that allows one to evaluate the transcriptome, effectively permitting single-transcript resolution of the expressed RNA transcripts at a particular snapshot in time, regardless of the transcript’s function or protein-coding potential (Trapnell, Pachter and Salzberg; Trapnell, Roberts, et al.; Trapnell, Williams, et al.). This is a powerful tool because it allows us to study expression levels without any *a priori* hypotheses about which genes or regulatory features may be differentially expressed. In this study, we focused on differential expression (*in vitro* vs. brain tissue) of both well-annotated protein-coding genes, as well as long intergenic noncoding RNAs (lincRNAs), both of which have been shown to exhibit tissue-specificity and are considered developmentally important (Krupp et al.; Ponten et al.; Cabili et al.; Ashburner et al.; Guttman et al.). Unlike other types of noncoding RNAs, lincRNAs do not overlap with well-annotated protein-coding genes allowing both features to be computationally tractable (Cabili et al.; Guttman et al.; Mercer, Dinger and Mattick).

In addition to transcriptome analyses, we also analyzed a subset of our samples for differences in genome-wide CpG methylation using an array-based platform (Bibikova et al.). CpG methylation has been linked to differential gene expression, in both developmental and pathological contexts, and has been extensively studied in human cancer (Salhia et al.; Irizarry et al.; Feinberg and Tycko; Deaton and Bird). In addition, previous studies have shown that CpG methylation can distinguish cell types in a tissue-specific manner (Irizarry et al.; Doi et al.), and that methylation patterns vary between different regions of the brain (Ladd-Acosta et al.). Likewise, the specific methylation states of various loci have been shown to exhibit dynamic changes in the brain during development and aging (Siegmund et al.; Sharma, Gavin and Grayson).

This study describes the transcriptional and methylation effects of *in vitro* neural differentiation and prolonged neural cell culture as it relates to the physiological levels exhibited by the endogenous brain tissue. We hope that our donor-identical comparisons will provide a valuable resource for those interested in the physiological or pathological relevance of iPSC-derived neurological disease models and the specific transcriptional progression of protein-coding genes and lincRNAs we observed i*n vitro*.

Materials and Methods

Autopsy Donor and Brain Tissue Collection

A 75-year-old male autopsy donor was identified as a neurological control (i.e., non-demented, without histological diagnostic levels of any major neurological disease) by both clinical criteria and a postmortem pathology exam. This subject was enrolled in the Banner Sun Health Research Institute (BSHRI) Brain and Body Donation Program as a whole-body donor and had previously signed informed consent approved by the BSHRI Institutional Review Board (IRB) (Beach, Sue, et al.). The brain of this autopsy donor was removed and specific regions or hemispheres were frozen after a short postmortem interval (PMI) (3.33hrs) and were stored at -80°C for available use in future studies. Frozen brain tissue from the temporal lobe, specifically the medial temporal gyrus, was selected as this region is pathological relevant to multiple neurological conditions. One piece of temporal lobe brain tissue containing both white and gray matter was divided into three pieces that were all of approximate size (1cm x 1cm x 0.2cm). Two of these pieces were subjected to RNA extraction and RNA-Seq, and were combined as replicates later during analysis (i.e., using Cuffdiff from the Cufflinks analysis package). The third piece was used for DNA extraction and subsequent CpG methylation array studies.

In Vitro Sample Collection and Neural Differentiation

Autopsy donor-derived dermal fibroblasts were used for iPSC generation and subsequent neural differentiation studies. Detailed methods regarding skin biopsies, fibroblast cell line establishment, iPSC generation, embryoid body (EB) formation and neural precursor cell (NPC) selection can be found in the Materials and Methods section of Chapter 2 (Hjelm, Rosenberg, et al.). For review, iPSCs were generated using a lentiviral cocktail (Allele Biotechnology, San Diego, CA, USA) of the Yamanaka Factors (Oct3/4, Sox2, Klf4, c-Myc) under feeder-free conditions using mTeSR1 growth media (STEMCELL Technologies, Vancouver, BC, Canada) and Matrigel hESC-qualified adherent matrix (BD Biosciences, San Jose, CA, USA) (Ludwig et al.; Xu et al.; Takahashi et al.; Chan et al.). EBs were generated using AggreWell 400 Plates (STEMCELL Technologies), followed by inductive loss of pluripotency (LOP), and NPCs were propagated and expanded in monolayer cultures using NeuroCult NS-A Proliferation media (STEMCELL Technologies) and Matrigel matrix (BD Biosciences) (Hjelm, Rosenberg, et al.; Schwartz et al.; Ma et al.).

Early-passage (p3), IPSC-derived NPCs were differentiated into neurons and glia as previously described (Hjelm, Rosenberg, et al.), except that in these studies, NPCs were seeded at a lower cell density ($2x10^3/cm^2$) so that a longer differentiation timecourse could be examined. NPCs were generated and maintained using the NeuroCult NS-A <u>Proliferation</u> Kit supplemented with bFGF (10ng/ml), rhEGF (20ng/ml), Heparin (2µg/ml) (STEMCELL Technologies), 100 units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich), and 5µg/ml Plasmocin prophylactic (Invivogen, San Diego, CA, USA). NPCs were expanded and passaged as monolayer cultures in wells pre-coated with BD Matrigel (BD Biosciences). NPCs were differentiated into forebrain, cortical neurons (and glia) on adherent Matrigel matrix using the Neurocult NS-A Differentiation Kit (STEMCELL Technologies) supplemented with 100 units/ml penicillin, 100µg/ml streptomycin (Sigma Aldrich), and 5µg/ml Plasmocin prophylactic (Invivogen). Neural cell cultures were allowed to differentiate for 35, 70, 105, or 140 days, at which time the RNA was extracted and frozen at -80°C for RNA-Seq studies. Two independent experiments were performed at different times, and replicates from each independent timepoint were RNA extracted, library prepped, and sequenced separately. Replicates were later combined during analysis (i.e., using Cuffdiff from the Cufflinks analysis package). The undifferentiated NPC sample and last differentiation timepoint (D140) were also used for DNA extractions and subsequent CpG methylation array analysis.

Copy Number Variation (CNV) Analysis

DNA was extracted from the IPSC line (2-13) and parental fibroblast (FO2AA1). DNA was extracted from both samples using the Qiagen Blood & Cell Culture DNA Mini Kit according to the manufacturer's instructions (Qiagen, Valencia, CA, USA). Genomic DNA was quantified using the Quant-iT PicoGreen dsDNA Assay (Life Technologies, Carlsbad, CA, USA). DNA quality was analyzed with both a 2% agarose gel and by evaluation of absorbance spectra from the ND-1000 Spectrophotometer (NanoDrop, Wilmington, DE, USA).

3.0µg genomic DNA per sample was used for next-generation sequencing library preparation, similar to our previously published methods (except that samples were not bar-coded for this study) (Craig, Pearson, et al.). See RNA-Seq library prep methods section following cDNA conversion for more details.

WGS libraries were sequenced across 13 lanes (IPSC, 8 lanes; fibroblast, 5 lanes) using the Illumina HiSeq 2000 (Bennett). High quality (> Q30), paired-end sequencing reads (104 cycles x 2) were obtained for both WGS samples. Base calling and bcl to qseq conversion was performed using the Off-Line Basecaller (OLB), and qseq to fastq conversion was performed using the Consensus Assessment of Sequence and Variation (CASAVA) software (Illumina, San Diego, CA, USA). Fastq files were aligned to build 37 of the human genome provided by the Genome Reference Consortium (GRCh37). Sequence alignment was performed using the Burrows-Wheeler Aligner (BWA), version 0.5.9-r16. PCR duplicates were removed during WGS analysis, and only uniquely mapped read numbers are reported.

CNV Analysis was performed using normalized sequencing coverage as previously described (Craig, O'Shaughnessy, et al.). The methods for this type of analysis have been recently described by our group for the identification of CNVs in cancer using WGS from tumor-normal pairs (Craig, O'Shaughnessy, et al.). Analysis was performed with both the raw data, as well as data masked for repetitive regions (RepeatMasker). CNV “hits” that were detected in both analyses were further evaluated by visual inspection. Only small focal amplifications (4x) and deletions (2x) were detected between the iPSC and parental fibroblast; however, both deletions identified have been previously detected in other somatic studies and are likely also false-positives. This analysis demonstrated the iPSC line used in this study had a normal, diploid karyotype and did not contain any major chromosomal aberrations.

Immunocytochemistry (ICC) Analysis

Differentiated neural cell cultures were grown on Matrigel-coated coverslips for 35 days (D35), at which point they were fixed in a solution of 4% paraformaldehyde (Thermo Scientific) in PBS (Invitrogen Carlsbad, CA, USA)) for 15min at RT, and were rinsed (and stored at 4°C) in PBS for later use. Coverslips were permeabilized with a PBS solution of 0.1% Triton X-100 (Sigma, St. Louis, MO, USA) for 10min, then were blocked in a solution of 2.5% BSA (Sigma) in PBS-T (PBS with 0.01% Tween 20 (VWR)) for 30min at room temperature (RT). Primary antibodies were all incubated overnight on a rotating shaker at 4°C. Primary antibodies included the following: TUBB3 (1:2000; Abcam ab18207), MAP2 (1:1000; EnCor Biotech. CPCA-MAP2), VGLUT1 (1:1000; Synaptic Systems 135-303), and GAD67 (1:300; Abcam ab26116). Coverslips were then washed 3X for 20min each in 2X PBS-T (PBS with 0.02% Tween 20), followed by another 30min blocking step. Alexa Fluor-conjugated secondary antibodies (1:2000; Alexa Fluor

488 or 647 (Invitrogen)) were then incubated on the coverslips for 1hr at RT. The coverslips were washed 3X again, and were then counterstained with DAPI (1µg/ml) for 10min. Coverslips were mounted onto slides with SlowFade Gold antifade reagent (Invitrogen) and were sealed with clear nail polish. All confocal microscopy images were obtained using an Olympus Fluoview FV1000 confocal microscope and the Olympus FV10-ASW 1.7 imaging analysis software. All confocal micrographs displayed are 3-D reconstructions from 10-15 1µm optical sections through the Z-axis.

RNA-Seq Library Preparation and Next-Generation Sequencing

RNA was extracted from both the *in vitro* neural samples and the endogenous brain tissue using TRIzol (Ambion, Life Technologies, Carlsbad, CA, USA) and the PureLink RNA Mini Kit along with an on-column DNase treatment (Life Technologies, Carlsbad, CA, USA) according to the manufacturer's instructions. Extracted RNA was quantified and qualified using Agilent RNA 6000 Nano kits and the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). All samples had an RNA Integrity Number (RIN) between 8.5 and 10. 100ng total RNA was linearly amplified and converted to double-stranded cDNA using the Ovation RNA-Seq System (NuGEN, San Carlos, CA, USA) as per the manufacturer's instructions (Tariq et al.). Double-stranded cDNA was quantified using the Quant-iT PicoGreen dsDNA Assay (Life Technologies).

Between 1.8µg and 3.0µg cDNA per sample was used for next-generation sequencing library preparation, similar to our previously published methods (except that samples were not bar-coded for this study) (Craig, Pearson, et al.). cDNA was fragmented by sonication in 6x16mm glass microtubes (Covaris #520045) using the Covaris S2 instrument (Covaris, Woburn, MA, USA). Settings for fragmentation included a duty of 5%, intensity = 3, 200 cycles/burst, and two 30 second cycles. The majority of the cDNA was between 200-650bp after sonication. Fragmented cDNA was subjected to end repair using the NEBNext end repair buffer and enzyme (New England BioLabs, Ipswich, MA, USA), followed by purification using Agencourt Ampure Beads (Beckman Coulter, Brea, CA, USA). End-repaired cDNA was subjected to A-tailing using the NEBNext dA-Tailing buffer and Klenlow Fragment (New England BioLabs), followed by purification using Agencourt Ampure Beads (Beckman Coulter). Samples were then quantified using the Quant-iT PicoGreen dsDNA Assay (Life Technologies). Illumina-compatible adapters (IDT) were ligated onto A-tailed samples at a 10:1 molar ratio (adaptor:DNA) using the NEBNext Quick T4 DNA Ligase and Quick Ligation buffer (New England BioLabs). Samples were ran on a 3% agarose gel containing GelStar (Lonza) for approximately 3hrs and DNA/gel was cut out of each lane at approximately 400bp and extracted using the Quantum Prep Freeze 'N Squeeze DNA extraction spin columns according to the manufacturer's instructions (Bio-Rad). Ligated samples were amplified by enrichment PCR (10 cycles) using primers specific to the adapter sequences. Amplified samples were isolated using a 2.5% agarose gel and Freeze N' Squeeze purification as previously described. Extracted libraries were further purified by ethanol precipitation and were resuspended in 50µl sterile H_2O. Libraries were quantified and qualified using the Agilent High Sensitivity DNA Kit, and RNA-Seq libraries had a final size distribution of 230-350bp. RNA-Seq libraries were sequenced with one sample per lane using the Illumina HiSeq 2000 (Bennett). High quality (> Q30), paired-end sequencing reads (104 cycles x 2) were obtained for all RNA-Seq samples.

Sequence Alignment and RNA-Seq Analysis

Base calling and bcl to qseq conversion was performed using the Off-Line Basecaller (OLB), and qseq to fastq conversion was performed using the Consensus Assessment of Sequence and Variation (CASAVA) software (Illumina, San Diego, CA, USA). Eight nucleotides were computationally trimmed off of the 5' end of each paired-end read, to avoid poor alignment due to the possible incorporation of the SPIA primer used during RNA-Seq library preparation (i.e., in Ovation RNA-Seq System). Fastq files were aligned to build 37 of the human genome provided by the Genome Reference Consortium (GRCh37). Transcript alignment was performed using TopHat (version 1.3.2) as previously described (Trapnell, Pachter and Salzberg).

Analysis of differential expression and transcript abundance was performed using Cuffdiff from the Cufflinks analysis package (version 1.3.0) (Trapnell, Roberts, et al.; Trapnell, Williams, et al.). All replicates from independent experiments or tissue pieces were combined analytically during Cuffdiff analysis. Cuffdiff run included the same reference as was previously used for TopHat alignment (GRCh37.62), and any transcript associated with ribosomal RNA (rRNA) genes or pseudogenes, transfer RNA (tRNA) genes or pseudogenes, or mitochondrial (mt) genes were ignored during analysis (using MASK file specific to these features created from the same genome reference). All samples were normalized to both the compatible-hits and upper-quartile. For Cuffdiff analysis on genes, data was annotated using the Human gtf file from Ensembl (release 63); for Cuffdiff analysis on lincRNAs, data was annotated to the lincRNA gtf file provided in the supplemental section of Cabili et al. (Cabili et al.).

For expression analysis on genes, a list was obtained from the Consensus CDS (CCDS) project (release 9/7/11) that originally contained 27,816 CCDS IDs. This list was limited to only "public" genes; any IDs "withdrawn," "pending," or "under review" were manually removed. This list was further limited to those with unique gene IDs and those that were present in our Cuffdiff output file, resulting in 18,062 CCDS genes that were used for transcriptome analysis. Lists of GO Processes specific to "Brain Development Genes" (443) and "Non-Brain Development Genes" (avg. 132) were obtained from the MetaCore search engine from GeneGo Inc. as previously described (Ashburner et al.). For expression analysis on lincRNAs, a list of 8,262 putative lincRNAs was obtained from the annotation file provided by Cabili et al. (Cabili et al.). Likewise, tissue-classified lists of lincRNAs specific to the brain (183) and other non-brain tissues (avg. 130) were obtained from the online supplemental data of Cabili et al. (Cabili et al.). Additional details about tissue-specific lists can be found in the Results section of this chapter.

CpG Methylation Array and Analysis

DNA was extracted from the NPC and D140 *in vitro* neural samples, along with the brain tissue sample (i.e., BRAIN). *In vitro* neural samples were treated with Proteinase K for 1hr prior to DNA extraction, and the frozen brain tissue sample was treated with Proteinase K for 24hr prior to DNA extraction. DNA was extracted from all samples using the Qiagen Blood & Cell Culture DNA Mini Kit according to the manufacturer's instructions (Qiagen). Genomic DNA was quantified using the Quant-iT PicoGreen dsDNA Assay (Life Technologies). DNA quality was analyzed with both a 2% agarose gel and by evaluation of absorbance spectra from the ND-1000 Spectrophotometer (NanoDrop).

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1μg genomic DNA per sample was used for the Illumina Infinium HumanMethylation450 Bead Chip, and the chip was prepared and ran according to the manufacturer's instructions (Illumina) (Bibikova et al.). This array had a total of 485,577 probe sites. Any probe with a detection p-value > 0.01 for any of the three samples was manually removed, resulting in 485,261 probes that were evaluated for differential methylation. Differential methylation was defined as a site that had a beta value difference of at least 20% (i.e., ≥ 0.2). Analysis of differential methylation for all methylation sites, as well as those specific to CpG Islands, shore or shelves, was performed using Microsoft Excel.

Data Access

Sequencing data will be deposited in the NIH database of Genotypes and Phenotypes (dbGaP).

Graphical Analysis and Figures

For the primary figures, density plots (Fig. 11) and heatmaps (Fig. 19) were created using R Studio. Brightfield images (Fig. 8) were taken using a Leica DM IL inverted microscope with the Leica DFC 290 digital camera and Leica Application Suite software (version 2.8.1). Confocal micrographs were obtained using an Olympus Fluoview FV1000 confocal microscope and the Olympus FV10-ASW 1.7 imaging analysis software (Fig. 10). Rank-order scatter plots (Fig. 11), line graphs (Fig. 14), and bar graphs (Figs. 16, 17, 18) were created using Microsoft Excel. Schematic diagram (Fig. 8) and figures were prepared using Microsoft Powerpoint. Scatter plots and rank correlations (Spearman's rank correlation tests; Figs. 12,13) were produced using R Studio. The number of mapped reads per chromosome was calculated using the flagstat command in SAMTools, and table was generated using Microsoft Word (Table 4). CNV plots were generated using R Studio (Fig. 9). Venn diagrams (Fig. 15) were created in Microsoft Powerpoint. List of genes found to be upregulated or downregulated *in vitro* in the published study of Patterson et al. were obtained from their heatmap figure, and those available for analysis in our dataset were evaluated further (Table 5) (Patterson et al.). Binomial distribution tests for overlap between our data and those of Patterson et al. were performed in Microsoft Excel (Table 5).

Results

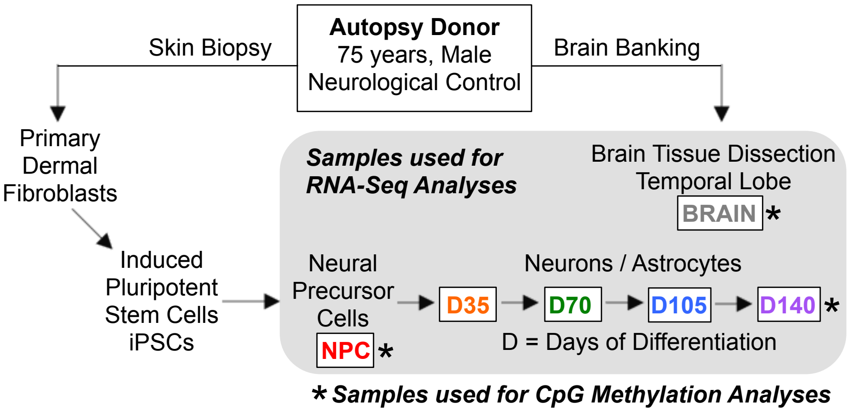
Samples and Experimental Design

We selected a 75-year-old, male autopsy-donor with no neurological conditions for these initial *in vitro* to brain tissue comparisons. This donor was cognitively normal, and the postmortem neuropathological exam revealed he had a Braak score (Stage 1) and a CERAD Neuritic Plaque score (0) consistent with an unaffected neurological control. A schematic diagram of our experimental design, along with samples selected for both RNA-Seq and CpG methylation analyses are shown (Fig. 8A). Briefly, early-passage (p3), iPSC-derived neural precursor cells (NPC) were used for two independent experiments, and were differentiated *in vitro* for a period of 35, 70, 105, or 140 days. Sample acronyms used for the neural differentiated samples in this study are listed (D35, D70, D105, D140) (Fig. 8A).

Differentiated neural samples were only selected for analysis in the case where at least 80% of the cells appeared neuronal by the first differentiation timepoint (D35) (i.e., exhibited neuritic cell-to-cell processes distinguishable by brightfield microscopy as shown in D140 sample) (Fig. 8B). A representative image of a piece of temporal lobe tissue used for RNA-Seq and CpG methylation analysis is also shown; all three tissue pieces had approximately the same amount of white matter (wm) and grey matter (gm) (Fig. 8B).

An average of 33.2 ± 11.7-million quality reads per sample library (mapped to GRCh37) were used for RNA-Seq analysis, and the number of sequencing reads for each RNA-Seq sample and replicate can be found in Table 4. The number of unique whole genome sequencing (WGS) reads (for both the iPSC and parental fibroblast) used for CNV analysis can also be found in Table 4. The CNV analysis demonstrated the iPSC line used in this study had a normal, diploid karyotype and did not contain any major chromosomal aberrations (Fig. 9).

Differentiated neural cell cultures that met our selection criterion were further evaluated by immunocytochemistry (ICC) for verification of neuronal identity and population architecture (Fig. 10). The differentiated neural cell cultures contained a mixed population of both immature (TUBB3+/MAP2-) and mature (TUBB3+/MAP2+) neurons at the first differentiation timepoint (D35) (Fig. 10). As a whole, the *in vitro* cell populations were mostly (≥ 85%) neurons (TUBB3+), A Schematic Diagram



B Images

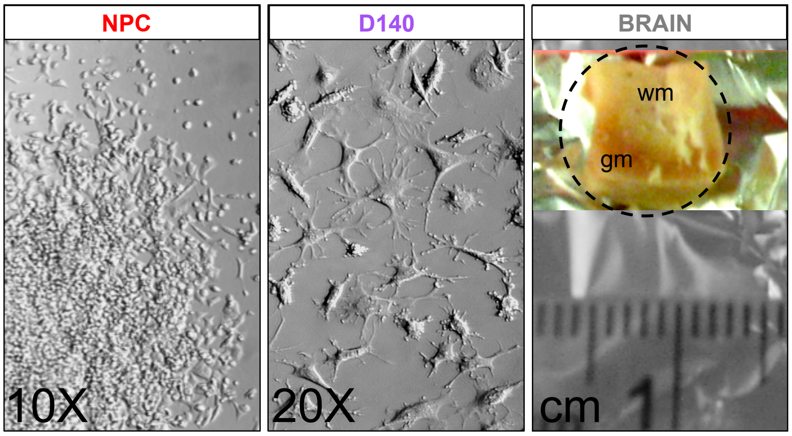


Figure 8.

In Vitro and Tissue-Derived Neural Samples. (A) Schematic diagram of experimental design, comparing *in vitro* iPSC-derived neural cell populations to donor-identical brain tissue. Samples used for RNA-Seq and CpG methylation analyses are displayed, along with the corresponding sample acronyms that are used in subsequent figures (i.e., NPC, D35-D140, BRAIN). (B) Brightfield images of neural cell cultures at the beginning (NPC) and end (D140) of the experimental timecourse. NPC images show clusters of undifferentiated cell populations, while D140 images show differentiated neurons with abundant neuritic processes. Photographic image of the frozen, temporal lobe brain tissue sample is also shown (in dashed circle). All tissue pieces used for RNA-Seq and CpG methylation analyses were approximately the same size and had the same proportion of white matter (wm) and gray matter (gm) (Hjelm, Salhia, et al.).

Table 4.

RNA-Seq and WGS Reads per Chromosome. The number of mapped reads for each autosome and sex chromosome, as well as the combined total, is shown for all samples sequenced by (A) transcriptome sequencing (RNA-Seq) and (B) whole genome sequencing (WGS). All read numbers shown are rounded to the nearest hundred thousand (Hjelm, Salhia, et al.).

A Transcriptome Sequencing (RNA-Seq)

	# (millions) Mapped Reads										
Chromosome	**NPC**	**D35$_a$**	**D35$_b$**	**D70$_a$**	**D70$_b$**	**D105$_a$**	**D105$_b$**	**D140$_a$**	**D140$_b$**	**BRAIN$_a$**	**BRAIN$_b$**
1	3.3	2.1	1.9	6.3	3.8	3.0	3.7	3.5	3.9	2.8	3.3
2	2.9	1.7	1.5	5.3	3.4	2.8	2.7	2.7	2.9	2.6	3.0
3	2.0	1.4	1.3	4.7	2.7	2.3	2.3	2.4	2.3	2.2	2.4
4	1.5	1.0	0.9	3.3	2.1	1.7	1.5	1.6	1.5	1.7	2.0
5	2.3	1.4	1.3	4.5	2.8	2.2	2.3	2.3	2.5	2.0	2.1
6	1.8	1.0	0.9	3.3	2.1	1.7	1.8	1.8	1.8	1.7	1.8
7	1.7	0.9	0.9	3.3	1.9	1.5	1.8	1.8	1.8	1.7	1.7
8	1.2	0.8	0.7	2.6	1.7	1.2	1.3	1.3	1.4	1.2	1.5
9	1.3	0.7	0.6	2.4	1.5	1.2	1.2	1.3	1.4	1.3	1.4
10	1.4	0.7	0.6	2.4	1.4	1.1	1.2	1.2	1.4	1.4	1.5
11	1.7	1.9	1.5	5.7	3.0	2.6	1.9	2.4	2.4	1.9	2.2
12	2.1	1.0	0.9	3.2	2.1	1.7	1.7	1.6	1.9	1.2	1.5
13	1.2	0.7	0.7	2.1	1.4	1.1	1.3	1.1	1.2	1.3	1.3
14	1.0	0.6	0.5	2.0	1.1	0.9	0.9	1.0	1.1	1.1	1.2
15	1.0	0.5	0.5	1.8	1.1	0.8	0.9	1.0	1.1	1.0	1.0
16	0.8	0.4	0.4	1.5	0.8	0.7	1.1	0.9	1.1	0.7	0.8
17	1.2	0.7	0.5	1.9	1.2	0.9	1.3	1.1	1.5	0.8	0.9
18	0.5	0.3	0.3	1.0	0.6	0.5	0.5	0.6	0.6	0.7	0.7
19	0.6	0.3	0.3	0.9	0.5	0.5	0.8	0.6	0.9	0.4	0.5
20	0.7	0.3	0.3	1.1	0.6	0.5	0.7	0.7	0.7	0.5	0.5
21	0.3	0.2	0.2	0.6	0.4	0.3	0.4	0.4	0.4	0.3	0.3
22	0.3	0.2	0.1	0.6	0.3	0.3	0.4	0.4	0.5	0.2	0.3
X	0.9	0.6	0.6	2.2	1.3	1.0	1.2	1.1	1.3	1.1	1.1
Y	0.1	0.0	0.0	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1
TOTAL	31.7	19.6	17.3	62.9	37.9	30.6	33.1	32.9	35.7	30.0	33.2

***a*, *b* = biological replicates from independent experiments or tissue pieces (combined as replicates during Cuffdiff analysis)**

B Whole Genome Sequencing (WGS)

	# (millions) Mapped Reads - Duplicates	
Chromosome	**Fibroblast**	**iPSC**
1	22.4	49.9
2	21.4	52.2
3	16.7	42.6
4	14.2	41.4
5	15.1	33.8
6	14.5	37.1
7	14.1	33.9
8	12.9	31.6
9	11.2	26.0
10	13.1	29.1
11	12.4	28.1
12	12.0	28.4
13	7.4	20.7
14	8.1	19.2
15	8.3	17.8
16	9.7	18.2
17	9.0	16.6
18	6.6	16.4
19	7.0	11.4
20	6.7	12.8
21	3.5	8.6
22	4.4	7.2
X	6.9	17.1
Y	1.6	3.9
TOTAL	259.5	604.0
Coverage	10X	22X

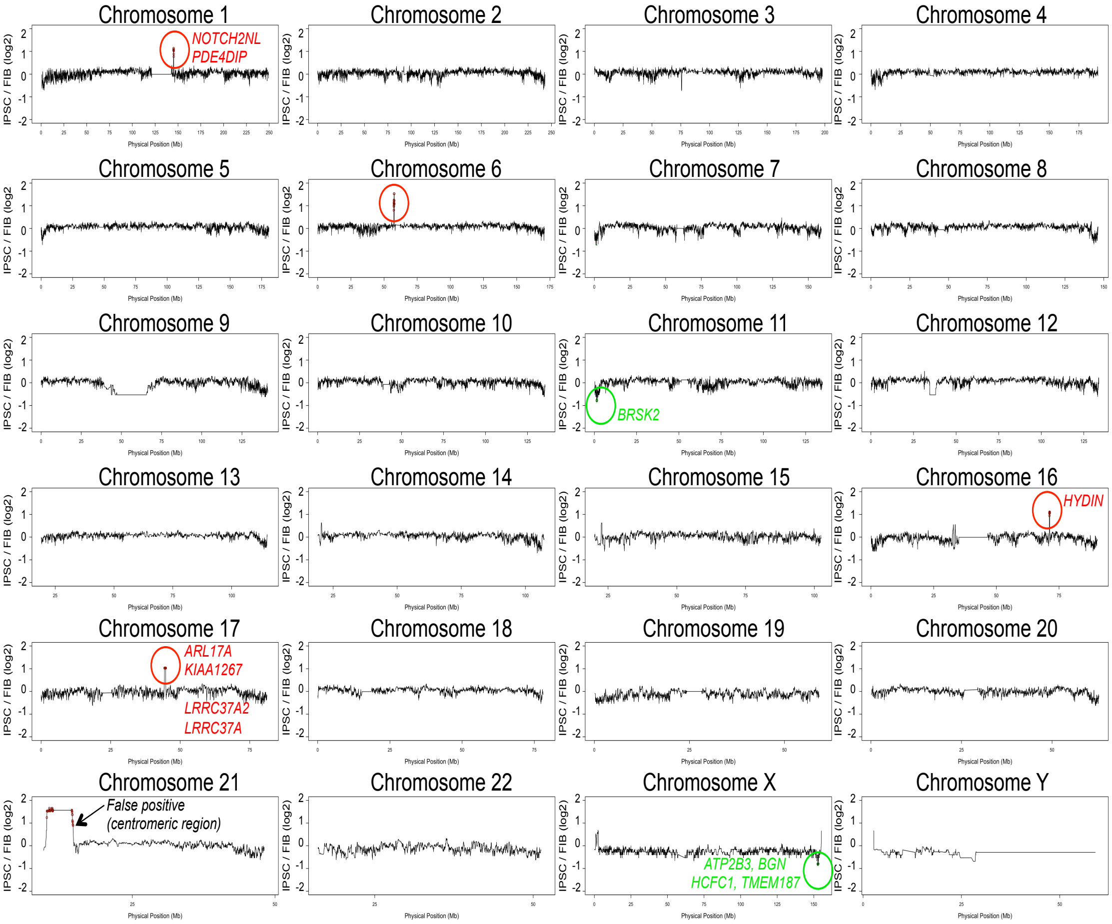


Figure 9.

Copy Number Variation (CNV) Analysis using Whole Genome Sequencing (WGS) Data. Chromosomal aberration plots comparing induced pluripotent stem cells (iPSC) line 2-13 to parental fibroblast cell line (F02AA1). Copy number variations (CNVs) were defined as regions or loci that had a log2 fold change (iPSC/FIB) > +0.75 (i.e., gain in iPSC) or < -0.75 (i.e., loss in iPSC) using normalized coverage comparisons obtained by whole genome sequencing (WGS). All detected CNVs were manually inspected at high resolution for false positives prior to annotation. Focal regions amplified (gain) are circled in red, while deletions (loss) are circled in green; any gene localized to a detected CNV is shown alongside the event in the corresponding color. The results from this analysis support that the iPSC line in these studies had a normal, diploid karyotype and contained no large-scale or major chromosomal aberrations (Hjelm, Salhia, et al.).

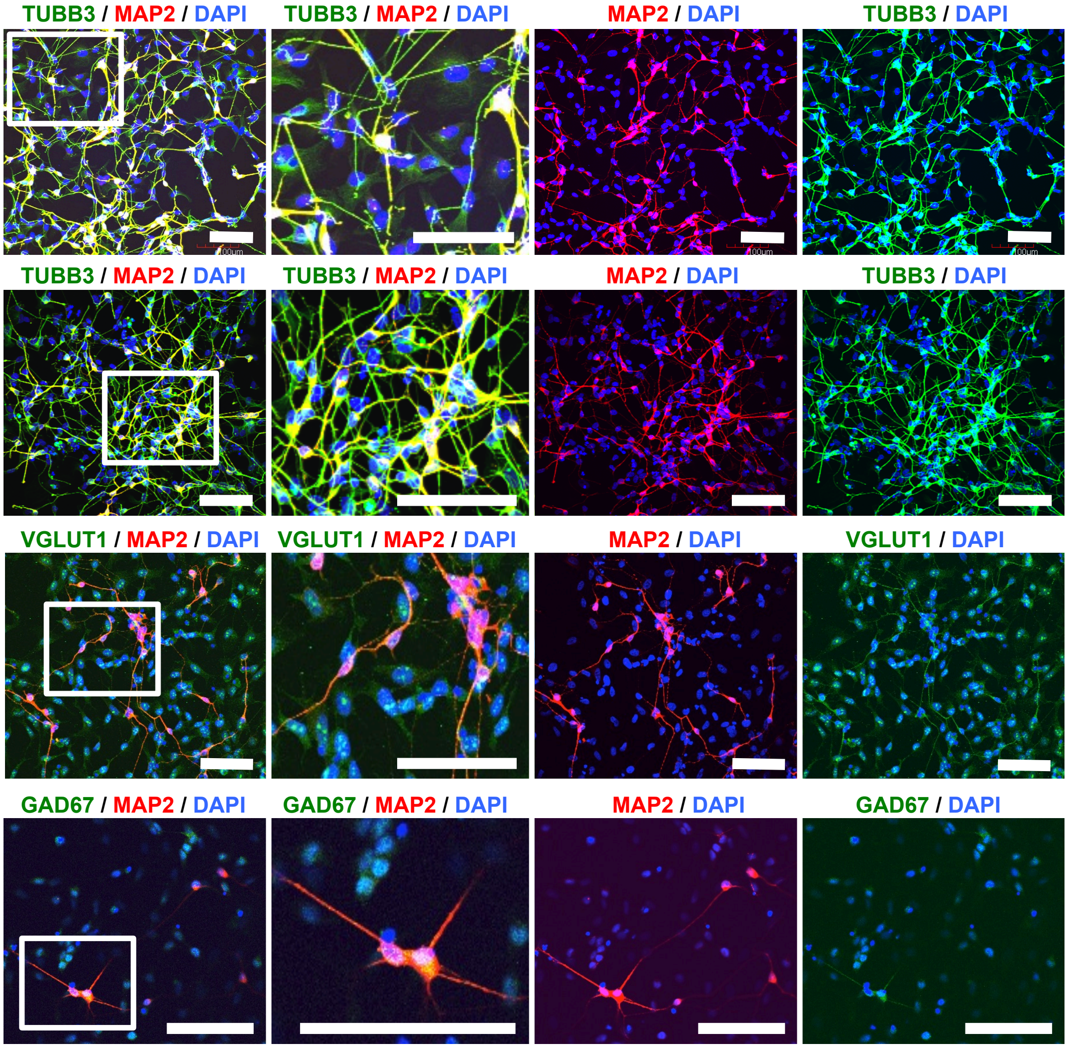


Figure 10.

Immunocytochemistry analysis of *in vitro* neural cell cultures at the first differentiation timepoint (D35). The neuronal marker TUBB3, glutamatergic marker VGLUT1, and GABAergic marker GAD67 (all green; Alexa Fluor 488) were counterstained against the mature neuronal marker MAP2 (red; Alexa Fluor 647). DAPI (blue) is shown in all images as a nuclear counterstain. All scale bars = 100 μm. All images (confocal micrographs) and are 3-D reconstructions from 10-15 1μm optical sections through the Z-axis. Region of interest (white box) in merged image (left most) is shown at higher magnification (2nd from left most). TUBB3/MAP2 image sets demonstrate regional heterogeneity of areas with both immature (TUBB3+/MAP2-) and mature (TUBB3+/MAP2+) neurons (1st row), and areas dominated by mature (TUBB3+/MAP2+) neurons (2nd row). VGLUT1 staining demonstrated vesicular-like localization in immature neurons and localization to both the cell body and neuritic processes in mature neurons (3rd row). GAD67 was only detected in mature neurons (4th row). See results section for population percentages (Hjelm, Salhia, et al.).

and about one third (30-35%) of these neurons were mature (MAP2+). Both glutamatergic (VGLUT1+) and GABAergic (GAD67+) neurons were identified (Fig. 10). VGLUT1 expression was detected in the majority (70-75%) of neurons, regardless if they were mature (MAP2+) or not. However, VLGUT1 expression in immature neurons appeared as strong, punctate staining in the cell body, consistent with a vesicular localization, while mature neurons (MAP2+) expressed VGLUT1 all along the neuritic processes in addition to the cell body. GAD67 expression was only detected in a subset (15-20%) of mature (MAP2+) neurons. ICC analyses were performed across three iPSC clones from the same donor, including the clone used for these RNA-Seq studies, verifying that the neural differentiation efficiency and percent of neuronal subtype markers evaluated were both reproducible. ICC analyses, previous studies, and our currently described RNA-Seq data, demonstrate a small proportion (≤ 5%) of the cell population was astrocytic glia (Hjelm, Rosenberg, et al.).

In Vitro Neural Cells Undergo Progressive Activation of Transcription and CpG Methylation

Studies using gene expression microarrays and RNA-Seq have demonstrated there are an increased number of actively transcribed genes in the brain compared to most other tissues, although there are exceptions (Ramskold et al.; Jongeneel et al.). This observation of increased transcriptional activation is presumably due to a high level of cell population complexity within the brain (Ramskold et al.; Jongeneel et al.; H. J. Kang et al.). In addition, functional features like postsynaptic membranes have been predicted to contain hundreds to thousands of proteins, and these numbers have been shown to increase during neuronal differentiation and subsequent equilibrium (Sugiyama et al.; Bayes and Grant).

Due to the possible added effects of population and functional complexity in the brain or cortex, we detected a high number of actively transcribed genes in our temporal lobe tissue sample (i.e., BRAIN). Specifically, out of 18,062 consensus CDS (CCDS) protein-coding genes evaluated, 82.9% (14,971) had detectable transcript expression values, or FPKM (i.e., Fragments Per Kilobase of exon per Million fragments mapped) above our cutoff (FPKM > 0.01), and 63.9% (11,538) had a FPKM > 1. Previous studies using RNA-Seq or gene expression arrays have reported a similar percentage of expressed genes (e.g., 71%, 76%, 82%, 86%) within the developing or adult brain (Ramskold et al.; H. J. Kang et al.; Johnson et al.). Differences in technologies used for transcript abundance estimations, in addition to differences in the total number of sequencing reads, may affect the total number of expressed transcripts detected; as such, these published values may not be directly comparable with our data.

An initial inspection of transcript data showed an increase in the number of actively transcribed, protein-coding genes as the *in vitro* neural samples progressed through our differentiation timecourse. Specifically and for comparison, 73.1% (13,199), 75.6% (13,661), 78.8% (14,239), 77.5% (14,003), and 82.0% (14,811) of CCDS genes had an FPKM > 0.01, for our NPC, D35, D70, D105, and D140 samples, respectively. Likewise, 50.2% (9,060), 53.5% (9,662), 56.2% (10,146), 56.9% (10,269), and 61.3% (11,066) of CCDS genes had an FPKM > 1 in these samples (listed in order). Statistical analysis showed a significant increasing monotonic correlation between the days of our timecourse and the percent (or number) of actively transcribed genes as determined by a one-tailed non-parametric Kendall's *tau* correlation test. This significant correlation was observed for both the cutoffs used to evaluate transcriptional activation (FPKM > 0.01, $p < 0.05$; FPKM > 1, $p < 0.01$).

In order to better characterize the transcript diversity, we conducted a density analysis of all transcripts under varying FPKM values. Density plots can be used for meta-analysis and visualization of the FPKM distributions, and have been previously described by Trapnell et al. in their published methods regarding RNA-Seq analysis and the CummeRbund analysis package (Trapnell, Roberts, et al.). For clarification, a pseudo-count of 0.01 was added to all FPKM values so that density plots could be displayed on a $\log_{10}$ scale. As such, density plots exhibit a bimodal distribution, whereby the first peak shows the density of inactive, non-expressed or 'off' genes, while the second peak shows the density and distribution of actively transcribed, expressed or 'on' genes in that sample. Density plots show a decrease in inactive genes (shrinkage in first peak) and an increase in actively transcribed genes (augmentation in second peak) as our differentiation timecourse progressed (Fig. 11A). The temporal lobe also showed a higher density of actively transcribed genes and is plotted alongside the *in vitro* samples as a reference

(Fig. 11A). In summation, the density plots and rank-ordered scatter plots show a systematic increase of area under the second curve, consistent with transcriptional activation of CCDS genes (Fig. 11A,D).

In addition to the progressive increase in the number of actively transcribed CCDS genes, we also observed a progressive increase in the number of lincRNA transcripts expressed, although this trend was less linear than that of protein-coding genes ($R^2 \cong 0.75$ vs. $R^2 \cong 0.91$) (data not shown). Out of 8,262 putative lincRNAs previously described by Cabili et al. (Cabili et al.), the temporal lobe sample (BRAIN) had 31.7% (2,623) of lincRNA actively expressed at an FPKM > 0.01, and 31.2% (2,581) had an FPKM > 1 in this sample. Comparatively, the *in vitro* neural samples showed 16.0% (1,318), 18.7% (1,544), 25.3% (2,087), 22.5% (1,855), and 25.4% (2,097) of lincRNAs had an FPKM > 0.01, for our NPC, D35, D70, D105, and D140 samples, respectively. Likewise, 15.5% (1,280), 18.1% (1,496), 24.0% (1,986), 21.5% (1,775) and 24.4% (2,020) of lincRNAs had an FPKM > 1 (listed in order). Statistical analysis showed a significant increasing monotonic correlation between the days of our timecourse and the percent (or number) of actively transcribed lincRNAs as determined by a one-tailed non-parametric Kendall's *tau* correlation test. This significant correlation was observed for both the cutoffs used to evaluate transcriptional activation (FPKM > 0.01, $p < 0.05$; FPKM > 1, $p < 0.05$).

There was a smaller percentage of lincRNAs expressed in both the *in vitro* neural samples and the endogenous brain tissue than there were protein-coding genes. These observations have been previously reported by others and are likely, in part, due to the high level of tissue-specificity in lincRNAs and a lower level that are constitutively active compared to protein-coding genes (Cabili et al.). On average, 23.2% to 22.5% of lincRNAs were expressed in our neural samples, for FPKM > 0.01 and > 1, respectively. In contrast, 78.3% to 57% of protein-coding genes were expressed (on average) in our neural samples, for FPKM > 0.01 and > 1. Density plots and rank-ordered scatter plots demonstrate this increase in transcriptional activation of lincRNAs, as previously described for CCDS genes (Fig. 11B,E). Interestingly, for both protein-coding genes (18,062) and putative lincRNAs (8,262), we saw an activation rate or slope of ≅2.2% per timepoint, or ≅0.4% per week, as determined by linear equation tests for our *in vitro* samples (data not shown). We also observed increased variation between our replicates (for both CCDS genes and lincRNAs) as our timecourse progressed, and more variability in progressive transcriptional activation at the middle stages of our timecourse, as determined by Spearman's correlation coefficients of the FPKM rankings (Figs. 12, 13).

As a final measure of the global differences between our *in vitro* samples and the endogenous brain tissue, we performed density analysis on methylation sites (485,261) with varying levels of methylation (i.e., beta values) obtained from a genome-wide methylation array. We observed an increased number of methylated CpG sites in the last neural differentiation timepoint (D140) compared to the methylated sites at the beginning or our timecourse (NPC), and this correlated with increased methylation in the tissue (BRAIN) (Fig. 11C). Beta value bins of < 0.2 (unmethylated) and > 0.8 (methylated) have been previously described by Illumina publications describing these arrays (Bibikova et al.). From the 485,261 methylation sites examined, the temporal lobe tissue sample (BRAIN) had 30.8% (149,561) of these sites with a beta value > 0.8. In comparison, the two *in vitro* samples examined had 17.6% (85,259) and 29.3% (142,285) of sites with a beta value > 0.8, for the NPC and D140 samples respectively. Conversely, 44.3% (215,021), 33.3% (161,552) and 35.8% (173,711) of these sites had a beta value < 0.2, for the NPC, D140, and BRAIN samples, respectively. Density plots and rank-order scatter plots demonstrate this increase in genome-wide DNA methylation (Fig. 11C,F).

The Percent of In Vitro to Tissue Differences Decreases During Differentiation, but Demonstrates Variation Dependent on Tissue-Specificity (Genes and lincRNAs) and Proximal Relation to CpG Islands (Methylation)

In order to stratify *in vitro* to brain tissue comparisons into more specific and informative datasets, statistical analysis of differential expression was performed between each *in vitro* neural sample (NPC, D35, D70, D105, D140) and the endogenous brain tissue (BRAIN), for all CCDS genes (18,062) and putative lincRNAs (8,262) using Cuffdiff from the Cufflinks analysis package (Trapnell, Williams, et al.). Specifically, genes and lincRNAs that had both a $\log_2$ fold-change > +2 and a p-value < 0.01 were defined as significantly upregulated *in vitro*, and those that had both a $\log_2$ fold-change < -2 and a p-value < 0.01 were defined as significantly downregulated *in vitro*.

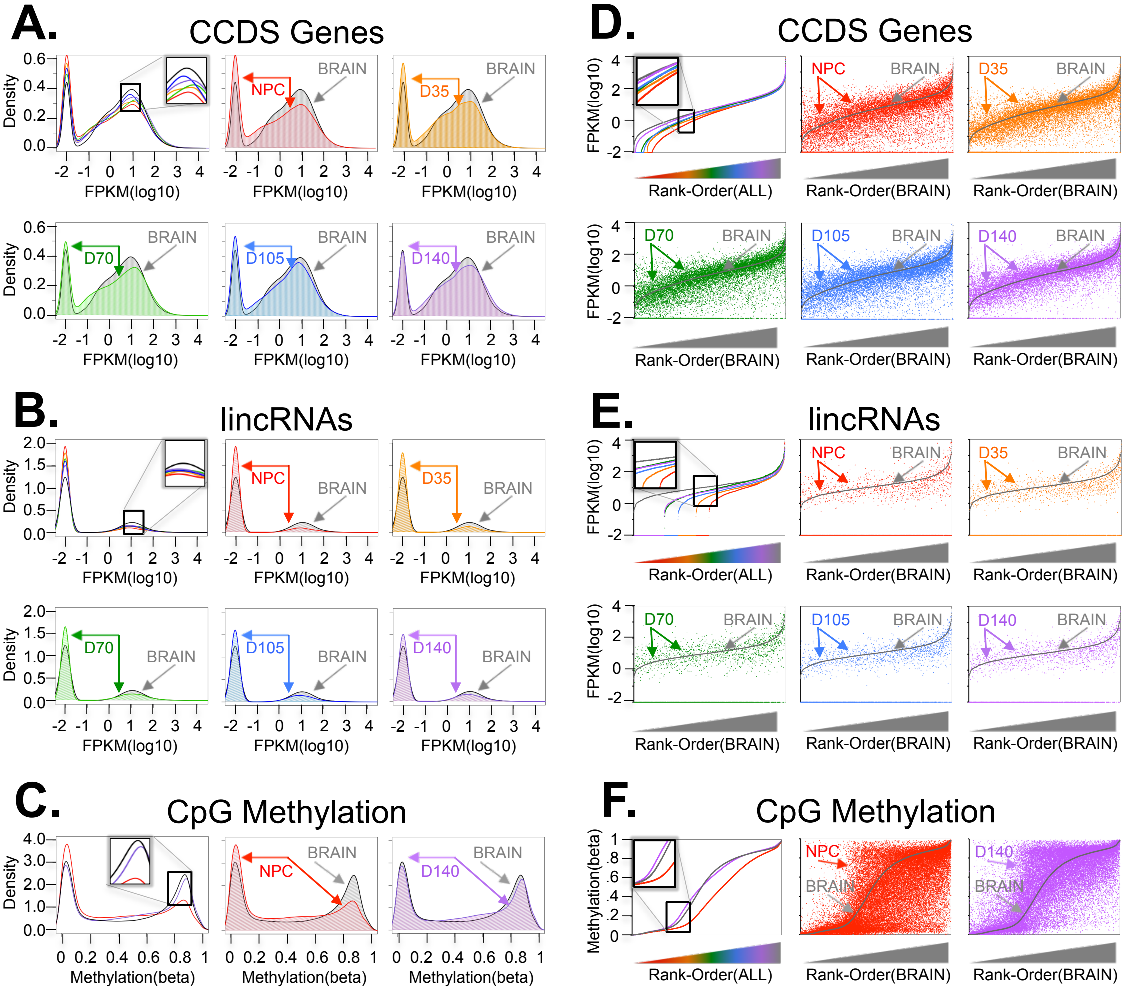


Figure 11.

Global Transcription and CpG Methylation. Density plots of RNA expression (i.e., FPKM($\log_{10}$)) for (A) CCDS genes (N=18,062) and (B) lincRNAs (N=8,262). First plot (top left) displays the overlay of all samples. Subsequent plots display the overlay of each individual *in vitro* sample along with the endogenous brain tissue. (C) Density plots of CpG methylation (i.e., beta values) for all sites on the Illumina Infinium HumanMethylation450 Bead Chip (N=485,261). First plot (left) displays overlay of the three samples analyzed for CpG methylation differences (NPC, D140, BRAIN). Subsequent plots display overlay of the two *in vitro* samples along with the brain tissue. Rank-order scatter plots for (D) CCDS genes, and (E) lincRNAs. First plot (top left) displays the overlay of all samples' RNA expression (y-axis: FPKM($\log_{10}$)), along with the Rank-order of each sample (x-axis: rank-order of FPKM, smallest to largest). Subsequent plots display the overlay of each individual *in vitro* sample along with the endogenous brain tissue, while using the BRAIN rank-order as the x-axis. (F) Rank-order scatter plots of 50,000 randomly selected CpG methylation sites. First plot (left) displays the overlay of the three analyzed samples' methylation (y-axis: beta values), along with the Rank-order of each sample (x-axis: rank-order of beta values, smallest to largest). Subsequent plots display the overlay of the two *in vitro* samples along with the brain tissue, while using the BRAIN rank-order as the x-axis (Hjelm, Salhia, et al.).

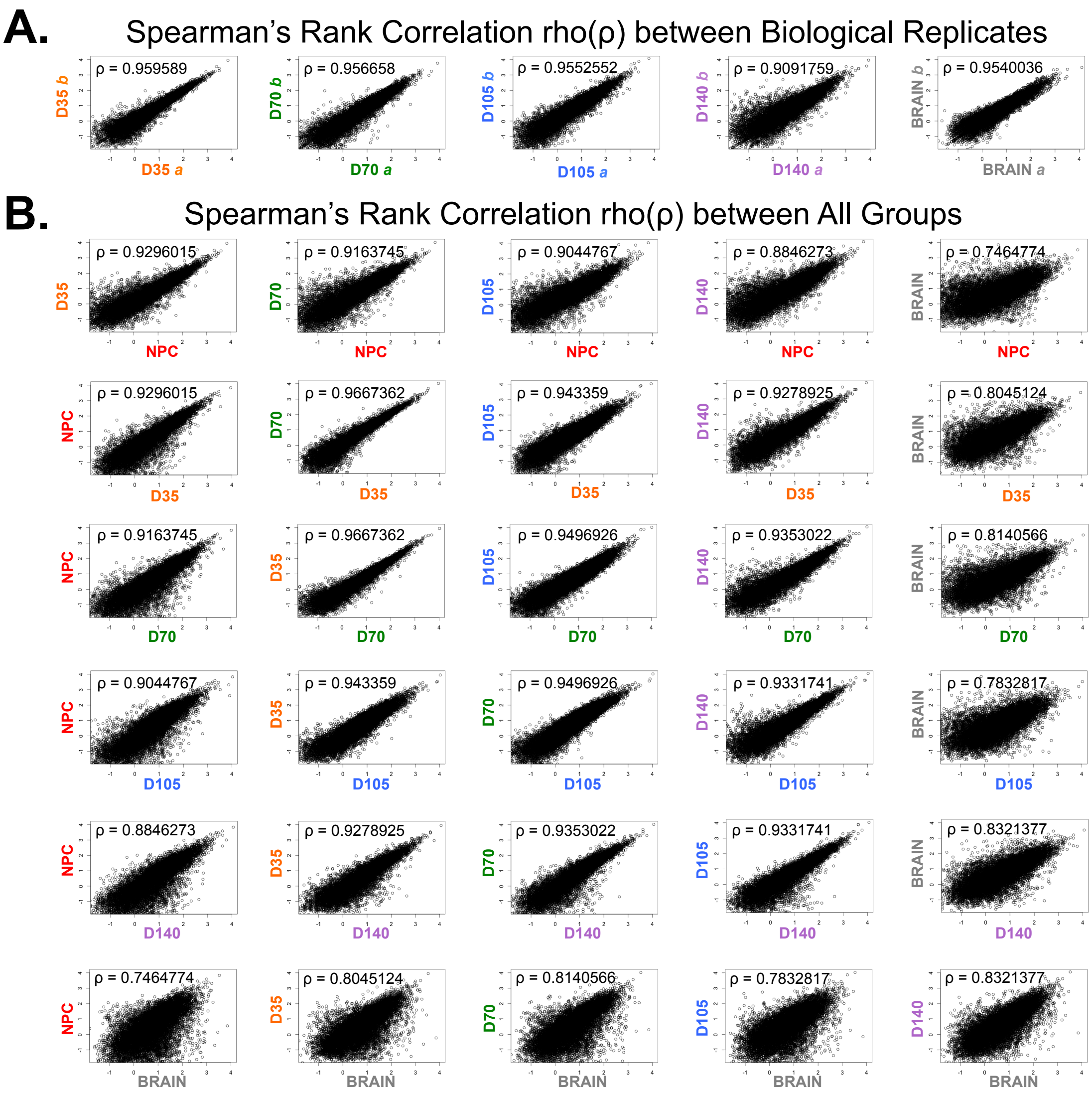


Figure 12.

Rank Correlations of Gene Expression between Replicates and Sample Groups. FPKM correlation scatter plots and Spearman's rank correlation coefficients, or rho(ρ), for (A) each set of replicates, and for (B) all possible group comparisons (Hjelm, Salhia, et al.).

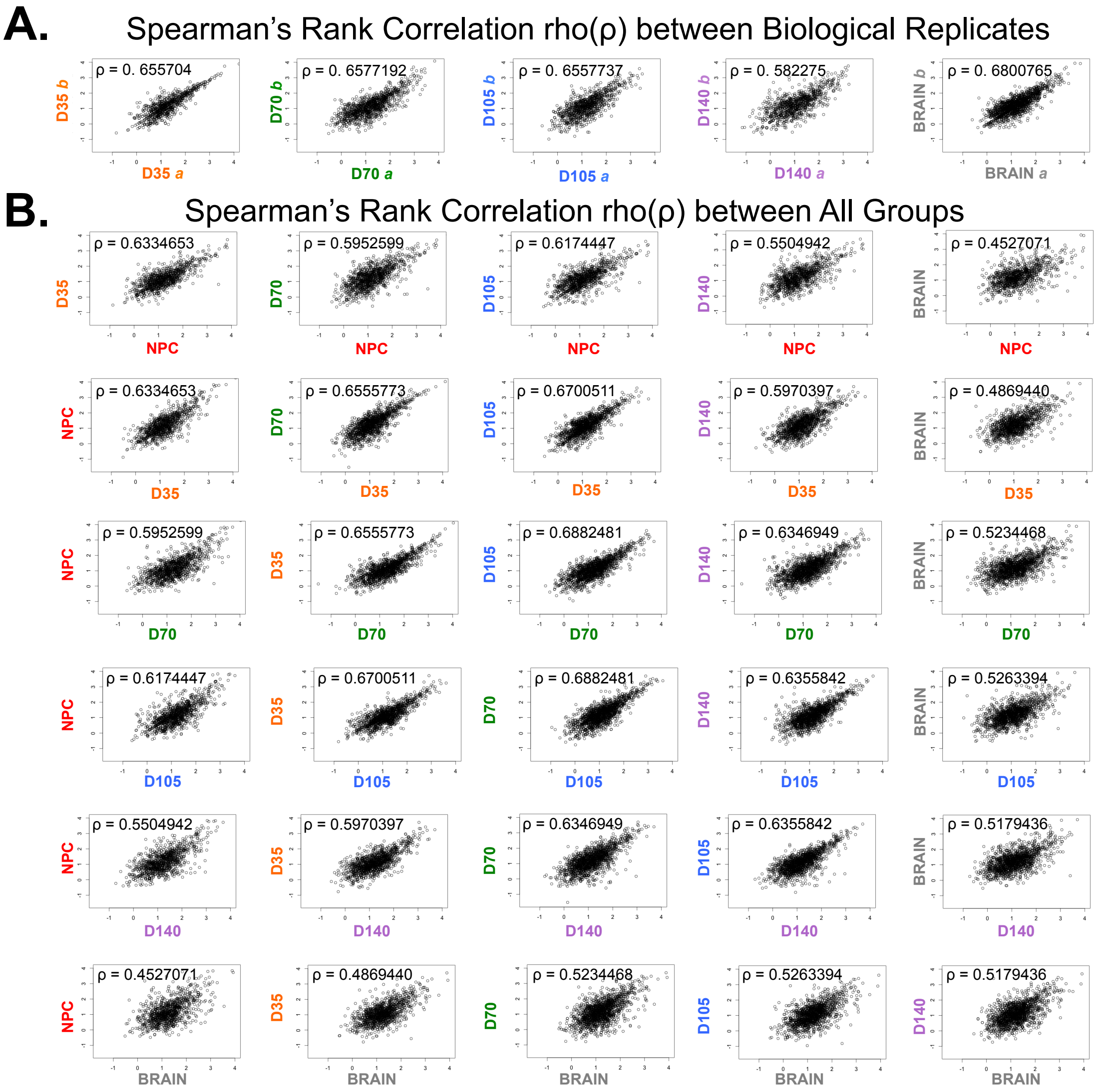


Figure 13.

Rank Correlations of lincRNA Expression between Replicates and Sample Groups. FPKM correlation scatter plots and Spearman's rank correlation coefficients, or rho(ρ), for (A) each set of replicates, and for (B) all possible group comparisons (Hjelm, Salhia, et al.).

Likewise, differential methylation between a subset of *in vitro* neural samples (NPC and D140) and the endogenous brain tissue (BRAIN) were evaluated for all methylation sites (485,261). Specifically, methylation sites that had a beta value difference ≤ -0.2 were defined as hypomethylated *in vitro*, and those that had a beta value difference ≥ +0.2 were defined as hypermethylated *in vitro*. The results of these comparisons provide the basis for our remaining figures (Figs. 14, 15, 16, 17, 18, 19).

We first looked at both the percentage of genes and the percentage of lincRNAs with significant differential expression, assessing all CCDS genes (18,062) and putative lincRNAs (8,262) along with tissue-specific gene lists (Fig. 14A,B). For brain tissue-specific gene lists, a list of "Brain Development Genes" (443) was obtained from the GO processes network using the MetaCore search engine from GeneGo Inc. (Ashburner et al.). As a negative control, lists of "Non-Brain Development Genes" were examined, using lists of GO processes from 8 different tissues (i.e., skin, eye, heart, bone, kidney, liver, lung, and pancreas development) (avg. 132), and the average number of differential genes was evaluated (Fig. 14A) (Ashburner et al.). For lincRNAs, a list of "Brain Tissue-specific lincRNAs" (183) was obtained from the annotated resource provided by Cabili et al., who separated lincRNAs into tissue-specific classes (Cabili et al.). As a negative control, "Non-Brain Tissue-specific lincRNAs" were examined, using lists of 8 different tissues (i.e., skeletal muscle, heart, placenta, liver, kidney, colon, lung, and testes) (avg. 130) also provided by Cabili et al., and the average number of differential lincRNAs was evaluated (Fig. 14B) (Cabili et al.).

Trends in differential gene expression showed that the percentage of *in vitro* to brain tissue differences declined as our timecourse progressed; however, only the "Brain Development Genes" (443) showed a significant decreasing monotonic correlation as determined by a one-tailed non-parametric Kendall's *tau* correlation test. This significant correlation was observed for both the total percentage of differences ($p < 0.01$), as well as the percentage of genes downregulated *in vitro* ($p < 0.05$), but was not significant for genes that were upregulated *in vitro* (Fig. 14A). Likewise, these trends were not significant for all CCDS genes (18,062) or "Non-Brain

Development Genes" (avg. 132). Taken together, these data show that for genes specific to brain developmental processes, there was a significant decrease in the percent of *in vitro* to brain tissue differences over our timecourse and that this observation was primarily due to the activation of genes that were originally downregulated *in vitro* (Fig. 14A).

Trends in differential lincRNA expression also showed a decrease in the percentage of *in vitro* to brain tissue differences. These trends showed more variation (or less linearity) than that of protein-coding genes, and the decrease only showed a significant decreasing monotonic correlation for the total number of differences of all putative lincRNAs (8,262) ($p < 0.05$) (Fig. 14B). Conversely, these trends were not significant for "Brain Tissue-specific" (183) or for "Non-Brain Tissue-specific" (avg. 130) lincRNAs, nor were they significant for trends specific to lincRNAs downregulated or upregulated *in vitro* (Fig. 14B). These data show that for all putative lincRNAs, we observed a significant decrease in the number of *in vitro* to brain tissue differences, but this trend was due to the combined effects of both activation of lincRNAs downregulated *in vitro,* and inactivation of lincRNAs upregulated *in vitro* (Fig. 14B). Also, there was less recovery (or progressive activation) of brain-specific lincRNAs than there was for protein-coding genes. Venn diagrams (for both CCDS genes and all putative lincRNAs) displaying the number and relative proportion of conserved *in vitro* to brain tissue differences between each adjacent step in the timecourse, as well as the differences conserved across all *in vitro* to tissue comparisons are also shown (Fig. 15).

Finally, differences in DNA methylation between two of the *in vitro* neural samples (NPC and D140) and the endogenous brain tissue (BRAIN) were also evaluated. Differential methylation was defined as a site that had a beta value difference of at least 20% (i.e., ≥ 0.2) between the brain tissue and respective *in vitro* sample. Trends in differential methylation were plotted for all methylation sites (485,261) on the array, as well as those specific to CpG islands (150,176), shores (North=62,827; South=49,166), and shelves (North=24,824; South=22,283). Shores are methylation regions 0-2 kilobases (kb) from CpG islands (CGI), and shelves are regions 2-4kb from CGI (Bibikova et al.; Doi et al.; Irizarry et al.). Overall, there was a decrease in the total number of differentially methylated sites from the beginning (NPC) to end (D140) of our timecourse compared to the brain (BRAIN). This trend was apparent for both CGI shores and shelves; however, for CGI themselves, there was a slight increase in the percent of *in vitro* to brain tissue differences (Fig. 14C). The percentage of methylation sites that were hypomethylated *in vitro* compared to the brain tissue decreased after differentiation (D140) for all methylation regions (islands, shores and shelves), which correlates with our previous observation of a global increase in DNA methylation. Conversely, the percentage of methylation sites that were hypermethylated *in vitro* compared to brain increased after differentiation (D140) for most of the methylation regions examined. The only exception to this trend was the percent of north-shore (N-Shore) methylation sites hypermethylated *in vitro*, which decreased after differentiation (D140) (Fig. 14C).

This observation was further examined by looking at CGI associated with a subset of genes that were originally downregulated *in vitro* and were transcriptionally activated during differentiation, or were originally upregulated *in vitro* and were transcriptionally inactivated during differentiation. Although we observed a global increase in CpG methylation, the percent of hypermethylated sites (for both NPC and D140 compared to BRAIN) was lower for genes activated during differentiation, than it was for genes inactivated during differentiation. These trends were most pronounced in the N-shore regions of associated CGI (Fig. 16). These observations are consistent with previous studies that have shown dynamic changes in CpG methylation in the developing and adult human brain (Siegmund et al.) and during *in vitro* differentiation, as well as previous reports that have identified the shore regions (0-2kb from CGI) as having the most tissue-specific methylation patterns (Irizarry et al.; Doi et al.).

Data sets comparing *in vitro* cell culture models versus tissue-derived counterparts are beneficial for evaluating the physiological and pathological relevance of iPSC-derived cell lines and disease models. Patterson et al. previously reported a comparison of several tissue types (i.e. hepatocytes, fibroblasts, and fetal neural progenitor cells) to their iPSC-derived counterparts (Patterson et al.). Using microarrays, they identified subsets of genes that were upregulated or downregulated in all *in vitro* samples compared to the endogenous tissues. We identified a significant number of genes in their data set that demonstrated the same pattern in our *in vitro* to

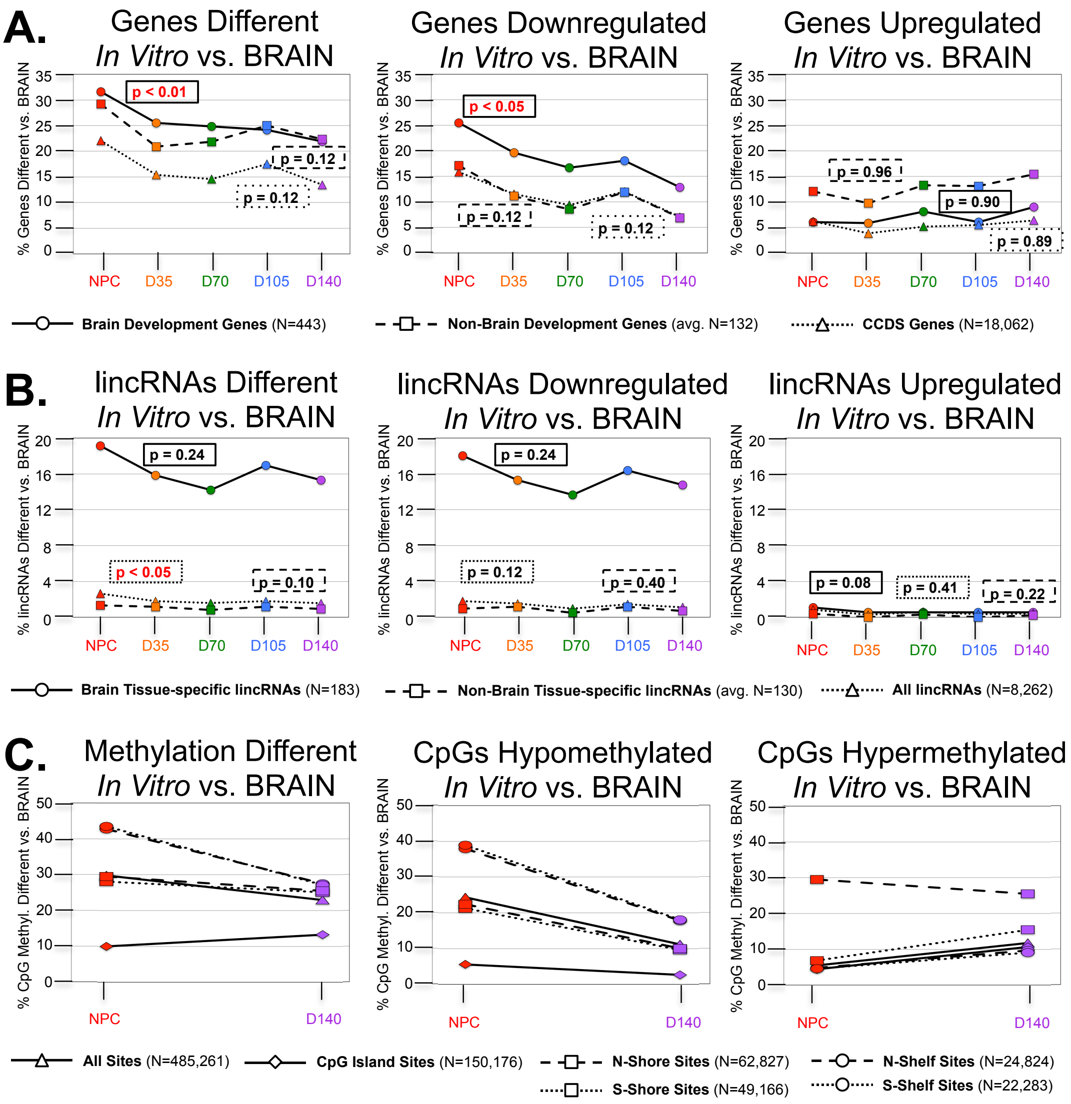


Figure 14.

Tissue-Specific Expression, Trends in Gene and lincRNA Expression, and CpG Methylation. Percentage of (A) genes and (B) lincRNAs that were differentially expressed between each *in vitro* sample and the endogenous brain tissue. Significant differential expression was defined as a comparison that had a $\log_2$ fold change > 2, as well as a p-value < 0.01. Trends are show for all genes/lincRNAs, as well as tissue specific lists (GeneGO and Cabili et al.). P-values shown are from a one-tailed, non-parametric Kendall's *tau* correlation test. (C) Percentage of CpG methylation sites differentially methylated between the two *in vitro* samples analyzed (NPC and D140) and the brain tissue. Differential methylation was defined as a site that had a beta value difference of at least 20% (i.e., ≥ 0.2). Trends are show for all methylation sites, as well as CpG islands and flanking regions (Hjelm, Salhia, et al.).

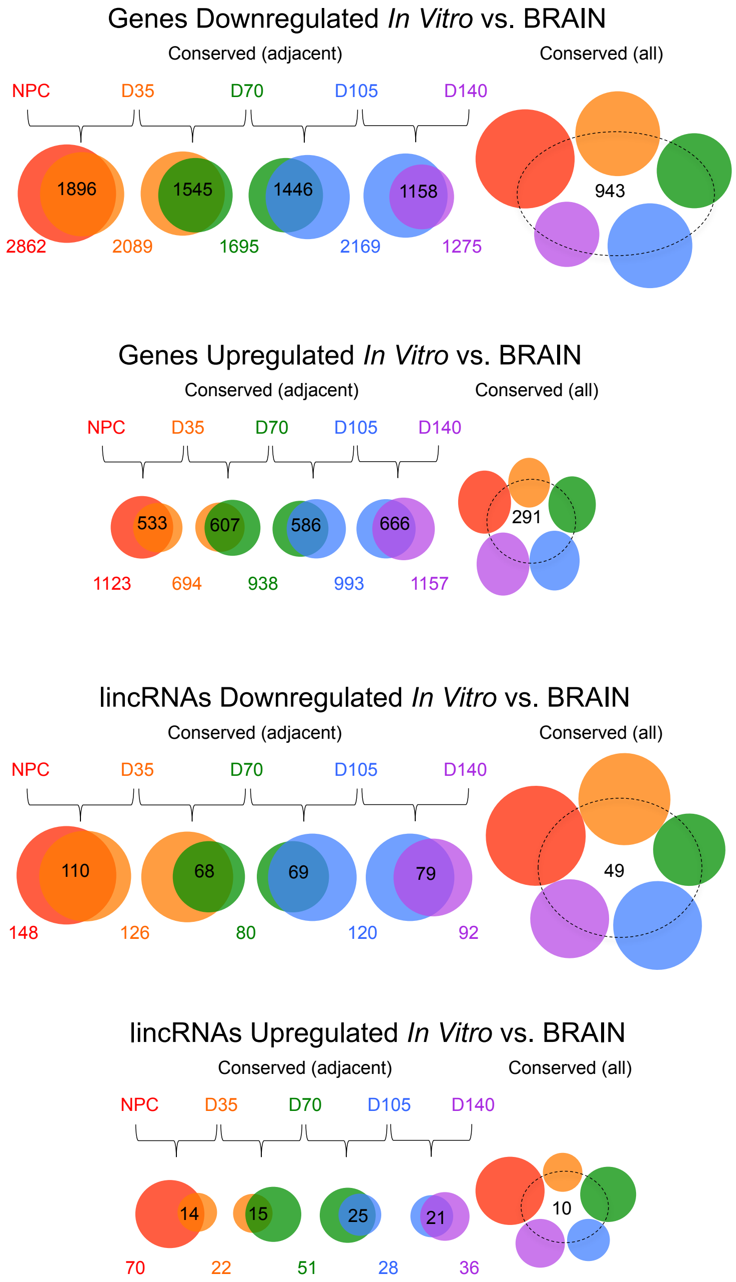


Figure 15.

Conserved *In Vitro* to Brain Tissue Differences. The number of significant differences between each *in vitro* sample and the *in vivo* brain tissue is shown below each Venn diagram. Circle sizes (area) for Venn diagram within each group are scaled in size relative to one another. Venn diagrams show the number of conserved differences between adjacent timepoints, and those conserved across all samples for (A) genes downregulated *in vitro*, (B) genes upregulated *in vitro*, (C) lincRNAs downregulated *in vitro*, and (D) lincRNAs upregulated *in vitro* (Hjelm, Salhia, et al.).

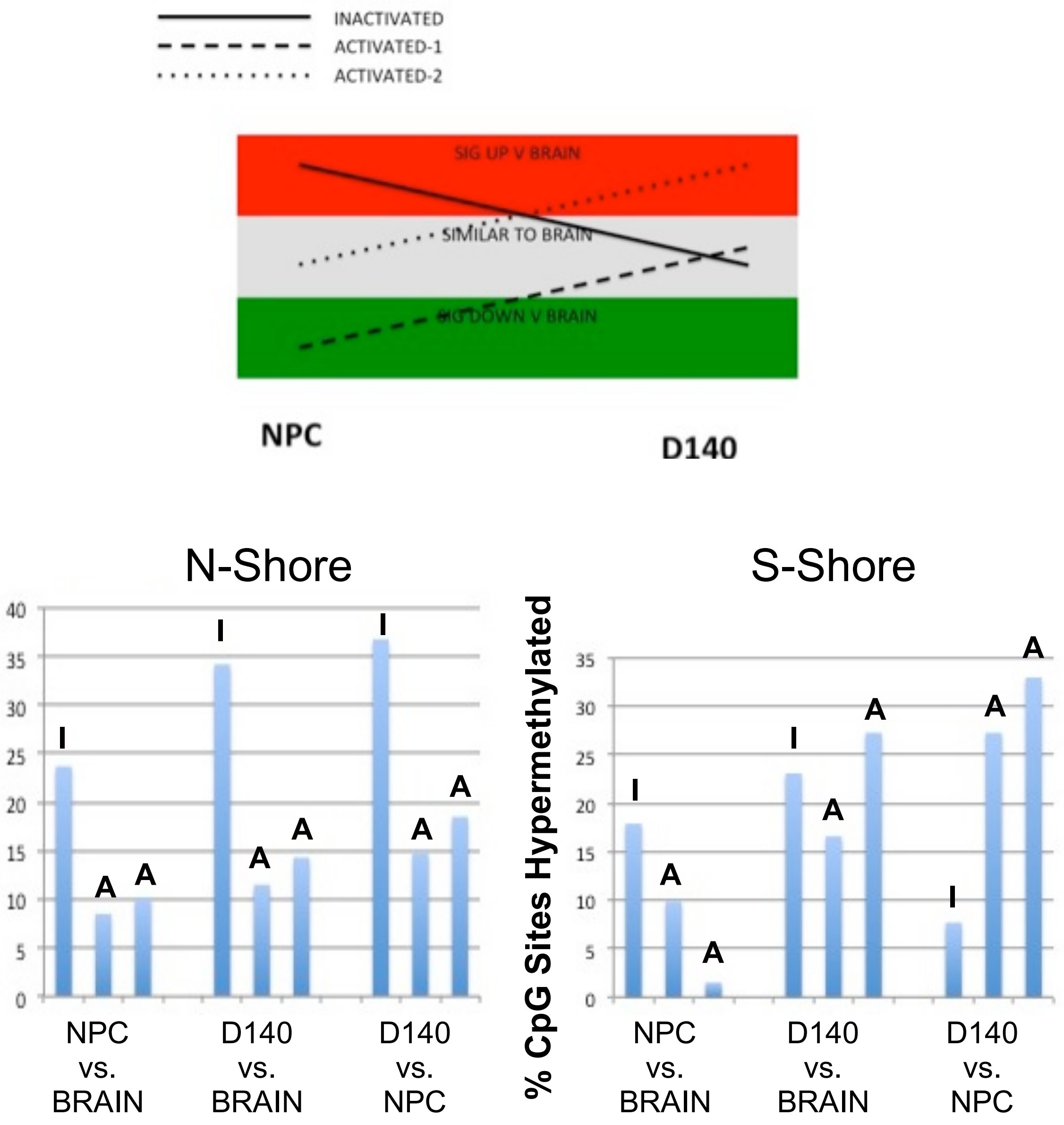


Figure 16.

Evaluation of Hypermethylated CpG Shores in Relation to Transcriptional Activation. Genes that followed a pattern of transcriptional inactivation (I), or transcriptional activation (A), were evaluated for differences in hypermethylated CpG sites. The percent of sites hypermethylated in both *in vitro* neural samples (NPC, D140) vs. the endogeous brain tissue (BRAIN) are shown, along with sites hypermethylated at the end of the timecourse (D14)) vs. the beginning (NPC). The North Shore (N-Shore) regions (0-2kb upstream of CpG Island) demonstrate a distinct association with transcriptional activation/inactivation (i.e., genes activated always had a lower % of hypermethylated sites compared to genes that were inactivated). These trends were not apparent in other flanking regions, like the South Shore (S-Shore), which is shown alongside for comparisons purposes as it has approximately the same density of CpG sites as the N-Shore.

Table 5.

Genes Significantly Different that Overlap with Previously Published Results. Genes that had *in vitro* to *in vivo* differences consistent with the results from Patterson et al. are shown. * = List of genes had significant overlap ($p < 0.05$) with Patterson et al., as determined by binomial distribution tests. Genes that were downregulated or upregulated at all timepoints are shown in dashed line (Hjelm, Salhia, et al.; Patterson et al.).
brain tissue comparisons (Table 5). Specifically, out of 33 genes they described as consistently

*	*		*	
NPC	D35	D70	D105	D140
ARNTL				
MGLL				
ZNF280D				
ZFP3				
CNTN3	*CNTN3*	*CNTN3*		
CREBL2	*CREBL2*		*CREBL2*	
PP1R3C	*PP1R3C*		*PP1R3C*	
SLC44A1			*SLC44A1*	
MAP3K5	*MAP3K5*	*MAP3K5*	*MAP3K5*	*MAP3K5*
ZNF662	*ZNF662*	*ZNF662*	*ZNF662*	*ZNF662*

In Vitro vs. *In Vivo* differences consistent with Patterson et al.

(left)
Downregulated *In Vitro*

(right)
Upregulated *In Vitro*

*	*	*	*	*
NPC	D35	D70	D105	D140
CORO2A				
ZCCHC3				
IGF2BP1	*IGF2BP1*	*IGF2BP1*	*IGF2BP1*	
EPHB4	*EPHB4*	*EPHB4*	*EPHB4*	*EPHB4*
LIN28B	*LIN28B*	*LIN28B*	*LIN28B*	*LIN28B*
MDK	*MDK*	*MDK*	*MDK*	*MDK*
TGIF2	*TGIF2*	*TGIF2*	*TG1F2*	*TGIF2*
	TCF7L1	*TCF7L1*	*TCF7L1*	*TCF7L1*
			PLAGL2	
				CLDN6
				DPPA4
				F11R
				GPC3

upregulated in iPSC-derived cell types, 7 to 9 of these genes were also upregulated in our samples compared to the endogenous brain tissue, from NPC to D140, respectively. All of the timepoints were significant when tested by binomial distribution tests (Table 5). Also, out of 19 genes that were consistently downregulated in iPSC-derived cell types in their study, 10 to 2 of these genes were also downregulated in our *in vitro* samples, from NPC to D140, respectively. Interestingly, this was only statistically significant at the NPC, D35 and D105 timepoints (Table 5). These data support the results of Patterson et al. and, in addition, suggest that *in vitro* activation of downregulated genes is more easily accomplished over time in culture than is the deactivation of upregulated genes. These deductions are consistent with our previously mentioned results of progressive and global transcriptional activation. Additional studies will need to be performed in order to determine if these results are specific to neural differentiation, or are likewise supported in prolonged culture of other iPSC-derived cell types.

In Vitro and Brain Tissue Transcript Abundance of Selected Neurologically Relevant Genes

We further investigated the physiological and pathological relevance of our *in vitro* iPSC-derived neural cell cultures by focusing on neurologically relevant genes. This includes genes important to neurogenesis and gliogenesis (Figs. 17, 18), and genes associated with certain neurological disorders and related pathways (Fig. 18). Genes were selected based on their redundancy in neurological GO processes, Pubmed, OMIM, and/or commercially available arrays containing neural-specific expression markers.

Neuronal expression markers included the following: *MAPT*, which was significantly downregulated *in vitro*; *MAP2*, which was significantly downregulated *in vitro* until the last differentiation timepoint (D140) when it was expressed at similar levels to the brain; *TUBB3*, which was expressed at similar levels to the brain until the last differentiation timepoint (D140) when it was significantly upregulated *in vitro*; the synaptic vesicle gene SYN1, which was also significantly downregulated *in vitro* (although an increase in expression was observed over time); and *DLG4*, the gene that encodes for the postsynaptic density protein, PSD-95, which was significantly downregulated *in vitro* until the last differentiation timepoint (D140) when it was expressed at similar levels to the brain (Fig. 17A). There was a progressive increase in expression for the three astrocyte genes, *SLC1A3(GLAST), GFAP* and S100B; however, all *in vitro* timepoints remained significantly downregulated compared to the brain tissue, as was expected for the smaller proportion of astrocytic glia in our *in vitro* neural cell cultures (Fig. 17B). Oligodendroglial markers *MBP* and *OLIG2* were both significantly downregulated *in vitro*, and did not increase during our timecourse suggesting these neural cell cultures did not contain terminally differentiated oligodendrocytes (Fig. 17B). Additional genes evaluated for differential expression included two neurotrophic growth factors (*BDNF* and *NGF*), as well as genes involved in neuronal cell adhesion (*CNTNAP2*), transcriptional repression (*MECP2*), and calcium channel signaling (*CACNA1C*) (Fig. 17C). Neuronal subtype-specific markers included genes for glutamatergic (*SLC17A7*), GABAergic (*GAD1*), and serotonergic (*SLC6A4*) neurons, as well as the forebrain developmental markers *PAX6* and *FOXG1*, all of which had some degree of transcriptional activation both *in vitro* and in the endogenous brain tissue (Fig. 17D). Lastly, evaluation of genes associated with excitatory (*OTX1* and *OTX2*) or inhibitory (*NKX2-1* and *GSX2*) neuronal activity demonstrated transcriptional activation occurred predominantly for the excitatory (not inhibitory) markers (Fig. 17E). Relative expression of some of these neurologically relevant genes, as well as a selected list of those associated with Alzheimer's disease and temporal lobe epilepsy are also displayed (Fig. 18).

Characterization of Genes and lincRNAs Ascribed to Early-to-Late Models of Differentiation

The differential expression results between our *in vitro* neural samples and the endogenous brain tissue were used to create five separate models of neural differentiation, based on the fact that we had five points in our timecourse. Genes and lincRNAs that were originally significantly different between the *in vitro* NPC sample and the BRAIN sample were divided into groups, based on if they changed to similar expression levels as the endogenous brain tissue (i.e., not significant vs. BRAIN) at early (D35; Model I), early-mid (D70; Model II), mid-late (D105; Model III), or late (D140; Model IV) timepoints, or if all *in vitro* samples remained significantly different compared to the brain (*in vitro* ≠ brain; Model V) (Fig. 19A). For genes that were originally upregulated in NPC compared to the brain tissue (1,123), 66% (740) fit into one of these five models, and for genes that were originally downregulated in NPC compared to the brain tissue (2,862), 77% (2,216) fit into one of these five models. Likewise, for lincRNAs upregulated in NPC compared to brain tissue (70), 86% (60) fit into one of these five models, and for lincRNAs downregulated in NPC (148), 64% (95) fit into one of these five models. The number of genes and lincRNAs in each model (for those both upregulated and downregulated *in vitro*) are shown, along with heatmaps of the relative expression (FPKM log2 vs. BRAIN) within each model (Fig. 19). For clarification of Models I-IV, those listed as upregulated were originally expressed *in vitro* at higher levels than the brain, then were inactivated to similar levels as the brain at a given step in our timecourse. Likewise, those listed as downregulated were originally expressed *in vitro* at lower levels than the brain, then were activated to similar levels as the brain during the differentiation timecourse. Heatmaps of differential expression for all genes in each of these models are shown, along with heatmaps of 20 selected neurologically relevant genes per model that were originally downregulated *in vitro* and demonstrated various rates of progressive activation (Fig. 19B). Likewise, heatmaps of differential expression for all lincRNAs in each of these models is shown (Fig. 19C).

Analysis of GO processes revealed the following sets of enriched processes for our neural differentiation models: genes inactivated during our neural differentiation timecourse (Model I-IV up) included those involved in mitosis, cell cycle control, biogenesis, chromatin assembly, and mitotic cell cycle checkpoints; genes activated during our neural differentiation timecourse (Models I-IV down) included those involved in nervous system development, neurogenesis, cell communication and signaling, and synaptic transmission. A description of each model can be found in Appendix A. The FPKM values for each gene and lincRNA corresponding to each of these models can be found in Appendix B. In addition, the significant GO processes associated with each of these models can be found in Appendix C. Future studies may use these lists as an initial association screen of which lincRNAs may be involved in mitosis, cell cycle control, neurogenesis and synaptic transmission. Likewise, genes and lincRNAs that remained significantly different between all our *in vitro* samples and the endogenous brain tissue

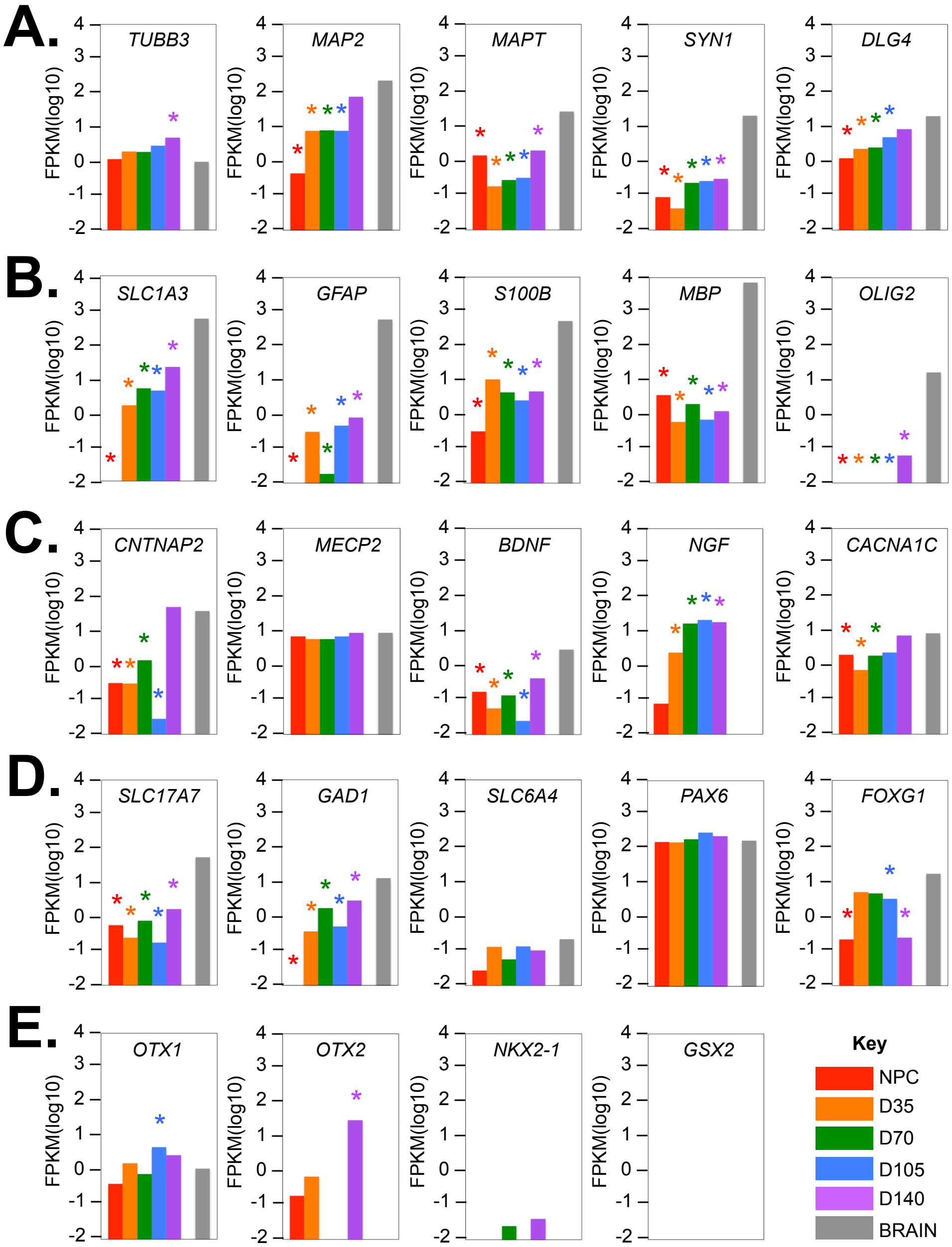


Figure 17.

Gene Expression of 24 Neurologically Relevant Genes. Bar graphs displaying the FPKM value ($\log_{10}$ scale) of various neurological genes for each *in vitro* sample along with the endogenous brain tissue. Significance (*) was defined as a comparison that had a $\log_2$ fold change > 2, as well as a p-value < 0.01. 24 genes associated with (A) neurons and synapses, (B) astrocytic and oligodendrocytic glia, (C) neurotrophic factors, adhesion, transcriptional repression, and calcium signaling, (D) neuronal subtypes (glutamatergic, GABAergic, serotonergic) and forebrain development, and (E) excitatory or inhibitory regional specificity are displayed. Gene lists were selected based on their redundancy in GeneGO, Pubmed, OMIM, and/or commercially available arrays containing neural-specific expression markers (Hjelm, Salhia, et al.).

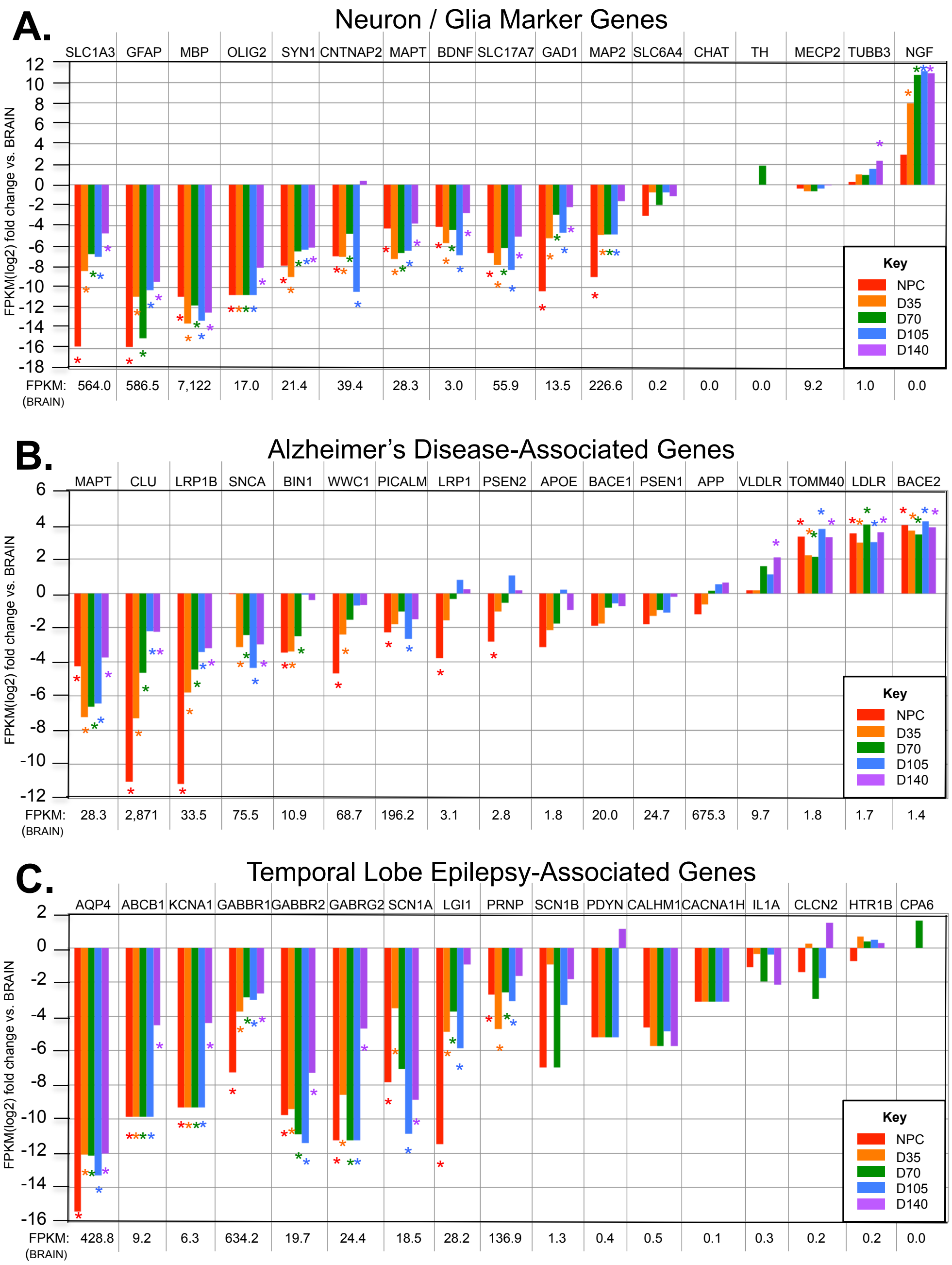
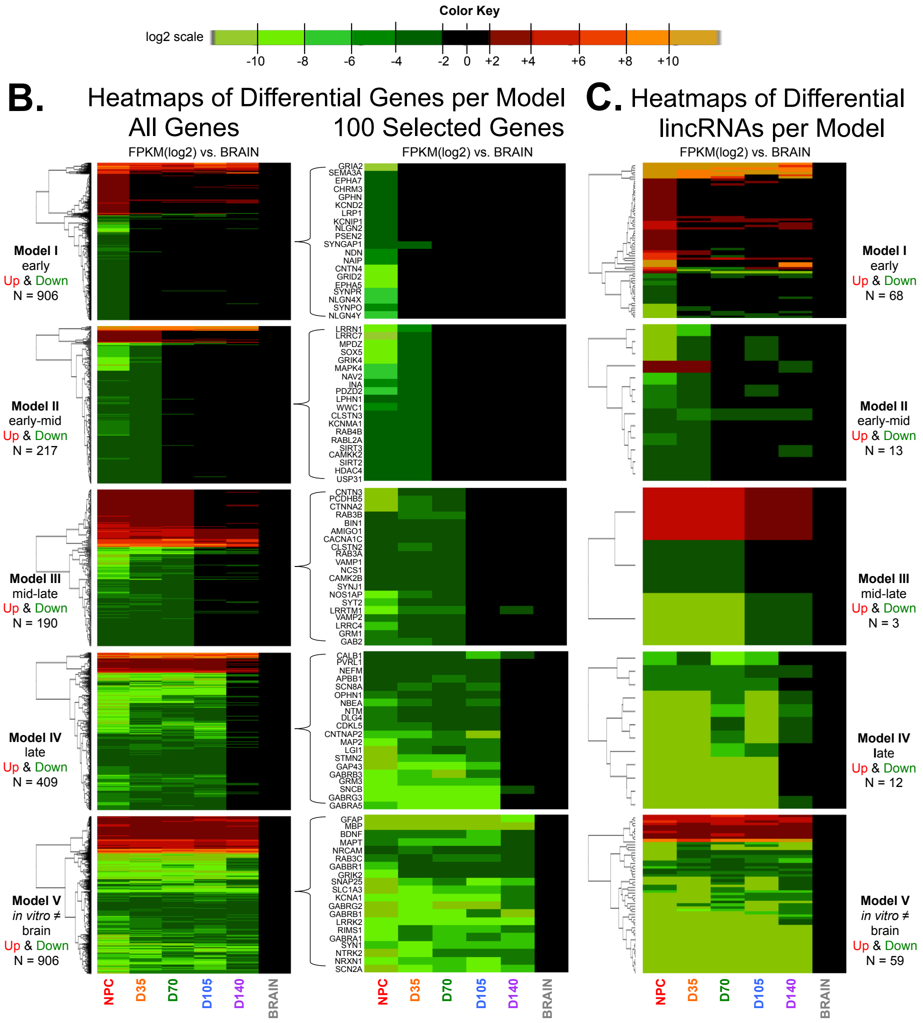


Figure 18.

Gene Expression of 50 Neurological and Disease-Associated Genes. Bar graphs displaying the $\log_2$ fold difference of each *in vitro* sample compared to the *in vivo* brain tissue. Significance (*) was defined as a comparison that had a $\log_2$ fold change > 2, as well as a p-value < 0.01. Above each graph has the list of 17 genes known to be (A) neurologically relevant, or have been associated with pathways involved in the pathogenesis of (B) Alzheimer's disease or (C) Temporal Lobe Epilepsy. Below each graph, the FPKM value for the BRAIN sample is given as a reference. Gene lists were selected based on their redundancy in neurological GO processes, Pubmed, OMIM, and/or commercially available arrays containing neural-specific expression markers (Hjelm, Salhia, et al.).

A. Models of Differentiation

Model	Differentiation Type	Significant vs. BRAIN (log2 fold >2 & p<0.01)	Not Significant vs. BRAIN (log2 fold <2 or p>0.01)	# Genes up / down / total vs. BRAIN	# lincRNAs up / down / total vs. BRAIN
I	early	NPC	D35, D70, D105, D140	305 / 601 / 906	48 / 20 / 68
II	early-mid	NPC, D35	D70, D105, D140	23 / 194 / 217	1 / 12 / 13
III	mid-late	NPC, D35, D70	D105, D140	70 / 120 / 190	1 / 2 / 3
IV	late	NPC, D35, D70, D105	D140	51 / 358 / 409	0 / 12 / 12
V	*in vitro* ≠ brain	NPC, D35, D70, D105, D140	-----	291 / 943 / 1234	10 / 49 / 59



B. Heatmaps of Differential Genes per Model

All Genes

100 Selected Genes

C. Heatmaps of Differential lincRNAs per Model

Figure 19.

Models of Neural Differentiation. Genes that were significantly different (log$_2$ fold change > 2 and p-value < 0.01) between the neural precursor (NPC) and brain tissue (BRAIN) samples were divided into five models of differentiation, based on if or when in the timecourse the gene became not significant (compared to the endogenous brain tissue). (A) Table of the five models (I-V), corresponding samples in each model, and the number of genes significantly upregulated or downregulated *in vitro* compared to the brain tissue in each model. (B) Heatmaps of all genes in each model, and heatmaps of 20 selected neurologically relevant genes per model that were downregulated in the NPC sample compared to the BRAIN and showed progressive activation at a given timepoint. Increasing models (I-IV) demonstrate the order in which these selected genes were transcriptionally activated/inactivated *in vitro* (i.e., early-to-late). Model V demonstrates selected genes that remained significantly different between all the *in vitro* neural samples compared to the endogenous brain tissue (i.e., *in vitro* ≠ brain). Genes were selected based on their redundancy in GO processes related to neural development, synaptogenesis, etc. (C) Heatmaps of all lincRNAs in each model (Hjelm, Salhia, et al.).

(Model V) may serve as a potential list of markers associated with highly specific features or terminal stages of neural differentiation.

Discussion

In this study, we focused on the *in vitro* to brain tissue differential expression of protein-coding genes and lincRNAs using RNA-Seq. We also evaluated some global differences in DNA CpG methylation using a genome-wide array. Future studies could also look at other functional features that may be predicted to have physiologically relevant differences. This includes, but is not limited to, microRNAs, histone methylation, protein translation and post-translational modifications, etc. In addition, RNA-Seq data could be further investigated beyond gene and lincRNA expression, for differences in alternative splicing, alternative promoter usage, intron retention, etc.

The variable we tested in this study was *time*, or time in neural differentiation conditions. Temporal effects are an intriguing variable to study, because they may be relevant to many cell culture systems regardless of the specific protocol. There are many additional variables, however, that are likely to influence the physiological or pathological relevance of *in vitro* neurological disease models. These variables include *what the neural cells were differentiated or grown on* (e.g., synthetic or biological scaffolds, adherent matrices, 3-dimensional vs. 2-dimensional cell culture conditions, polymer coated surfaces, feeder layers), *what cell culture media and conditions were used* (e.g., differentiation protocol, growth factors and their concentrations, ambient oxygen levels, feeder layers), and *what additional steps were performed that may affect the cell population complexity* (e.g., purification or cell sorting steps, genetic modification, cell seeding density, passage of NPC used, etc.). Future studies may include RNA-Seq analyses on some of these *in vitro* variables in order to determine their effects on physiological transcription.

Here, we focused on *in vitro* comparisons to temporal lobe brain tissue from an elderly, male autopsy donor identified as a neurological control. In addition to this specific comparison, it will be interesting to examine the *in vitro* to brain tissue differences using other brain regions, as well as comparisons with donors of different ages, sexes, and those with different stages of neurological disease progression. Likewise, larger data sets that include multiple donors and/or multiple iPSC clones (potentially generated by various methods or independent research groups) will be valuable in order to examine the variation that may exist and which aspects of the *in vitro* neural transcriptome are more fixed or plastic.

Also, additional studies should not only look at comparisons of complex cell populations and tissues, but also investigate more simplified or specific cell types obtained after purification/isolation by flow cytometry or laser capture microdissection (LCM). One particularly intriguing question that has important technical implications is- if our neural cell cultures described herein contain both immature and mature neurons, *how much* of the observed transcriptional activation (and hence brain-specific progression) is due to neuronal maturation? If this accounts for even a portion of the observed transcriptional progression, one would predict that cell sorting techniques specific to mature neuronal markers could demonstrate temporal progression and an increase in physiological transcription. Future studies may include RNA-Seq evaluations of *in vitro* neural cell populations and *in vivo* brain tissue, where both samples are analyzed prior to and following single-cell isolation or cell sorting.

While homogenous neuronal cell cultures offer many technical advantages, evaluation of more complex cell culture models, that may include the additional co-culture of astrocytes, oligodendrocytes, microglia, capillary endothelial cells, etc., may also be beneficial RNA-Seq studies as they allow us to evaluate the transcriptome while different cell types are in communication or contact with one another. Some transcriptional, and possibly even pathological, effects may not be present in monotypic cell culture models.

Overall, our analysis demonstrates the power of RNA-Seq and CpG methylation array data sets in evaluating the temporal effects of *in vitro* development and maturation of an iPSC-derived neural cell culture model. *In vitro* and tissue comparisons like these are not only useful resources, but also provide unique opportunities for collaboration amongst experts in genomics, stem cell biology, neuroscience, neuropathology, and bioengineering. We hope that this study provides a valuable resource for those interested in the physiological or pathological relevance of iPSC-derived neural cell culture models, and encourages others to collaborate and consider performing *in vitro* to tissue comparisons when evaluating their model system(s).

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APPENDIX A

DESCRIPTION OF MODELS (I-V) OF NEURAL DIFFERENTIATION

Model	Significant vs. BRAIN	Not Significant vs. BRAIN	Description	Pattern
I up	NPC	D35, D70, D105, D140	early	Originally upregulated in NPC, then inactivated to similar levels as BRAIN by D35
I down	NPC	D35, D70, D105, D140	early	Originally downregulated in NPC, then activated to similar levels as BRAIN by D35
II up	NPC, D35	D70, D105, D140	early-mid	Originally upregulated in NPC&D35, then inactivated to similar levels as BRAIN by D70
II down	NPC, D35	D70, D105, D140	early-mid	Originally downregulated in NPC&D35, then activated to similar levels as BRAIN by D70
III up	NPC, D35, D70	D105, D140	mid-late	Originally upregulated in NPC&D35&D70, then inactivated to similar levels as BRAIN by D105
III down	NPC, D35, D70	D105, D140	mid-late	Originally downregulated in NPC&D35&D70, then activated to similar levels as BRAIN by D105
IV up	NPC, D35, D70, D105	D140	late	Originally upregulated in NPC&D35&D70&D105, then inactivated to similar levels as BRAIN by D140
IV down	NPC, D35, D70, D105	D140	late	Originally downregulated in NPC&D35&D70&D105, then activated to similar levels as BRAIN by D140
V up	NPC, D35, D70, D105, D140		*in vivo* specific	Upregulated in all *in vitro* samples, NPC&D35&D70& D105&D140
V down	NPC, D35, D70, D105, D140		*in vivo* specific	Downregulated in all in vitro samples, NPC&D35&D70& D105&D140

APPENDIX B

FPKMS FOR ALL GENES / LINCRNAS IN MODELS (I-V)

Gene / lincRNA	ID	UP / DOWN (in vitro)	Model	Type	NPC (FPKM)	D35 (FPKM)	D70 (FPKM)	D105 (FPKM)	D140 (FPKM)	BRAIN (FPKM)
Gene	FABP4	UP	I	early	17.363	0.01	0.01	0.01	0.01	0.01
Gene	KRT18	UP	I	early	9.24333	0.502807	0.726268	0.01	0.77445	0.01
Gene	GAL	UP	I	early	8.0785	0.68174	1.6583	1.6127	0.837218	0.01
Gene	ODAM	UP	I	early	5.17817	1.15765	0.689352	1.12956	0.01	0.01
Gene	KRT25	UP	I	early	5.14986	0.643092	0.759947	0.192975	0.01	0.01
Gene	HIST1H3B	UP	I	early	5.10666	2.66459	1.15297	7.1207	3.26108	0.01
Gene	HIST1H2BL	UP	I	early	5.08622	3.34654	1.18232	7.62017	4.05453	0.01
Gene	CSN3	UP	I	early	4.9494	0.01	0.01	0.371625	0.273954	0.01
Gene	SFRP5	UP	I	early	4.93195	0.01	0.01	0.01	0.01	0.01
Gene	KRT8	UP	I	early	4.84173	0.299933	0.01	0.01	0.58329	0.01
Gene	ETV4	UP	I	early	4.55848	0.29035	0.181384	0.416495	3.32672	0.01
Gene	CD70	UP	I	early	4.5219	0.01	0.01	0.01	0.569416	0.01
Gene	ZCCHC3	UP	I	early	4.05778	0.60023	0.659799	0.574652	0.0702157	0.01
Gene	NMB	UP	I	early	3.73694	1.12387	0.66883	0.542431	0.378133	0.01
Gene	EIF4EBP1	UP	I	early	3.48664	1.07343	1.56644	3.73857	1.68741	0.01
Gene	SLC23A3	UP	I	early	3.38989	0.479758	0.925294	1.03181	0.117412	0.01
Gene	TRAPPC5	UP	I	early	3.27103	2.08734	1.13913	3.1525	2.4694	0.01
Gene	HIST1H3J	UP	I	early	2.96005	0.851213	0.930967	2.00409	1.06509	0.01
Gene	RD3	UP	I	early	2.88711	0.690372	0.121812	0.743054	1.5023	0.01
Gene	UNC93A	UP	I	early	2.39486	0.51156	0.01	0.01	0.0914826	0.01
Gene	RHOH	UP	I	early	2.32954	0.0900847	0.221742	0.0801966	1.3224	0.01
Gene	SLC25A10	UP	I	early	2.26947	0.883098	1.55997	3.36239	0.507862	0.01
Gene	TK1	UP	I	early	2.15481	0.402932	0.571112	0.81985	0.512841	0.01
Gene	ENDOG	UP	I	early	2.00382	0.308474	0.137878	0.748734	0.317341	0.01
Gene	TNFSF12-TNFSF13	UP	I	early	1.97653	0.320182	0.01	0.0581281	0.000454864	0.01
Gene	C11orf52	UP	I	early	1.96314	0.601428	0.78412	4.1278	1.05836	0.01
Gene	MTFP1	UP	I	early	1.82177	0.899341	0.68344	2.2938	0.498489	0.01
Gene	NDST4	UP	I	early	12.1545	0.760958	0.358852	0.15015	0.315871	0.0710939
Gene	KIF18B	UP	I	early	1.67856	0.91657	0.652462	1.39642	1.34834	0.01
Gene	MACROD1	UP	I	early	1.659	1.22374	0.373829	1.06353	0.830244	0.01
Gene	YDJC	UP	I	early	1.62309	0.426243	0.302805	0.967591	0.781194	0.01

Gene	GSDMD	UP	I	early	1.52431	0.443662	0.253274	0.884339	0.339038	0.01
Gene	TRPC7	UP	I	early	1.36528	0.01	0.01	0.0461169	0.01	0.01
Gene	PRSS21	UP	I	early	1.35896	0.388035	1.39368	0.01	0.611426	0.01
Gene	SDR42E1	UP	I	early	1.34832	0.817806	0.701413	0.79777	1.51665	0.01
Gene	TNNI3	UP	I	early	1.27376	0.989124	0.01	0.01	1.69811	0.01
Gene	CMA1	UP	I	early	1.26925	0.525128	0.190766	0.236944	0.235253	0.01
Gene	CPNE7	UP	I	early	1.26082	0.757155	0.2204	0.781889	0.431732	0.01
Gene	RAC2	UP	I	early	1.23033	1.32397	1.96688	3.35621	0.788159	0.01
Gene	SMR3B	UP	I	early	1.17468	0.293121	0.614136	1.51721	0.01	0.01
Gene	PRPS1L1	UP	I	early	1.16407	0.152021	0.01	0.213815	0.268969	0.01
Gene	CLPP	UP	I	early	1.13776	0.410592	0.616268	1.11283	1.54856	0.01
Gene	SKA1	UP	I	early	8.96681	4.98974	4.64132	6.85726	7.52027	0.0808942
Gene	RGS21	UP	I	early	1.09224	0.100916	0.0310284	0.113012	0.184683	0.01
Gene	CREB3L4	UP	I	early	1.06485	0.669788	0.802366	0.707653	0.687378	0.01
Gene	LRP5	UP	I	early	1.04628	0.93252	2.30436	4.63983	2.66165	0.01
Gene	FAM150A	UP	I	early	0.992967	0.01	0.298069	0.722028	0.01	0.01
Gene	RHOD	UP	I	early	0.979354	0.365503	1.85895	1.82797	1.14051	0.01
Gene	ESPL1	UP	I	early	0.958751	0.346136	0.46142	0.878525	1.08349	0.01
Gene	WDR34	UP	I	early	0.848006	0.27367	0.444162	0.535801	0.309043	0.01
Gene	RIPK4	UP	I	early	0.827516	0.0695989	0.0100313	0.01	3.40319	0.01
Gene	GABRR1	UP	I	early	0.79932	0.487604	0.0590941	0.370295	0.01	0.01
Gene	CABS1	UP	I	early	0.79354	0.616522	0.23545	0.139742	0.01	0.01
Gene	B3GNT3	UP	I	early	0.782199	0.01	0.01	0.01	0.0598412	0.01
Gene	MAGEA11	UP	I	early	0.780747	0.365086	0.030124	0.283898	0.01	0.01
Gene	E2F2	UP	I	early	0.777111	0.65203	0.60701	0.728427	0.530479	0.01
Gene	PLA2G3	UP	I	early	0.774941	0.272015	0.111991	0.150826	0.42929	0.01
Gene	MAGEA2	UP	I	early	0.769283	0.877683	0.189781	0.881698	7.04254	0.01
Gene	FAM109B	UP	I	early	0.751758	1.13869	0.953024	2.27231	0.755482	0.01
Gene	RAB43	UP	I	early	0.737179	0.01	0.137449	0.01	0.01	0.01
Gene	STEAP3	UP	I	early	6.67092	2.54845	3.97658	2.82647	4.43115	0.0973044
Gene	KBTBD8	UP	I	early	93.3065	3.62706	5.9442	2.06167	4.25339	1.68683
Gene	FAM159B	UP	I	early	32.8433	9.35302	0.01	0.01	0.783868	0.639555
Gene	CDCA2	UP	I	early	16.5713	10.1735	10.0162	9.30018	7.53336	0.375326
Gene	SGCG	UP	I	early	16.0163	0.683357	0.415935	0.184016	1.65358	0.380417

Gene	SKA3	UP	I	early	21.711	16.4203	16.7805	5.20831	8.82811	0.581476
Gene	AQP3	UP	I	early	13.9164	5.64171	9.83499	7.09067	0.94173	0.448419
Gene	ORC1	UP	I	early	3.53642	2.1927	1.558	1.21496	3.8307	0.117173
Gene	TRIB3	UP	I	early	2.64401	0.32975	0.2615	0.732872	0.544787	0.0923836
Gene	LRR1	UP	I	early	8.14887	3.89022	4.45317	2.28392	1.78244	0.30204
Gene	KIF2C	UP	I	early	3.76136	1.51977	1.89207	1.47876	1.55525	0.152165
Gene	IL18RAP	UP	I	early	1.91553	1.0517	0.713547	0.536253	0.01	0.0780139
Gene	ZPLD1	UP	I	early	6.41015	0.324497	0.0709367	0.0484571	0.411803	0.297855
Gene	CDC45	UP	I	early	11.0457	5.62721	3.88862	5.9083	6.25091	0.552801
Gene	AIM1	UP	I	early	30.6586	0.836323	0.413944	0.44897	2.08538	1.61845
Gene	MOCOS	UP	I	early	0.965234	0.0324019	0.185566	0.0828186	0.3804	0.0577295
Gene	GPX1	UP	I	early	9.97624	2.13866	1.3877	5.33787	2.16799	0.625335
Gene	DCPS	UP	I	early	8.58055	3.26766	3.29781	6.82721	4.70777	0.539624
Gene	AGPAT9	UP	I	early	10.1884	0.480237	1.71243	0.0705546	1.42391	0.656486
Gene	CARD11	UP	I	early	2.62748	0.01	0.157522	0.01	0.155867	0.171688
Gene	MICB	UP	I	early	4.93579	0.494185	1.07972	0.297874	1.38159	0.346642
Gene	TMEM171	UP	I	early	12.171	1.59844	0.580206	2.06744	2.81229	0.861596
Gene	CA12	UP	I	early	8.48939	1.79996	1.6124	0.668916	1.05058	0.625056
Gene	CORO2A	UP	I	early	4.51333	0.01	0.10801	0.0804905	0.934732	0.342724
Gene	SLC16A6	UP	I	early	9.76386	0.69897	2.81584	0.30042	2.87709	0.827135
Gene	PLS1	UP	I	early	12.7942	2.92658	1.11723	0.719727	1.87964	1.09908
Gene	FDXR	UP	I	early	8.16152	1.81042	1.11748	2.68388	1.74903	0.705343
Gene	TSEN34	UP	I	early	8.16742	2.92181	4.15849	3.82891	3.21147	0.706395
Gene	TNFAIP8L3	UP	I	early	10.986	0.0620785	0.01	0.0231674	0.374758	0.971213
Gene	SDF2L1	UP	I	early	13.0445	5.76902	4.42604	1.61183	1.18802	1.15389
Gene	BOLA3	UP	I	early	115.185	35.2484	36.2673	36.1166	24.4537	10.2241
Gene	MRTO4	UP	I	early	7.27327	2.59963	3.09877	4.21636	3.83971	0.647289
Gene	CSK	UP	I	early	4.6651	1.02279	0.955785	2.14969	1.24066	0.415756
Gene	MSTN	UP	I	early	10.5998	0.826943	0.797646	0.711102	0.163275	0.955773
Gene	RPL26L1	UP	I	early	13.0099	6.13166	9.64066	6.57211	9.02287	1.20729
Gene	TFAP2C	UP	I	early	24.0674	5.48997	6.89545	2.15729	8.23349	2.23503
Gene	ACLY	UP	I	early	108.024	50.4904	56.9639	61.5798	88.06	10.045
Gene	KAZALD1	UP	I	early	4.12056	0.960704	1.1245	2.28373	0.667947	0.397918
Gene	FAM72D	UP	I	early	3.4723	2.43515	2.45993	0.721833	3.21391	0.342262
Gene	MIF	UP	I	early	8.95255	0.868587	4.53451	8.64134	7.16053	0.891423

Gene	HIST1H4B	UP	I	early	20.1725	8.85679	9.45147	12.6068	16.3739	2.01338
Gene	ACAT2	UP	I	early	125.895	45.4523	28.8549	20.5283	29.4642	12.6568
Gene	MRPL11	UP	I	early	16.7748	4.15344	6.46336	6.68825	5.60183	1.78395
Gene	NPY2R	UP	I	early	5.99046	1.01407	1.53949	0.39496	0.242545	0.638706
Gene	DOT1L	UP	I	early	9.4912	3.57175	2.67171	3.42612	4.09509	1.03849
Gene	CYP1A1	UP	I	early	2.42895	0.137648	0.165165	0.01	0.322363	0.278263
Gene	C4orf49	UP	I	early	10.94	1.05509	0.406439	0.300253	0.96844	1.26341
Gene	TECTA	UP	I	early	8.58465	0.649879	0.521956	0.7996	0.676503	1.00133
Gene	C9orf140	UP	I	early	4.26779	1.3494	0.446596	1.37222	1.28409	0.50853
Gene	EYA4	UP	I	early	35.1287	7.52429	8.52749	1.15679	10.7675	4.20615
Gene	C3orf37	UP	I	early	42.0578	8.74896	10.4637	11.8908	13.8603	5.04402
Gene	AEN	UP	I	early	3.0492	1.56095	1.19062	0.948393	2.11899	0.367111
Gene	C16orf91	UP	I	early	8.43463	3.72843	4.04251	6.38789	4.93123	1.01906
Gene	BDKRB2	UP	I	early	1.48796	0.138515	0.109145	0.244586	0.241124	0.181485
Gene	IL18R1	UP	I	early	9.09447	4.88848	5.0108	1.44326	0.905654	1.1237
Gene	COQ3	UP	I	early	17.3358	6.73551	6.78735	4.37874	4.17512	2.17404
Gene	POP1	UP	I	early	39.0835	15.9743	14.089	17.5705	13.4242	4.95608
Gene	MRPS15	UP	I	early	152.703	67.4899	52.2058	68.3921	57.5045	19.954
Gene	ZNRD1	UP	I	early	7.17983	2.99623	5.58797	5.70909	6.13972	0.949699
Gene	TRIM7	UP	I	early	10.1404	1.1923	1.10714	0.263306	0.01	1.34425
Gene	C16orf80	UP	I	early	84.3654	23.5338	24.3668	35.1645	33.2514	11.2007
Gene	JAG2	UP	I	early	2.35052	0.562362	0.837062	1.05521	0.971241	0.312964
Gene	CHRNA5	UP	I	early	38.964	15.8656	15.6549	4.18857	10.8624	5.20235
Gene	CTSC	UP	I	early	37.7168	20.433	17.0332	9.69969	56.1816	5.18358
Gene	PKP2	UP	I	early	9.52634	0.797126	0.0480199	0.464881	2.98309	1.33977
Gene	PSMA7	UP	I	early	249.853	106.501	138.61	119.714	91.172	35.2443
Gene	EBPL	UP	I	early	8.70363	5.75118	4.94338	4.32309	4.67401	1.23721
Gene	SCIN	UP	I	early	58.8241	5.13018	21.6615	20.9911	16.2542	8.41589
Gene	CCDC86	UP	I	early	8.4909	2.55934	2.1813	5.81399	3.72635	1.22557
Gene	PNP	UP	I	early	17.734	5.40885	5.42125	6.26005	5.68526	2.56187
Gene	PGK1	UP	I	early	189.53	85.2674	104.469	64.3325	102.71	27.7774
Gene	PPP1CA	UP	I	early	20.199	10.1785	5.87987	8.06815	9.07464	2.99816
Gene	CHAF1B	UP	I	early	10.475	5.78056	5.15426	4.35136	8.41082	1.56989
Gene	TUBG1	UP	I	early	10.8319	3.64283	2.71501	6.27834	3.30252	1.63052
Gene	TACO1	UP	I	early	21.2974	8.20055	5.97266	7.65376	10.8142	3.22067

Gene	NUP88	UP	I	early	53.4596	29.1598	23.6539	17.9241	22.8173	8.11055
Gene	PGAM4	UP	I	early	7.13793	2.81397	3.17721	2.22288	1.80608	1.08338
Gene	LYN	UP	I	early	20.9637	3.40578	5.48496	2.89339	7.51406	3.18298
Gene	NDUFAB1	UP	I	early	77.8404	38.874	42.24	22.9881	22.2754	11.9379
Gene	CCNF	UP	I	early	2.88134	1.14791	0.823606	1.40477	1.51532	0.443525
Gene	PERP	UP	I	early	29.6484	2.67159	6.24286	2.35175	5.76522	4.61558
Gene	MRPS9	UP	I	early	40.4805	12.352	13.1573	11.4628	13.656	6.30932
Gene	CENPP	UP	I	early	8.84489	2.2625	1.30227	2.55893	3.507	1.37962
Gene	UCK2	UP	I	early	19.8056	6.34881	5.99917	8.96618	8.64349	3.10057
Gene	UMPS	UP	I	early	25.0718	10.5096	14.3649	12.4791	12.7089	3.95484
Gene	TIMM50	UP	I	early	6.93826	2.37312	2.83589	5.19078	4.07289	1.0962
Gene	LRRC59	UP	I	early	21.5112	9.0226	11.6145	11.5027	9.91865	3.45961
Gene	MCTP2	UP	I	early	6.31177	1.33361	1.12451	0.364897	0.858101	1.01697
Gene	PFKP	UP	I	early	82.385	22.8242	21.036	38.6428	33.7435	13.3929
Gene	MTHFD1L	UP	I	early	27.1911	6.62281	17.2616	10.4757	13.8784	4.45981
Gene	MRPL4	UP	I	early	2.98568	1.42207	1.17585	2.45517	1.47898	0.491033
Gene	CXorf57	UP	I	early	69.0246	24.5033	9.63276	4.60874	9.66475	11.375
Gene	SMYD2	UP	I	early	60.3609	19.0465	16.5154	12.144	14.2722	10.0116
Gene	UTP14A	UP	I	early	31.0984	16.745	16.7728	20.2923	19.1837	5.19408
Gene	TRIM14	UP	I	early	56.9319	18.2948	12.5228	26.8784	17.0719	9.52083
Gene	FAM96A	UP	I	early	56.5915	17.3056	23.2074	9.14836	15.2265	9.50434
Gene	SPRY4	UP	I	early	86.6761	13.5904	25.0044	11.4962	41.5787	14.5724
Gene	DTYMK	UP	I	early	7.59237	6.11415	5.62683	6.58336	3.54855	1.28344
Gene	DIAPH1	UP	I	early	26.2606	8.21396	13.7348	13.9869	14.4146	4.45923
Gene	THAP4	UP	I	early	10.5028	3.36268	3.68634	5.96789	3.82452	1.79354
Gene	MRPL47	UP	I	early	22.3144	12.959	13.5026	8.73533	14.7256	3.85641
Gene	EXPH5	UP	I	early	32.881	9.12941	13.4745	2.86666	7.84896	5.69103
Gene	FAM162B	UP	I	early	8.54232	3.95305	3.02861	0.855543	0.01	1.48507
Gene	SNRPD3	UP	I	early	76.4982	48.0977	51.5169	36.2261	41.4755	13.3047
Gene	CYC1	UP	I	early	14.1226	5.23164	3.92799	9.43869	6.00529	2.46273
Gene	APOL2	UP	I	early	132.36	25.4994	29.8729	64.5087	44.7066	23.0817
Gene	WDR77	UP	I	early	25.0925	11.4512	12.6187	8.15141	13.4245	4.39209
Gene	PTDSS1	UP	I	early	27.6892	10.5579	14.3534	17.4678	16.1511	4.86101
Gene	CD3EAP	UP	I	early	4.78313	2.28204	3.63511	3.51195	3.87789	0.844777
Gene	HNRNPD	UP	I	early	1317.19	762.874	740.522	490.718	808.967	233.219

Gene	HNRNPM	UP	I	early	291.3	170.287	157.002	126.523	151.998	51.7598
Gene	SLC16A7	UP	I	early	42.0933	15.4477	19.574	9.27915	9.51387	7.57506
Gene	TUBA1B	UP	I	early	956.561	121.345	168.231	382.95	105.248	172.258
Gene	LTV1	UP	I	early	154.43	83.636	84.7822	39.3686	51.69	27.8886
Gene	EXOSC8	UP	I	early	57.859	27.687	32.106	20.7596	36.3661	10.5026
Gene	SAMM50	UP	I	early	28.8484	12.4608	12.7162	14.374	15.3481	5.24922
Gene	MTHFD1	UP	I	early	14.8737	8.96049	8.54657	10.4516	7.17086	2.70737
Gene	VDAC1	UP	I	early	533.509	274.978	274.496	180.138	290.134	97.2701
Gene	LBR	UP	I	early	78.8657	29.8054	24.8188	20.5891	39.7449	14.4425
Gene	ANXA11	UP	I	early	37.8726	12.6828	11.6517	23.6286	20.084	6.9684
Gene	KDELC2	UP	I	early	29.6686	17.3119	19.4312	8.99899	16.7706	5.46075
Gene	BLMH	UP	I	early	36.9517	17.9621	22.5318	23.0132	20.6582	6.80317
Gene	CCT4	UP	I	early	87.7126	52.0459	60.5549	35.4495	51.43	16.1881
Gene	CASP7	UP	I	early	19.3629	7.72853	8.81205	7.92308	5.78654	3.57959
Gene	AFG3L2	UP	I	early	13.4574	7.60398	8.68303	7.26866	7.92797	2.50041
Gene	EIF3C	UP	I	early	142.365	48.8377	60.5127	84.9763	83.3774	26.513
Gene	COASY	UP	I	early	4.87893	1.13343	1.12947	2.2476	2.14414	0.923601
Gene	PDSS1	UP	I	early	16.4421	11.7303	10.123	6.12543	6.32154	3.12081
Gene	CCDC110	UP	I	early	14.3914	6.26856	5.0386	1.73503	2.38592	2.73212
Gene	MAPKAPK3	UP	I	early	6.19958	1.34123	1.64821	2.96001	5.08072	1.18793
Gene	ATP5F1	UP	I	early	210.455	113.492	117.375	65.7849	97.2	40.6174
Gene	RRP15	UP	I	early	68.4379	40.6512	44.9581	29.5676	35.3346	13.2112
Gene	SLC25A39	UP	I	early	5.11365	1.42573	2.52248	3.664	4.06997	0.98742
Gene	PDIA6	UP	I	early	155.916	58.917	93.4711	62.3557	78.6988	30.2101
Gene	NDNL2	UP	I	early	59.5741	31.9018	38.3191	7.2548	3.43786	11.5694
Gene	SRSF7	UP	I	early	169.089	110.476	100.037	59.4528	113.362	32.8952
Gene	RPS12	UP	I	early	41.0767	30.2709	24.2896	20.735	24.0518	8.00708
Gene	MRPS23	UP	I	early	58.5843	20.792	20.461	19.4841	25.667	11.4469
Gene	ARPC1B	UP	I	early	95.8531	27.262	44.1138	39.6107	33.4967	18.7293
Gene	MRPL34	UP	I	early	47.9576	18.2174	16.4722	27.1843	17.8408	9.44037
Gene	TOMM5	UP	I	early	94.1796	64.8084	66.4671	44.9822	73.3126	18.618
Gene	EIF3CL	UP	I	early	124.018	43.5802	54.5965	75.7585	75.14	24.533
Gene	HSPA4	UP	I	early	387.184	140.665	174.717	87.1679	118.649	76.5989
Gene	RAD23A	UP	I	early	56.9862	24.3152	22.5824	43.7437	25.8439	11.2867
Gene	HNRNPF	UP	I	early	64.2781	29.3648	42.6576	25.8119	27.4134	12.7614

Gene	WDR76	UP	I	early	21.4591	14.6396	13.3193	10.6479	13.2655	4.26099
Gene	RPA3	UP	I	early	15.6452	5.10262	10.1973	3.64687	2.61419	3.11721
Gene	EIF3D	UP	I	early	53.5424	30.1053	38.0167	33.4458	33.3365	10.6911
Gene	FKBP4	UP	I	early	149.776	51.0103	47.6911	65.4372	54.5481	29.9213
Gene	GOT2	UP	I	early	87.4922	28.3725	25.1607	32.6497	40.707	17.4854
Gene	CHAC2	UP	I	early	6.4934	4.27642	4.42785	0.717074	1.06867	1.3003
Gene	VPS25	UP	I	early	5.18051	3.0264	2.65099	5.85141	4.03623	1.03999
Gene	CACYBP	UP	I	early	241.628	89.814	60.7292	53.6246	48.6755	48.7911
Gene	MRPL40	UP	I	early	33.7746	11.8894	17.4545	26.9513	15.7002	6.82253
Gene	C15orf23	UP	I	early	12.2186	6.26043	6.59771	5.9032	7.91216	2.47531
Gene	FERMT1	UP	I	early	25.974	8.01788	7.32059	3.96923	8.01015	5.27869
Gene	PSMB5	UP	I	early	169.63	114.956	136.346	128.151	83.5972	34.7221
Gene	ATP5A1	UP	I	early	277.135	168.774	148.223	166.835	195.865	56.8296
Gene	GTF2A2	UP	I	early	126.176	66.071	92.9504	40.2199	59.6313	26.0279
Gene	C20orf20	UP	I	early	28.0288	10.4878	11.0219	7.89608	7.85479	5.81403
Gene	IFI16	UP	I	early	117.971	66.3008	86.7031	23.0155	35.2751	24.541
Gene	MASTL	UP	I	early	22.6228	16.9113	22.128	7.30685	14.9782	4.74357
Gene	EFTUD2	UP	I	early	14.5398	7.42544	7.07682	8.95092	8.84535	3.07369
Gene	SERPINB6	UP	I	early	71.0601	9.27315	9.0356	10.3924	12.439	15.0359
Gene	ERCC6L	UP	I	early	7.04419	4.19278	4.68492	1.87041	4.32819	1.49428
Gene	VRK1	UP	I	early	62.2602	36.8919	31.028	11	26.2552	13.2197
Gene	MRPS7	UP	I	early	21.1649	10.6518	10.3553	10.0994	10.5306	4.4941
Gene	MRPL14	UP	I	early	11.2639	6.50191	7.58496	9.62244	8.08197	2.3952
Gene	SAC3D1	UP	I	early	6.71924	2.96149	2.37808	5.55435	3.80855	1.43514
Gene	PSMD14	UP	I	early	116.305	56.7364	63.6665	35.183	78.9939	24.8699
Gene	POU3F1	UP	I	early	3.15245	2.16979	1.7028	0.924761	1.07218	0.679579
Gene	ISOC1	UP	I	early	41.5737	16.4634	11.3131	7.79029	8.56767	8.97319
Gene	CCDC109B	UP	I	early	8.05682	2.49341	4.4501	3.78706	5.58407	1.73931
Gene	PSME1	UP	I	early	126.05	69.3963	89.5734	96.8557	76.7207	27.298
Gene	EIF3B	UP	I	early	27.7895	14.1816	14.9478	15.0514	14.1534	6.0289
Gene	CMBL	UP	I	early	24.8901	2.89502	4.86221	5.11885	8.77966	5.4033
Gene	EBNA1BP2	UP	I	early	210.495	107.032	116.713	159.038	151.253	46.0138
Gene	PGAM1	UP	I	early	73.2606	26.7353	28.9724	32.9523	47.8003	16.0153
Gene	TTLL12	UP	I	early	3.07617	1.46381	1.81567	2.11377	2.36894	0.673712
Gene	NSUN2	UP	I	early	29.9744	18.3261	21.5585	15.8521	23.4519	6.56594

Gene	EXOSC2	UP	I	early	14.7806	9.20035	6.85684	8.90115	11.0277	3.24864
Gene	CHCHD3	UP	I	early	58.9155	35.3762	37.4425	28.3242	43.0198	12.9864
Gene	RPS27L	UP	I	early	97.4469	62.064	83.3655	57.793	55.8631	21.5217
Gene	PRPS2	UP	I	early	13.4762	6.3708	5.31096	1.84726	2.48558	2.97662
Gene	WBSCR22	UP	I	early	40.8143	16.9105	26.0674	30.6478	32.4642	9.0454
Gene	ST3GAL2	UP	I	early	5.52544	2.24515	3.62426	4.7928	3.90934	1.22497
Gene	NIP7	UP	I	early	22.4004	13.4916	18.5559	7.03949	17.2687	4.96698
Gene	ATP5C1	UP	I	early	114.996	85.263	83.2259	78.6852	88.9715	25.5674
Gene	PGR	UP	I	early	2.70306	0.0512697	0.0698244	0.0545845	0.387762	0.602037
Gene	ARPC2	UP	I	early	297.902	219.692	227.826	151.778	252.087	66.8954
Gene	POLR3K	UP	I	early	44.6058	37.0914	27.701	19.1516	27.9804	10.0232
Gene	SUV39H1	UP	I	early	7.41213	4.0877	1.44428	3.45213	4.03881	1.66556
Gene	HIGD2A	UP	I	early	41.2685	35.1676	27.7458	34.3836	27.9387	9.28211
Gene	C6orf211	UP	I	early	21.8402	15.8054	13.0848	3.10225	13.7633	4.91707
Gene	ALDOA	UP	I	early	28.6994	11.6645	10.0287	21.2164	20.9366	6.47316
Gene	SEPHS1	UP	I	early	28.5653	19.7347	21.2879	12.1818	16.3406	6.4449
Gene	DAPK1	UP	I	early	145.789	84.2455	70.1687	78.432	97.1709	33.0405
Gene	JAGN1	UP	I	early	5.73809	4.70837	3.60852	4.06046	5.33581	1.3015
Gene	CYP4X1	UP	I	early	6.92905	3.32485	1.53768	0.664399	0.848962	1.57407
Gene	ILF3	UP	I	early	31.9258	23.1889	20.3157	27.3488	35.5107	7.26392
Gene	SURF2	UP	I	early	64.4163	12.2905	22.3428	29.0294	26.7814	14.7159
Gene	DTD1	UP	I	early	73.3643	26.6731	23.5815	32.6355	61.3347	16.7812
Gene	SORD	UP	I	early	10.6484	6.63654	5.61322	4.63694	5.22829	2.43671
Gene	PSPH	UP	I	early	16.749	5.63642	7.35082	10.8542	10.2599	3.83741
Gene	SLC7A5	UP	I	early	8.29696	1.92975	1.06968	1.5005	0.805086	1.90646
Gene	XRCC5	UP	I	early	221.509	158.242	160.867	116.152	185.274	51.0885
Gene	CCT3	UP	I	early	146.17	77.5024	100.853	133.769	119.258	33.8032
Gene	FRMPD2	UP	I	early	3.89074	0.286572	0.459051	0.716458	1.04418	0.902431
Gene	DSN1	UP	I	early	8.35332	6.10852	10.9981	7.57772	11.7147	1.94087
Gene	RNF128	UP	I	early	2.64186	1.72022	1.10609	0.320526	0.643895	0.614113
Gene	CPNE3	UP	I	early	92.8527	24.8331	29.6264	15.0427	22.9787	21.5968
Gene	SDHB	UP	I	early	44.5667	23.7163	20.823	17.0807	12.765	10.3769
Gene	PRMT6	UP	I	early	11.4831	8.20763	9.79601	5.77219	1.54275	2.6805
Gene	NDUFA12	UP	I	early	310.414	168.135	160.649	141.934	221.262	72.5377
Gene	CIRH1A	UP	I	early	35.5361	19.3066	15.6819	27.7286	30.0827	8.33932

Gene	STIP1	UP	I	early	244.101	105.554	100.617	171.688	168.753	57.3223
Gene	FARSB	UP	I	early	50.7799	27.8575	28.2004	28.4723	42.038	11.9309
Gene	NUP37	UP	I	early	17.3255	9.44046	12.6042	7.52616	11.9677	4.07441
Gene	RPIA	UP	I	early	15.9552	12.9551	11.601	6.26167	11.6862	3.76895
Gene	RPUSD4	UP	I	early	39.4404	27.845	29.6717	22.295	25.7123	9.32189
Gene	EIF4B	UP	I	early	122.602	69.3199	67.2076	56.1625	98.8626	29.1086
Gene	TIPIN	UP	I	early	28.535	12.2709	12.4982	6.00745	8.10597	6.78459
Gene	MRPL51	UP	I	early	881.573	485.617	478.701	805.844	893.959	210.631
Gene	TRMT112	UP	I	early	189.082	121.099	109.952	158.771	130.242	45.3559
Gene	LETM1	UP	I	early	9.44342	2.65958	2.93929	7.13374	4.63223	2.26823
Gene	NHEJ1	UP	I	early	12.984	10.0008	9.30053	11.7457	11.1407	3.12584
Gene	LARS2	UP	I	early	49.3624	46.5631	43.1722	42.4082	42.7976	11.9052
Gene	SDCCAG3	UP	I	early	12.0004	5.95488	4.41279	7.08396	8.41972	2.89444
Gene	TSR1	UP	I	early	31.6617	15.1941	14.5396	13.488	24.875	7.65453
Gene	NDUFS5	UP	I	early	205.829	96.6506	127.409	155.875	130.817	49.8
Gene	KLHL29	UP	I	early	4.25917	0.876756	1.44105	2.46809	1.56165	1.031
Gene	ITPR3	UP	I	early	1.20071	0.291836	0.135134	0.205104	0.242128	0.291282
Gene	HSPA9	UP	I	early	289.696	105.234	113.102	111.064	122.096	70.9026
Gene	EXOSC9	UP	I	early	35.9766	28.6068	24.1006	11.5688	17.4762	8.81349
Gene	BUD31	UP	I	early	41.2809	24.5659	30.2018	25.2011	34.5265	10.1332
Gene	U2AF1	UP	I	early	109.804	94.298	105.223	89.4442	37.1685	26.9648
Gene	PSMB6	UP	I	early	30.2376	10.8177	14.217	26.5202	20.7162	7.4455
Gene	HMGN2	UP	I	early	51.9573	36.5453	41.9571	27.0406	29.5073	12.794
Gene	GMNN	UP	I	early	23.5389	12.6689	9.77149	4.2821	5.84962	5.80697
Gene	RRS1	UP	I	early	21.9736	12.4244	12.968	9.71964	8.33081	5.44302
Gene	VMA21	UP	I	early	36.565	15.6549	15.6326	3.91821	8.29484	9.0589
Gene	RBM34	UP	I	early	240.275	218.741	205.091	110.502	179.579	59.601
Gene	YEATS4	UP	I	early	57.9352	33.9181	37.371	10.9607	7.92205	14.3903
Gene	DRG1	UP	I	early	54.4401	32.1873	39.5269	41.8972	48.9959	13.5517
Gene	TFB1M	UP	I	early	24.6992	11.6083	17.7051	17.2961	22.6029	6.15529
Gene	HIST1H2BI	UP	II	early-mid	12.6957	4.01273	4.28649	12.9633	4.91834	0.01
Gene	HIST1H3I	UP	II	early-mid	11.8664	13.9892	5.72165	28.5781	22.4838	0.01
Gene	HIST1H2BO	UP	II	early-mid	11.8369	6.43726	4.0738	10.1967	3.08411	0.01
Gene	CENPA	UP	II	early-mid	8.14601	3.55395	7.24246	0.974116	1.79542	0.01

Gene	HIST1H2BM	UP	II	early-mid	7.09741	5.57296	2.84608	8.72795	13.9404	0.01
Gene	FAM64A	UP	II	early-mid	1.8706	1.90818	1.08935	2.67938	2.57179	0.01
Gene	GPRC5A	UP	II	early-mid	23.9528	16.3403	8.01347	8.76918	4.80459	0.237759
Gene	ERP27	UP	II	early-mid	8.89644	5.85818	2.52176	0.119394	0.747521	0.727111
Gene	RACGAP1	UP	II	early-mid	54.3518	26.0167	19.9518	20.5253	19.9926	5.74452
Gene	MIXL1	UP	II	early-mid	3.6412	6.04185	2.33826	2.27378	0.530999	0.39
Gene	HIST1H1A	UP	II	early-mid	11.2864	15.3797	4.66522	6.47065	4.85665	1.42535
Gene	FAM65B	UP	II	early-mid	22.8557	11.9477	8.95499	6.04951	5.65423	2.98652
Gene	C1orf135	UP	II	early-mid	6.4062	3.86638	3.33706	3.21736	3.08547	0.907369
Gene	TCERG1L	UP	II	early-mid	2.51895	2.1562	1.88124	2.1018	0.948937	0.366191
Gene	POLE2	UP	II	early-mid	2.81763	2.74439	2.17489	0.684857	2.28492	0.454514
Gene	CYCS	UP	II	early-mid	822.928	561.651	438.857	314.169	417.484	138.975
Gene	SERBP1	UP	II	early-mid	280.348	202.785	164.851	81.7401	145.306	49.0875
Gene	LANCL3	UP	II	early-mid	6.17257	5.1526	3.22167	1.56941	2.83515	1.08858
Gene	HDAC1	UP	II	early-mid	104.058	77.3349	51.1561	59.2535	70.8653	19.3113
Gene	IDH2	UP	II	early-mid	20.1978	16.8289	11.1061	14.4354	5.71413	3.88688
Gene	CCDC58	UP	II	early-mid	48.3454	43.227	34.2777	24.1551	25.6554	10.0911
Gene	HSPE1	UP	II	early-mid	377.166	384.639	265.084	208.463	222.15	83.2387
Gene	ZNF732	UP	II	early-mid	4.35318	5.65254	3.43861	1.85597	1.77503	1.02763
Gene	HOXD8	UP	III	mid-late	31.1366	16.2076	25.4225	3.96661	3.84163	0.0484361
Gene	MYBL2	UP	III	mid-late	3.66404	1.72302	1.59744	2.75706	1.67271	0.01
Gene	HOXA5	UP	III	mid-late	3.51213	2.99899	3.33875	3.62481	2.24097	0.01
Gene	HOXA13	UP	III	mid-late	2.53594	2.91398	2.34338	1.16806	0.419265	0.01
Gene	CDK1	UP	III	mid-late	22.6619	19.31	22.1391	2.52898	1.05787	0.0896141
Gene	NPSR1	UP	III	mid-late	2.52812	2.24852	1.15825	0.136066	1.11836	0.01
Gene	HOXB7	UP	III	mid-late	2.48001	1.8343	3.0015	0.540706	1.10039	0.01
Gene	KIAA0101	UP	III	mid-late	15.4799	10.3397	14.7537	4.87024	1.7302	0.122694
Gene	C3orf55	UP	III	mid-late	0.784391	1.8069	2.69596	0.494032	1.54022	0.01
Gene	AGMO	UP	III	mid-late	12.3456	2.66374	6.57738	1.50537	1.42278	0.181025
Gene	CASC5	UP	III	mid-late	43.5881	29.7604	28.4445	6.2619	8.53113	0.692275

Gene	CKS2	UP	III	mid-late	44.7741	26.4989	32.4683	6.36566	9.05517	0.837844
Gene	SIX1	UP	III	mid-late	7.66985	3.0083	2.96544	0.936823	1.99258	0.159537
Gene	CERKL	UP	III	mid-late	8.3371	2.62656	2.44565	1.11827	1.19431	0.196413
Gene	FAM83D	UP	III	mid-late	7.76887	3.91065	3.95618	1.84739	1.81628	0.221432
Gene	TTK	UP	III	mid-late	23.5188	23.8834	14.4983	6.37897	7.2526	0.708033
Gene	NEIL3	UP	III	mid-late	7.4825	12.2142	6.94568	3.65599	1.89119	0.243555
Gene	DLX2	UP	III	mid-late	4.17327	5.814	7.05168	0.870944	2.21377	0.148256
Gene	ITGA4	UP	III	mid-late	45.4241	11.6658	14.0405	5.32919	5.22583	1.6937
Gene	FAM72A	UP	III	mid-late	6.10154	3.4601	4.9234	1.15715	2.64739	0.228904
Gene	CEP55	UP	III	mid-late	28.6594	15.5373	14.2276	6.91272	8.23881	1.19451
Gene	MAD2L1	UP	III	mid-late	18.1164	11.6071	13.3473	3.4461	2.45909	0.789811
Gene	DBF4	UP	III	mid-late	27.1441	20.329	18.6896	4.08339	1.52648	1.22136
Gene	AKAP2	UP	III	mid-late	46.9486	18.8501	20.7009	6.89385	3.79677	2.44648
Gene	COCH	UP	III	mid-late	21.7077	9.59599	5.20214	2.11187	3.71059	1.21839
Gene	GGH	UP	III	mid-late	176.718	66.279	66.749	39.7979	26.5655	10.1104
Gene	IKZF3	UP	III	mid-late	4.08312	8.28584	5.74821	1.95154	1.14268	0.237734
Gene	LMNB1	UP	III	mid-late	138.566	48.9783	35.9507	29.3737	32.312	8.60001
Gene	FAM72B	UP	III	mid-late	6.45911	3.31106	4.08469	0.952471	2.22147	0.418112
Gene	OSTM1	UP	III	mid-late	171.532	63.567	57.8155	20.9209	31.2724	11.3222
Gene	ULBP3	UP	III	mid-late	9.38538	10.1646	14.5821	4.58005	7.00096	0.729776
Gene	CCNA2	UP	III	mid-late	37.0575	17.1974	15.6737	4.41578	7.38705	2.97073
Gene	DDX21	UP	III	mid-late	124.214	67.389	73.7654	38.1992	46.0081	11.6053
Gene	SLC25A5	UP	III	mid-late	269.273	126.1	118.275	106.366	89.5077	27.1923
Gene	SPC25	UP	III	mid-late	14.3235	12.5958	11.0166	2.35998	2.72142	1.47637
Gene	RANBP1	UP	III	mid-late	74.9429	40.4723	35.2797	16.6865	11.8048	7.92407
Gene	MCM4	UP	III	mid-late	78.0733	55.7944	43.7416	25.2823	32.4588	8.51756
Gene	CKAP2	UP	III	mid-late	74.8817	76.9483	75.9329	21.7773	25.0653	8.45208
Gene	SMC4	UP	III	mid-late	469.645	457.651	476.598	88.6062	64.7157	54.7126
Gene	HMGB2	UP	III	mid-late	387.477	315.022	402.138	129.584	136.109	45.4058
Gene	MIS18A	UP	III	mid-late	24.5086	12.4174	13.4275	3.87505	12.2554	2.96165
Gene	TLL2	UP	III	mid-late	3.92559	2.15422	4.10378	1.69713	1.20992	0.477759
Gene	DARS2	UP	III	mid-late	15.5499	10.4759	8.19855	4.75594	5.95291	1.94326

Gene	PCNA	UP	III	mid-late	53.9617	29.122	28.5632	10.9338	13.9228	7.014
Gene	DOCK11	UP	III	mid-late	16.3303	17.8238	9.34571	4.2822	6.05996	2.21247
Gene	HNRNPA3	UP	III	mid-late	949.686	663.767	553.587	235.505	391.065	130.603
Gene	RPS13	UP	III	mid-late	416.454	271.545	309.112	107.794	183.834	57.3296
Gene	RFWD3	UP	III	mid-late	23.9882	15.7896	18.3356	10.0032	13.0808	3.34003
Gene	TMPO	UP	III	mid-late	81.9778	46.4175	52.2688	20.676	33.6044	11.4381
Gene	SNRPG	UP	III	mid-late	181.948	152.969	124.046	44.6397	23.4877	25.6097
Gene	HAUS1	UP	III	mid-late	8.16978	6.42732	6.35887	3.80729	6.31123	1.16468
Gene	PUS7	UP	III	mid-late	30.3094	18.7511	23.0665	12.5768	15.4448	4.33527
Gene	PPPDE1	UP	III	mid-late	64.6379	37.7841	45.0864	23.9402	25.1495	9.29778
Gene	MYH15	UP	III	mid-late	9.43161	7.95394	8.49358	4.85353	3.47179	1.36468
Gene	SGOL2	UP	III	mid-late	11.1196	9.91216	12.2107	2.69593	1.58819	1.67532
Gene	ZNF367	UP	III	mid-late	5.16965	3.80469	4.25994	0.622499	0.305971	0.790714
Gene	SNRPE	UP	III	mid-late	52.5585	72.5035	57.5831	21.6511	9.27867	8.06769
Gene	PIM2	UP	III	mid-late	5.68875	3.86378	3.54591	2.59318	4.80622	0.87878
Gene	MINA	UP	III	mid-late	95.3087	76.9886	74.1973	39.8629	27.9797	15.1043
Gene	KIF20B	UP	III	mid-late	50.154	33.2906	52.0939	16.4821	20.6698	8.06513
Gene	SMC2	UP	III	mid-late	110.325	86.4279	83.2255	41.2975	69.9389	18.7396
Gene	PLK4	UP	III	mid-late	29.6087	40.1316	26.8322	12.0422	20.1807	5.0516
Gene	IKBIP	UP	III	mid-late	10.4747	7.73514	16.1573	3.0376	4.98381	1.79725
Gene	C4orf43	UP	III	mid-late	41.9927	32.6552	33.7471	18.1081	24.8679	7.55584
Gene	HAT1	UP	III	mid-late	203.824	176.666	182.405	53.9454	135.834	38.3856
Gene	VDAC2	UP	III	mid-late	170.192	157.077	149.188	117.634	109.54	35.0379
Gene	OSTC	UP	III	mid-late	29.4727	29.2419	49.8923	9.88988	20.7782	6.07898
Gene	NMI	UP	III	mid-late	7.84286	7.35719	10.4016	3.23077	4.95162	1.74403
Gene	LSM6	UP	III	mid-late	37.6649	37.2585	41.9155	18.9177	16.2461	8.40477
Gene	RPL22L1	UP	III	mid-late	9.78986	9.51333	13.636	6.0899	8.10571	2.37362
Gene	RRM2	UP	IV	late	67.9237	34.7113	33.6775	13.3768	17.6154	0.01
Gene	HIST1H2AJ	UP	IV	late	13.951	10.1294	8.65238	20.5634	11.8205	0.01
Gene	NEK2	UP	IV	late	13.1824	7.76696	5.90729	2.04673	5.03702	0.01
Gene	HIST1H1B	UP	IV	late	10.7462	3.77638	4.33803	7.65638	6.4831	0.01
Gene	GSG2	UP	IV	late	3.72115	2.24653	2.21415	1.66106	2.51941	0.01

Gene	ISL1	UP	IV	late	2.99051	9.57871	5.51527	3.35796	0.809667	0.01
Gene	IGF2BP1	UP	IV	late	2.38499	3.573	3.68521	3.27452	9.29564	0.01
Gene	RGS13	UP	IV	late	1.75441	13.8155	2.21251	4.01955	0.376299	0.01
Gene	POU2F3	UP	IV	late	1.71591	4.43205	2.66264	2.88034	1.65273	0.01
Gene	HOXD4	UP	IV	late	1.62814	2.46504	2.19357	1.43997	0.798633	0.01
Gene	OR51F1	UP	IV	late	1.30658	16.1633	23.1214	15.5836	4.56099	0.01
Gene	PBK	UP	IV	late	45.7326	33.8475	28.9719	9.3	2.79627	0.356567
Gene	EN2	UP	IV	late	1.14653	3.98318	8.5693	2.75683	5.04104	0.01
Gene	IRX3	UP	IV	late	1.05763	7.5178	13.6298	8.5065	6.26942	0.01
Gene	HOXA3	UP	IV	late	0.853364	2.8792	4.51269	5.03597	2.01025	0.01
Gene	HOXA10	UP	IV	late	14.2986	13.262	13.1655	9.21647	6.32746	0.195221
Gene	FOXM1	UP	IV	late	15.9636	7.02385	5.88438	5.44371	3.06383	0.274095
Gene	NPM3	UP	IV	late	24.768	16.7231	12.3669	34.4324	3.97995	0.527561
Gene	NUSAP1	UP	IV	late	68.4066	69.6114	61.3141	25.7069	31.6285	1.52357
Gene	ZWINT	UP	IV	late	40.2918	39.6023	44.9569	10.5538	3.23772	1.12487
Gene	SHCBP1	UP	IV	late	9.82754	3.03586	4.28384	1.84924	1.86887	0.337096
Gene	BZW2	UP	IV	late	93.7738	79.4908	78.0135	45.7159	64.31	4.71446
Gene	C1QBP	UP	IV	late	183.024	53.7375	57.5758	53.7616	46.4965	9.74272
Gene	CENPK	UP	IV	late	15.864	18.5789	15.9905	5.69753	5.20605	1.06669
Gene	NCAPD2	UP	IV	late	46.1647	31.255	23.1355	50.5939	26.312	3.65021
Gene	PPP1R14C	UP	IV	late	39.8659	30.8334	42.4505	35.3236	12.2945	3.46417
Gene	DIRAS3	UP	IV	late	17.4958	14.4257	27.4329	13.0912	7.01398	1.65038
Gene	SNRPC	UP	IV	late	23.2632	17.5368	19.2835	19.124	9.38091	2.38153
Gene	RUNX3	UP	IV	late	1.68475	1.8904	1.93784	2.95664	1.1962	0.174666
Gene	AHCY	UP	IV	late	112.978	109.856	88.7567	127.349	45.3887	11.8844
Gene	RPL10A	UP	IV	late	121.865	82.1178	94.6418	122.828	66.0033	13.1143
Gene	DDT	UP	IV	late	133.629	79.125	78.1742	86.1256	35.7829	14.5749
Gene	ATP5G3	UP	IV	late	353.524	180.254	200.865	175.81	119.22	41.451
Gene	TUBA1C	UP	IV	late	249.878	129.11	169.731	130.388	55.653	30.219
Gene	RRP36	UP	IV	late	9.77024	5.93544	5.93831	8.44073	7.15731	1.26624
Gene	FRAT2	UP	IV	late	3.63699	3.66873	3.36793	3.5385	3.10085	0.509789
Gene	TCF19	UP	IV	late	3.6908	2.58839	2.32772	2.85142	1.37196	0.528475
Gene	BTF3	UP	IV	late	201.885	239.669	248.124	123.032	78.9294	29.1051
Gene	TFAM	UP	IV	late	84.3307	58.4173	55.5112	55.9865	60.0625	12.442
Gene	SH2D4A	UP	IV	late	41.8356	35.3761	39.8931	61.8866	19.2159	6.39088
Gene	TIMM22	UP	IV	late	6.27573	4.5858	4.00044	13.4085	4.13777	0.970344

Gene	RPL19	UP	IV	late	551.298	352.021	422.845	580.13	283.824	86.197
Gene	HNRNPL	UP	IV	late	26.1655	18.5873	16.8161	17.3628	15.8564	4.11959
Gene	YRDC	UP	IV	late	5.63714	5.35632	4.83621	4.37111	3.16713	0.929475
Gene	ECT2	UP	IV	late	59.8977	72.3106	49.2683	50.2722	26.0801	10.212
Gene	NKIRAS2	UP	IV	late	4.0854	4.71841	4.16802	7.84725	8.07757	0.740802
Gene	RPS3A	UP	IV	late	216.163	229.095	255.192	184.507	161.671	42.8927
Gene	GEN1	UP	IV	late	8.63311	12.5139	17.6842	8.07734	7.11824	1.75005
Gene	RPL39	UP	IV	late	41.9559	40.831	63.9783	37.483	33.6771	9.31378
Gene	HSBP1L1	UP	IV	late	10.436	9.88612	10.7106	18.372	11.0324	2.32491
Gene	MRPL36	UP	IV	late	38.1956	38.4832	43.9271	44.201	24.4987	8.95216
Gene	GPR50	UP	V	In Vivo-sp.	168.001	91.8413	54.0289	37.994	29.8306	0.01
Gene	UBE2C	UP	V	In Vivo-sp.	26.2926	20.5681	14.5762	20.7589	26.0457	0.01
Gene	NDC80	UP	V	In Vivo-sp.	20.3097	19.6911	19.6874	13.434	12.2143	0.01
Gene	PITX2	UP	V	In Vivo-sp.	16.5205	11.7094	12.9234	39.2614	6.81938	0.01
Gene	TFAP2A	UP	V	In Vivo-sp.	13.6887	14.3383	18.6789	10.2782	33.6167	0.01
Gene	MCM10	UP	V	In Vivo-sp.	60.8936	27.3915	22.6939	45.8975	38.1117	0.0573954
Gene	HOXC6	UP	V	In Vivo-sp.	10.4127	14.9936	33.9138	24.1339	14.6997	0.01
Gene	HMGA2	UP	V	In Vivo-sp.	9.35744	8.77125	13.0938	2.24705	32.4585	0.01
Gene	SHOX2	UP	V	In Vivo-sp.	8.78579	13.7402	12.6671	7.07075	7.45502	0.01
Gene	HOXC9	UP	V	In Vivo-sp.	8.39442	8.9806	12.5985	24.6084	7.29107	0.01
Gene	DTL	UP	V	In Vivo-sp.	28.9868	17.0238	13.034	13.9234	24.5239	0.0395957
Gene	ESCO2	UP	V	In Vivo-sp.	6.48753	8.55418	4.68786	3.0746	2.14529	0.01
Gene	TROAP	UP	V	In Vivo-sp.	6.4697	7.44579	3.19496	6.343	2.79748	0.01
Gene	SALL4	UP	V	In Vivo-sp.	6.2704	7.0054	10.312	9.42735	38.3165	0.01
Gene	AURKB	UP	V	In Vivo-sp.	6.24624	4.02577	2.88724	3.07322	7.24882	0.01

Gene	GTSE1	UP	V	In Vivo-sp.	5.64082	3.25976	1.42542	2.97378	3.78641	0.01
Gene	TOP2A	UP	V	In Vivo-sp.	95.5566	69.5566	78.0382	22.7828	53.397	0.207085
Gene	DLGAP5	UP	V	In Vivo-sp.	48.0114	28.4895	23.3649	8.22209	20.4484	0.132452
Gene	STC1	UP	V	In Vivo-sp.	35.5457	55.0052	18.2285	27.7961	26.2435	0.103083
Gene	KIF20A	UP	V	In Vivo-sp.	66.3375	25.9775	15.9779	14.4216	18.3878	0.218202
Gene	MMP14	UP	V	In Vivo-sp.	2.74653	5.16968	6.23125	4.7196	5.6929	0.01
Gene	HOXC10	UP	V	In Vivo-sp.	121.246	139.365	246.349	557.574	114.646	0.506434
Gene	UGT3A1	UP	V	In Vivo-sp.	2.31289	11.3586	3.59632	12.3378	6.02621	0.01
Gene	PCSK9	UP	V	In Vivo-sp.	12.3204	6.25378	11.5264	12.5664	5.38087	0.0615409
Gene	KIF4A	UP	V	In Vivo-sp.	17.4081	13.3025	13.2573	7.17383	15.5294	0.0891807
Gene	HOXA7	UP	V	In Vivo-sp.	16.9606	29.0682	20.9978	75.1248	17.295	0.0903434
Gene	MEOX2	UP	V	In Vivo-sp.	67.3222	36.0784	29.7849	12.063	4.81572	0.362828
Gene	CDCA5	UP	V	In Vivo-sp.	12.5225	5.43845	5.0905	9.29233	4.73798	0.0782112
Gene	POU5F1B	UP	V	In Vivo-sp.	13.3495	11.0374	8.74866	16.9463	23.9217	0.0850768
Gene	CRABP1	UP	V	In Vivo-sp.	339.921	14.9986	31.2863	15.8322	398.443	2.25077
Gene	COL3A1	UP	V	In Vivo-sp.	79.1246	283.53	311.694	101.971	71.1639	0.584066
Gene	TPX2	UP	V	In Vivo-sp.	67.9556	35.1121	31.5179	24.3309	40.3852	0.503749
Gene	BUB1B	UP	V	In Vivo-sp.	38.2688	28.247	23.125	16.5024	28.0427	0.285509
Gene	CKAP2L	UP	V	In Vivo-sp.	11.6936	7.42429	8.63179	4.22983	4.1977	0.0878136
Gene	PAX3	UP	V	In Vivo-sp.	27.3951	48.5064	59.8329	69.2617	45.4796	0.210554
Gene	IGFBP2	UP	V	In Vivo-sp.	10.084	3.40274	6.37575	5.7776	2.3003	0.0810349
Gene	DEPDC1	UP	V	In Vivo-sp.	12.6171	8.52833	8.74457	1.43197	1.99782	0.107542

Gene	IGF2BP3	UP	V	In Vivo-sp.	27.4213	21.2582	27.0459	8.31128	41.7383	0.252416
Gene	TGFBI	UP	V	In Vivo-sp.	17.3392	14.2293	24.4925	14.2042	25.3172	0.162101
Gene	BHLHE22	UP	V	In Vivo-sp.	51.7192	81.4688	47.6433	11.6365	10.9782	0.484144
Gene	CCNB2	UP	V	In Vivo-sp.	24.41	14.6754	11.0676	8.69315	11.8165	0.238907
Gene	HJURP	UP	V	In Vivo-sp.	21.2168	9.97079	10.98	11.4688	13.8864	0.207751
Gene	C15orf42	UP	V	In Vivo-sp.	5.2324	3.59423	2.76734	3.91111	3.4773	0.0524508
Gene	CENPF	UP	V	In Vivo-sp.	75.4276	69.9555	62.3877	39.3591	48.6539	0.767844
Gene	CCL2	UP	V	In Vivo-sp.	0.972323	20.3084	54.3725	31.3034	132.319	0.01
Gene	HMMR	UP	V	In Vivo-sp.	136.389	107.355	85.9259	23.2909	21.0234	1.42644
Gene	CRISPLD1	UP	V	In Vivo-sp.	148.678	54.9577	61.2686	19.0555	16.9555	1.76799
Gene	HIST1H2AL	UP	V	In Vivo-sp.	172.839	69.342	46.9111	143.37	31.519	2.17237
Gene	EHF	UP	V	In Vivo-sp.	85.9961	18.0007	6.68984	9.3738	56.4347	1.09612
Gene	TFAP2B	UP	V	In Vivo-sp.	8.01767	73.0748	131.792	250.499	105.609	0.102849
Gene	NCAPH	UP	V	In Vivo-sp.	17.4668	9.25578	7.66365	9.0613	11.0465	0.227263
Gene	PRSS12	UP	V	In Vivo-sp.	110.423	132.287	265.774	196.459	386.21	1.52859
Gene	C12orf48	UP	V	In Vivo-sp.	14.6629	11.7041	14.0704	2.84042	3.95993	0.207019
Gene	EXO1	UP	V	In Vivo-sp.	24.3884	18.3995	12.2557	14.4235	9.6588	0.356697
Gene	NTF3	UP	V	In Vivo-sp.	15.3859	31.024	39.1249	26.2453	15.7193	0.233309
Gene	ASPM	UP	V	In Vivo-sp.	20.851	17.8839	17.2613	4.2674	6.00179	0.33844
Gene	HIST1H4L	UP	V	In Vivo-sp.	43.2057	29.2596	16.329	49.0229	16.8506	0.727696
Gene	KIF23	UP	V	In Vivo-sp.	52.9944	33.3572	34.4975	21.0128	23.5558	0.912453
Gene	PLK1	UP	V	In Vivo-sp.	113.041	43.4324	21.0667	45.4547	18.9813	2.02256

Gene	CLSPN	UP	V	In Vivo-sp.	135.269	102.086	71.6593	79.3456	60.0975	2.45679
Gene	NCAPG	UP	V	In Vivo-sp.	40.0178	39.974	37.1241	12.2641	17.4821	0.740276
Gene	E2F7	UP	V	In Vivo-sp.	25.8608	12.5982	10.356	3.37678	5.74706	0.504315
Gene	ULBP1	UP	V	In Vivo-sp.	5.55176	7.36072	13.0251	2.93999	7.63766	0.114873
Gene	BIRC5	UP	V	In Vivo-sp.	13.8937	7.8656	7.02546	7.40889	6.44015	0.289289
Gene	MLF1IP	UP	V	In Vivo-sp.	69.5974	42.9978	33.0865	16.8462	36.8434	1.46833
Gene	CCNB1	UP	V	In Vivo-sp.	108.536	48.3975	40.1314	36.013	40.4488	2.30836
Gene	KIF18A	UP	V	In Vivo-sp.	19.9034	33.3602	33.5287	11.1867	16.8195	0.516104
Gene	PTTG1	UP	V	In Vivo-sp.	276.41	211.457	152.061	247.161	126.379	7.23857
Gene	SLC38A4	UP	V	In Vivo-sp.	16.7361	21.2497	22.6451	8.54738	3.70812	0.468342
Gene	PLA2G4A	UP	V	In Vivo-sp.	145.342	45.1711	47.3476	40.6997	37.6931	4.12765
Gene	RPRM	UP	V	In Vivo-sp.	126.479	128.432	130.772	227.277	141.903	3.62126
Gene	CNN2	UP	V	In Vivo-sp.	24.7178	22.6634	38.267	56.0998	59.746	0.721037
Gene	TACC3	UP	V	In Vivo-sp.	16.6782	7.60041	6.79504	7.87064	7.96187	0.490735
Gene	MYC	UP	V	In Vivo-sp.	34.9332	25.9304	33.1824	39.4648	36.1505	1.08193
Gene	EZH2	UP	V	In Vivo-sp.	117.525	83.2449	79.0318	44.1198	100.862	3.68769
Gene	FAM54A	UP	V	In Vivo-sp.	26.1768	25.8271	15.5381	26.1853	32.7601	0.834968
Gene	EMP1	UP	V	In Vivo-sp.	136.072	22.0429	96.8045	19.1594	20.36	4.44407
Gene	ANXA2	UP	V	In Vivo-sp.	108.544	107.312	141.602	245.742	171.926	3.57445
Gene	VGLL3	UP	V	In Vivo-sp.	19.2118	176.143	283.656	69.3842	81.5957	0.640122
Gene	ADAMTS3	UP	V	In Vivo-sp.	44.3158	49.0586	33.1418	12.7133	11.2617	1.48938
Gene	KIF11	UP	V	In Vivo-sp.	39.4187	32.1325	33.9016	7.66443	9.42191	1.41854

Gene	NOP16	UP	V	In Vivo-sp.	119.705	31.1811	38.5966	49.249	34.3536	4.33946
Gene	ORC6	UP	V	In Vivo-sp.	17.0541	8.87666	9.12414	4.94165	8.52625	0.636943
Gene	CDC25A	UP	V	In Vivo-sp.	8.59933	5.03112	5.10595	2.13583	7.31989	0.332983
Gene	DEPDC1B	UP	V	In Vivo-sp.	28.5332	15.6545	12.1625	13.0113	8.84481	1.11197
Gene	CDKN1A	UP	V	In Vivo-sp.	162.239	50.0483	109.088	166.838	366.817	6.45959
Gene	MYL9	UP	V	In Vivo-sp.	15.7454	22.4064	32.4193	92.6977	59.0983	0.628481
Gene	HIST1H2BG	UP	V	In Vivo-sp.	98.3281	51.1603	41.292	54.5789	58.9616	4.0352
Gene	DUSP4	UP	V	In Vivo-sp.	4.63833	5.75862	6.79825	2.44407	7.06084	0.192206
Gene	CENPE	UP	V	In Vivo-sp.	40.7409	45.7842	44.1144	11.373	9.03349	1.69933
Gene	CDKN3	UP	V	In Vivo-sp.	129.197	74.7445	62.3931	33.0165	35.2918	5.39401
Gene	CDCA7	UP	V	In Vivo-sp.	38.8736	38.7448	28.6864	29.3394	26.3291	1.62365
Gene	APOBEC3C	UP	V	In Vivo-sp.	56.728	23.1655	18.6399	53.6826	32.3335	2.3703
Gene	SAMD5	UP	V	In Vivo-sp.	14.2556	22.6343	30.8561	8.3921	12.0385	0.598459
Gene	CPXM2	UP	V	In Vivo-sp.	3.35747	3.38601	15.7358	20.9758	21.4344	0.146794
Gene	IFI30	UP	V	In Vivo-sp.	30.2539	6.94506	17.7092	25.3268	24.0858	1.34233
Gene	IQGAP3	UP	V	In Vivo-sp.	2.93289	2.0159	1.80749	1.73145	2.56282	0.130503
Gene	TBX15	UP	V	In Vivo-sp.	11.1081	23.0464	26.6229	16.2065	17.2827	0.507584
Gene	PRC1	UP	V	In Vivo-sp.	84.0382	45.7975	35.3903	27.2384	16.4179	3.92523
Gene	CHEK1	UP	V	In Vivo-sp.	71.4533	37.9062	38.1949	16.3601	83.7985	3.47362
Gene	TIMELESS	UP	V	In Vivo-sp.	19.4481	9.3909	6.10526	7.00416	6.90291	0.972091
Gene	HIST1H2BF	UP	V	In Vivo-sp.	23.2125	14.6058	12.0052	41.1865	37.1576	1.16908
Gene	SHMT2	UP	V	In Vivo-sp.	22.8644	10.0369	8.52256	15.6227	13.3952	1.15572

Gene	CDC6	UP	V	In Vivo-sp.	59.3318	48.7959	31.6351	40.7251	58.6795	3.00162
Gene	RUVBL1	UP	V	In Vivo-sp.	62.4727	26.2119	26.5763	34.4336	39.832	3.19047
Gene	TUBB6	UP	V	In Vivo-sp.	48.3448	17.7444	28.3849	19.2701	13.2977	2.51189
Gene	AURKA	UP	V	In Vivo-sp.	77.2282	28.4696	20.1734	23.5345	21.1846	4.04648
Gene	MCM6	UP	V	In Vivo-sp.	78.3917	30.9333	24.5329	29.1072	25.0341	4.28572
Gene	ARHGAP11A	UP	V	In Vivo-sp.	27.6454	18.3921	18.1419	8.11421	14.5429	1.53727
Gene	RCN1	UP	V	In Vivo-sp.	301.76	488.026	624.437	173.809	208.997	17.0282
Gene	UBE2T	UP	V	In Vivo-sp.	19.708	16.0972	12.8533	13.59	12.0443	1.11462
Gene	FANCI	UP	V	In Vivo-sp.	17.7743	13.8893	9.55464	5.07263	14.5578	1.02999
Gene	SLC35F2	UP	V	In Vivo-sp.	11.6966	4.89232	4.48906	5.02856	7.3067	0.681715
Gene	KPNA2	UP	V	In Vivo-sp.	134.673	88.5483	110.391	49.2104	68.0643	7.96876
Gene	LIN28B	UP	V	In Vivo-sp.	5.06315	10.3177	8.11932	2.91102	21.2519	0.299926
Gene	ARHGAP11B	UP	V	In Vivo-sp.	13.477	10.36	10.9603	9.66591	15.7039	0.800354
Gene	MME	UP	V	In Vivo-sp.	15.3941	40.5723	101.332	50.4338	55.2236	0.915839
Gene	BRIP1	UP	V	In Vivo-sp.	4.20666	6.95376	7.44467	4.55259	6.09505	0.250612
Gene	H2AFZ	UP	V	In Vivo-sp.	716.116	393.943	234.995	230.262	374.543	43.5219
Gene	HIST1H2BC	UP	V	In Vivo-sp.	120.714	57.6159	44.0988	98.2822	97.316	7.3842
Gene	NPM1	UP	V	In Vivo-sp.	3093.44	1992.98	2198.19	1572.86	2273.42	189.242
Gene	PCDH20	UP	V	In Vivo-sp.	46.6465	42.5374	47.6329	27.3472	24.1751	2.86584
Gene	GINS2	UP	V	In Vivo-sp.	11.4231	6.90645	5.22578	8.52079	7.22666	0.705294
Gene	ATP5B	UP	V	In Vivo-sp.	1626.67	1090.56	617.825	773.749	901.783	100.772
Gene	MND1	UP	V	In Vivo-sp.	46.2336	41.9629	38.4333	20.5844	59.3064	2.89059

Gene	HIST1H2BK	UP	V	In Vivo-sp.	47.1777	27.8853	28.3708	42.9177	81.1134	2.98511
Gene	CCND1	UP	V	In Vivo-sp.	868.096	347.054	378.198	254.226	483.576	54.9532
Gene	BACE2	UP	V	In Vivo-sp.	22.2957	17.9833	15.4766	26.4468	20.334	1.41254
Gene	MCM2	UP	V	In Vivo-sp.	9.56802	6.34124	7.10422	10.2702	7.18523	0.60674
Gene	NRG1	UP	V	In Vivo-sp.	60.5607	54.7975	54.3908	77.7245	47.022	3.87686
Gene	FEN1	UP	V	In Vivo-sp.	27.5539	9.91141	13.2553	12.7137	11.5315	1.81057
Gene	RAN	UP	V	In Vivo-sp.	937.684	696.123	514.973	420.815	426.751	61.8178
Gene	NME1	UP	V	In Vivo-sp.	391.448	226.766	247.023	336.177	348.643	25.8333
Gene	TOM1L1	UP	V	In Vivo-sp.	62.5994	43.2982	60.5992	38.847	70.5696	4.17524
Gene	RPS5	UP	V	In Vivo-sp.	116.071	45.5971	54.6065	89.5029	92.2993	7.76821
Gene	CDCA4	UP	V	In Vivo-sp.	4.52882	2.80186	4.26334	3.22828	2.46591	0.308718
Gene	RPL13A	UP	V	In Vivo-sp.	519.595	327.146	412.173	908.186	208.074	35.8127
Gene	WEE1	UP	V	In Vivo-sp.	56.2737	91.2919	86.6327	55.3147	136.28	3.89242
Gene	CDCA8	UP	V	In Vivo-sp.	5.12941	2.87479	2.52328	2.56177	3.72519	0.361763
Gene	ZYG11A	UP	V	In Vivo-sp.	3.36209	2.93086	4.47341	4.78372	2.49475	0.238474
Gene	PRR11	UP	V	In Vivo-sp.	9.78543	8.84473	7.68104	9.35224	8.70445	0.696149
Gene	MRPS24	UP	V	In Vivo-sp.	65.2172	25.7764	19.7131	34.1901	29.6808	4.6613
Gene	FRRS1	UP	V	In Vivo-sp.	4.02564	5.44364	4.9398	3.7331	5.87957	0.287863
Gene	HMCN1	UP	V	In Vivo-sp.	5.62332	33.9016	56.744	24.1287	17.0525	0.403383
Gene	ANTXR2	UP	V	In Vivo-sp.	155.264	139.014	233.867	151.291	141.636	11.2161
Gene	GAS2L3	UP	V	In Vivo-sp.	36.9112	51.4366	86.0908	39.9561	79.1955	2.67765
Gene	MCM3	UP	V	In Vivo-sp.	30.5688	17.7822	14.8124	16.0687	20.7556	2.23304

Gene	LAMC1	UP	V	In Vivo-sp.	195.953	65.6484	113.892	110.401	144.157	14.3455
Gene	EPHB4	UP	V	In Vivo-sp.	7.00761	2.70695	3.3359	5.11084	3.77004	0.515057
Gene	TES	UP	V	In Vivo-sp.	50.7504	18.8287	61.2314	34.2535	59.8021	3.74314
Gene	HMGA1	UP	V	In Vivo-sp.	14.0441	5.33823	4.90042	11.4345	17.1666	1.04358
Gene	MDK	UP	V	In Vivo-sp.	31.0077	100.962	67.222	170.206	225.538	2.30471
Gene	RPS3	UP	V	In Vivo-sp.	522.246	227.072	292.326	335.529	423.836	38.9852
Gene	EIF4A1	UP	V	In Vivo-sp.	58.4896	41.8061	39.8256	49.7463	39.0415	4.54035
Gene	TCF3	UP	V	In Vivo-sp.	10.3253	12.8196	11.678	20.4622	13.4511	0.804504
Gene	PGD	UP	V	In Vivo-sp.	121.497	65.8934	46.0013	94.4892	89.3587	9.53391
Gene	DLX1	UP	V	In Vivo-sp.	33.5965	23.9184	36.1255	15.7343	47.8187	2.66953
Gene	C11orf82	UP	V	In Vivo-sp.	3.43911	3.5294	3.91702	2.07888	2.51231	0.273954
Gene	TNFRSF10D	UP	V	In Vivo-sp.	7.41101	4.61437	9.08977	11.5163	14.6577	0.600657
Gene	PFAS	UP	V	In Vivo-sp.	5.23025	3.64273	2.86941	3.32943	2.64446	0.427514
Gene	TRIP6	UP	V	In Vivo-sp.	14.6646	8.00571	13.8314	21.9806	20.625	1.2056
Gene	FAM60A	UP	V	In Vivo-sp.	36.2003	61.138	56.6053	16.2652	54.8577	3.03351
Gene	SLC1A5	UP	V	In Vivo-sp.	17.895	11.1998	12.3634	13.5204	10.9483	1.51515
Gene	HNRNPAB	UP	V	In Vivo-sp.	186.841	122.811	107.356	136.503	120.798	15.9423
Gene	CAV1	UP	V	In Vivo-sp.	48.7218	65.4269	77.972	77.8037	49.6198	4.16963
Gene	EEF1G	UP	V	In Vivo-sp.	164.619	75.7462	82.8243	95.4913	101.864	14.1186
Gene	ASS1	UP	V	In Vivo-sp.	24.3398	12.9584	28.037	50.5036	46.0772	2.09856
Gene	HK2	UP	V	In Vivo-sp.	25.7068	26.0752	32.0365	23.1147	58.7162	2.24008
Gene	AIMP2	UP	V	In Vivo-sp.	42.3018	20.182	23.0738	31.0613	28.561	3.70062

Gene	LDLR	UP	V	In Vivo-sp.	19.5075	13.4213	28.066	13.6798	20.3026	1.71164
Gene	LMNB2	UP	V	In Vivo-sp.	74.233	61.1228	46.9124	104.73	55.7122	6.53523
Gene	RND3	UP	V	In Vivo-sp.	121.711	651.884	1132.11	654.261	745.021	10.9424
Gene	KIF4B	UP	V	In Vivo-sp.	3.56514	2.88438	2.12294	1.43442	2.42323	0.323425
Gene	HMGB3	UP	V	In Vivo-sp.	51.9207	37.2674	32.8566	26.7717	45.5672	4.72252
Gene	RPS2	UP	V	In Vivo-sp.	177.73	134.703	181.906	315.109	146.427	16.3648
Gene	GCH1	UP	V	In Vivo-sp.	54.0505	94.754	113.816	64.0705	93.4712	5.06895
Gene	CD44	UP	V	In Vivo-sp.	147.795	73.2063	367.135	486.376	667.273	13.9876
Gene	RBM3	UP	V	In Vivo-sp.	95.0636	69.5518	86.7933	67.8293	86.1157	9.00628
Gene	PAICS	UP	V	In Vivo-sp.	166.026	126.455	121.264	94.7892	150.716	16.0915
Gene	THOC3	UP	V	In Vivo-sp.	112.283	58.5662	59.4798	77.8434	109.005	10.992
Gene	WDR3	UP	V	In Vivo-sp.	33.1667	26.8233	21.0342	23.8481	32.7516	3.31458
Gene	TNFRSF10B	UP	V	In Vivo-sp.	20.2119	12.6159	24.007	15.4313	25.9976	2.02987
Gene	TOMM40	UP	V	In Vivo-sp.	18.0872	8.62853	7.99908	24.581	17.7942	1.82048
Gene	SOSTDC1	UP	V	In Vivo-sp.	7.1973	26.2917	46.3648	17.1222	15.8604	0.73739
Gene	NME1-NME2	UP	V	In Vivo-sp.	57.4525	46.314	56.2914	86.7215	72.5527	5.94743
Gene	S100A10	UP	V	In Vivo-sp.	159.995	105.977	193.928	253.376	239.706	16.7199
Gene	HIST1H4H	UP	V	In Vivo-sp.	225.957	146.164	114.295	303.404	159.208	23.9012
Gene	DLX6	UP	V	In Vivo-sp.	6.83206	8.45091	9.99877	5.96709	6.83297	0.733385
Gene	RAB11FIP1	UP	V	In Vivo-sp.	3.79085	2.47661	3.11519	3.62593	3.52672	0.413389
Gene	PNPLA3	UP	V	In Vivo-sp.	8.70305	13.5841	9.39988	20.1536	14.7881	0.95006
Gene	IQGAP2	UP	V	In Vivo-sp.	25.9119	39.9	29.4587	24.7026	51.0705	2.83271

Gene	VCL	UP	V	In Vivo-sp.	80.5376	62.7941	97.5129	72.4734	93.2944	8.82424
Gene	DLX5	UP	V	In Vivo-sp.	13.2509	11.3824	21.3607	14.9266	16.0672	1.4523
Gene	NUP93	UP	V	In Vivo-sp.	90.8975	65.2202	53.4513	61.5296	76.2732	9.97223
Gene	CCT5	UP	V	In Vivo-sp.	571.353	276.598	310.445	416.315	344.005	63.3424
Gene	TPM2	UP	V	In Vivo-sp.	208.778	173.683	399.163	502.304	598.166	23.5012
Gene	TXNRD1	UP	V	In Vivo-sp.	97.6514	46.0423	71.0674	52.5192	116.991	11.1543
Gene	KIRREL	UP	V	In Vivo-sp.	15.3736	17.8918	33.6473	33.5737	53.477	1.7794
Gene	PTX3	UP	V	In Vivo-sp.	3.13062	3.91967	8.03848	4.37237	27.6577	0.363735
Gene	EIF4A3	UP	V	In Vivo-sp.	19.1711	10.4527	13.0952	8.94506	11.962	2.23028
Gene	PSMC1	UP	V	In Vivo-sp.	39.7111	25.011	23.5069	20.3162	25.7675	4.62271
Gene	QPRT	UP	V	In Vivo-sp.	8.30471	13.1508	17.6789	40.8813	29.7716	0.977179
Gene	ARHGAP18	UP	V	In Vivo-sp.	33.0074	53.4172	64.3758	28.9659	76.2702	3.88447
Gene	FSTL1	UP	V	In Vivo-sp.	51.2382	52.3561	188.553	183.311	263.618	6.11298
Gene	PTBP1	UP	V	In Vivo-sp.	60.5047	35.6162	41.6901	76.9687	51.4812	7.25312
Gene	AIFM1	UP	V	In Vivo-sp.	50.3094	33.0688	31.9348	36.1932	40.1244	6.03396
Gene	BEND7	UP	V	In Vivo-sp.	16.3371	13.0197	15.2441	11.3007	22.2701	1.9607
Gene	C20orf24	UP	V	In Vivo-sp.	17.3931	10.0526	9.48661	8.88681	13.2252	2.09426
Gene	GNL3	UP	V	In Vivo-sp.	166.069	125.309	118.871	113.024	135.983	20.0042
Gene	PFN1	UP	V	In Vivo-sp.	170.727	90.8074	94.5626	243.481	425.117	20.6538
Gene	TGIF2	UP	V	In Vivo-sp.	1.73904	2.69441	3.49785	3.08187	4.40262	0.21131
Gene	TP53	UP	V	In Vivo-sp.	35.0134	49.7742	47.1056	69.5221	82.2238	4.29679
Gene	ZNF618	UP	V	In Vivo-sp.	12.3809	10.5687	12.8802	11.6869	16.158	1.52528

Gene	NOP10	UP	V	In Vivo-sp.	53.9396	30.1692	31.7266	40.2571	32.527	6.72937
Gene	MET	UP	V	In Vivo-sp.	11.6835	9.25143	7.96688	7.18881	10.0786	1.46369
Gene	PSMA6	UP	V	In Vivo-sp.	61.4076	63.5669	62.1744	31.4064	52.7171	7.70129
Gene	SKP2	UP	V	In Vivo-sp.	35.8401	37.7341	37.9483	36.1575	44.0162	4.54427
Gene	TRIM38	UP	V	In Vivo-sp.	16.4925	19.2741	22.5711	11.7646	10.3533	2.09439
Gene	TMEM97	UP	V	In Vivo-sp.	24.5294	32.2246	31.2532	40.9888	35.4439	3.12817
Gene	SLC25A6	UP	V	In Vivo-sp.	114.62	65.2636	71.1863	115.723	72.5243	14.6885
Gene	CDK4	UP	V	In Vivo-sp.	59.1986	44.8965	48.1175	71.9145	57.6926	7.59197
Gene	CKS1B	UP	V	In Vivo-sp.	32.9855	19.8976	23.9299	20.5928	21.0941	4.23728
Gene	KARS	UP	V	In Vivo-sp.	90.6459	48.936	53.7038	102.221	75.0177	11.7281
Gene	PDIA4	UP	V	In Vivo-sp.	33.8398	25.1147	32.8895	22.5205	25.9336	4.43054
Gene	PRDX4	UP	V	In Vivo-sp.	33.0819	17.9502	28.8129	18.4461	18.1551	4.35668
Gene	IMPDH2	UP	V	In Vivo-sp.	27.1541	19.6063	20.1518	30.5466	19.2778	3.58688
Gene	TRIM58	UP	V	In Vivo-sp.	4.14175	9.44159	14.9425	9.65581	3.08982	0.548857
Gene	PSMA4	UP	V	In Vivo-sp.	137.221	108.639	113.22	73.9211	135.735	18.1979
Gene	RPL23	UP	V	In Vivo-sp.	444.979	281.943	330.992	311.318	444.304	59.2155
Gene	THG1L	UP	V	In Vivo-sp.	15.9077	11.199	12.1715	13.5302	11.3425	2.11972
Gene	HAUS8	UP	V	In Vivo-sp.	11.6016	6.52222	12.3973	9.05673	10.4837	1.55167
Gene	GNB2L1	UP	V	In Vivo-sp.	192.927	122.258	144.074	221.826	178.215	25.947
Gene	ALDH18A1	UP	V	In Vivo-sp.	21.9507	15.6481	28.1239	34.9331	37.5108	2.95461
Gene	KIF15	UP	V	In Vivo-sp.	8.54514	11.1471	9.17069	6.91384	10.7312	1.1713
Gene	PPRC1	UP	V	In Vivo-sp.	7.72133	6.32984	7.20134	9.24973	7.40224	1.06272

Gene	SERPINH1	UP	V	In Vivo-sp.	19.8951	42.869	63.8449	125.355	60.2873	2.76043
Gene	LIPG	UP	V	In Vivo-sp.	2.35573	1.97663	7.52905	11.401	9.38816	0.328435
Gene	APEX1	UP	V	In Vivo-sp.	152.724	165.921	136.249	192.072	196.643	21.5629
Gene	POLR1E	UP	V	In Vivo-sp.	14.7691	9.70834	11.5011	13.178	13.0281	2.08935
Gene	CASP8	UP	V	In Vivo-sp.	20.881	17.3275	23.1926	15.3763	14.2257	2.95717
Gene	IER3	UP	V	In Vivo-sp.	41.6541	129.09	215.885	160.216	470.223	5.89908
Gene	CARM1	UP	V	In Vivo-sp.	4.81228	3.23987	3.34743	7.93859	5.25346	0.68435
Gene	PPIA	UP	V	In Vivo-sp.	2936.24	1912.71	2043.57	2776.3	2793.36	420.61
Gene	RSL1D1	UP	V	In Vivo-sp.	784.471	453.194	497.704	476.704	821.255	112.493
Gene	PTGFRN	UP	V	In Vivo-sp.	20.4905	17.9145	28.5681	55.5302	42.9111	2.93909
Gene	VCAM1	UP	V	In Vivo-sp.	9.4041	18.6866	20.3367	14.1879	26.4526	1.35063
Gene	RPLP1	UP	V	In Vivo-sp.	27.7005	22.34	20.5083	33.4227	22.9623	3.99333
Gene	ABCC1	UP	V	In Vivo-sp.	7.34133	9.88903	8.77927	11.048	15.7386	1.05851
Gene	MYD88	UP	V	In Vivo-sp.	7.74832	9.86048	11.5634	15.3695	14.5197	1.12474
Gene	RPLP0	UP	V	In Vivo-sp.	55.8695	54.5592	82.5033	60.4164	42.8789	8.12915
Gene	PYGL	UP	V	In Vivo-sp.	15.2369	17.777	18.2736	16.0897	28.333	2.234
Gene	ZC3HAV1L	UP	V	In Vivo-sp.	6.87606	11.1647	13.8127	13.9633	8.34867	1.02337
Gene	GARS	UP	V	In Vivo-sp.	355.088	273.222	276.426	273.015	218.419	53.7516
Gene	EFNA5	UP	V	In Vivo-sp.	92.3827	151.259	364.528	627.875	553.877	14.0011
Gene	SPSB4	UP	V	In Vivo-sp.	2.75669	4.80398	5.72808	3.58185	6.21164	0.421499
Gene	ARPC5	UP	V	In Vivo-sp.	199.167	155.471	181.982	148.204	141.46	30.7753
Gene	MTCH2	UP	V	In Vivo-sp.	142.521	104.126	110.662	116.53	99.5442	22.1168

Gene	QARS	UP	V	In Vivo-sp.	40.6774	34.3879	30.6363	58.2473	57.8522	6.37415
Gene	F2R	UP	V	In Vivo-sp.	5.83953	6.23843	11.34	4.21893	17.9349	0.937587
Gene	RPL35A	UP	V	In Vivo-sp.	1154.28	784.277	1009.2	1352.32	1503.51	186.064
Gene	LGI2	UP	V	In Vivo-sp.	5.00387	17.645	20.2569	14.778	9.49157	0.820346
Gene	ATF5	UP	V	In Vivo-sp.	12.3986	17.888	23.334	22.509	24.6251	2.0544
Gene	RCC1	UP	V	In Vivo-sp.	12.8049	16.6399	10.0913	10.3453	11.1405	2.14253
Gene	RPL3	UP	V	In Vivo-sp.	190	135.047	142.954	377.283	329.362	32.461
Gene	PRRC1	UP	V	In Vivo-sp.	92.9342	179.455	224.381	264.622	355.309	15.9847
Gene	EIF3E	UP	V	In Vivo-sp.	319.364	364.457	384.219	283.011	250.808	55.4076
Gene	MAP7D3	UP	V	In Vivo-sp.	64.7785	90.8351	136.95	91.3686	121.913	11.2961
Gene	LMNA	UP	V	In Vivo-sp.	25.076	22.8372	37.4107	53.8689	30.2376	4.38147
Gene	HCCS	UP	V	In Vivo-sp.	40.4146	31.1773	43.1795	32.9286	39.1226	7.11632
Gene	ILF2	UP	V	In Vivo-sp.	118.166	111.588	112.296	119.427	222.273	20.8786
Gene	TRIM5	UP	V	In Vivo-sp.	18.1471	28.3937	36.0837	24.268	35.9624	3.25084
Gene	CDK2	UP	V	In Vivo-sp.	9.57382	11.003	12.1385	8.84536	9.77173	1.72285
Gene	PPIB	UP	V	In Vivo-sp.	32.8106	27.5029	35.5219	49.2308	42.8019	6.20993
Gene	NANP	UP	V	In Vivo-sp.	3.1191	3.40219	4.77728	2.70523	5.82398	0.596732
Gene	MYL12A	UP	V	In Vivo-sp.	161.65	162.382	220.63	141.096	250.19	31.633
Gene	GANAB	UP	V	In Vivo-sp.	66.6052	61.8547	66.2063	96.3314	97.9629	13.1384
Gene	WWTR1	UP	V	In Vivo-sp.	53.3592	68.3146	79.4788	64.3086	69.2407	10.8647
Gene	HIST1H2BD	UP	V	In Vivo-sp.	21.3516	25.1165	21.0908	18.5673	45.252	4.38966
Gene	CCT2	UP	V	In Vivo-sp.	441.093	598.321	559.056	536.697	874.731	91.9126

Gene	RCC2	UP	V	In Vivo-sp.	30.6016	26.5352	27.3062	28.2217	26.0221	6.4212
Gene	DAB1	UP	V	In Vivo-sp.	33.5911	29.8372	34.5392	31.9306	37.7054	7.13458
Gene	NONO	UP	V	In Vivo-sp.	392.522	585.89	464.895	963.63	787.283	83.4359
Gene	FKBP7	UP	V	In Vivo-sp.	10.9471	23.7497	29.6741	15.7601	14.6037	2.36697
Gene	SLC4A2	UP	V	In Vivo-sp.	113.757	135.884	138.776	645.763	129.832	25.4563
Gene	RPS24	UP	V	In Vivo-sp.	523.751	539.258	663.687	734.042	793.143	119.19
Gene	RREB1	UP	V	In Vivo-sp.	4.84307	5.67687	6.54606	12.5195	8.24031	1.10517
Gene	RPL26	UP	V	In Vivo-sp.	444.884	411.164	481.227	426.005	602.559	102.031
Gene	TRIM6	UP	V	In Vivo-sp.	1.97486	5.99592	5.36575	3.71023	3.2228	0.45509
Gene	TRAF5	UP	V	In Vivo-sp.	16.5976	29.558	45.5053	24.7671	62.6739	4.02022
Gene	CYR61	UP	V	In Vivo-sp.	13.9068	86.243	134.98	34.9683	151.685	3.37694
Gene	GNL2	UP	V	In Vivo-sp.	106.103	113.646	119.647	129.087	163.337	26.2992
Gene	GRIA2	DOWN	I	early	0.01	354.062	374.944	357.818	407.833	521.085
Gene	CFH	DOWN	I	early	0.0058227	23.1134	45.2783	20.9704	12.8457	17.76
Gene	PCDH15	DOWN	I	early	0.01	24.684	24.5944	6.65492	13.6352	20.5292
Gene	ZNF711	DOWN	I	early	0.0201074	19.8557	28.6272	9.22222	35.5077	26.1322
Gene	SOX6	DOWN	I	early	0.0186252	6.50441	15.3244	13.1577	6.38765	18.863
Gene	BEND5	DOWN	I	early	0.01	3.31567	5.91994	3.47907	7.37857	10.029
Gene	CCND2	DOWN	I	early	0.0630804	47.7283	114.698	57.9708	154.356	60.3871
Gene	CNTN4	DOWN	I	early	0.01	17.2732	3.31116	14.6524	13.9653	9.56171
Gene	SLC24A5	DOWN	I	early	0.0176812	5.03554	11.4212	4.16837	6.01453	15.9749
Gene	PALMD	DOWN	I	early	0.01	6.33658	7.85717	5.9967	2.31607	7.67324
Gene	GYPB	DOWN	I	early	0.01	0.132516	0.0929535	0.149752	0.120879	7.35409
Gene	FBXL7	DOWN	I	early	0.01	5.98913	7.82124	6.93121	5.96442	7.22009
Gene	MYRIP	DOWN	I	early	0.01	3.55395	15.1314	13.7215	7.37838	6.10141
Gene	EPHA5	DOWN	I	early	0.01	6.71715	11.7345	3.61644	2.37013	5.7194
Gene	MAMLD1	DOWN	I	early	0.01	2.9897	13.2141	6.74256	4.40601	5.6522
Gene	DTX4	DOWN	I	early	0.01	0.62849	1.57131	3.7131	2.5181	4.74818

Gene	GLDC	DOWN	I	early	0.01	1.9029	1.25035	3.57038	12.46	4.6788
Gene	ITGB8	DOWN	I	early	0.0851869	11.9084	43.5265	13.9098	10.1668	37.9503
Gene	CBLN2	DOWN	I	early	0.01	11.2268	12.4819	6.03247	1.26015	4.24101
Gene	SEMA4A	DOWN	I	early	0.01	0.757138	1.67794	1.22754	3.73746	4.10999
Gene	CFHR1	DOWN	I	early	0.01	4.63711	9.20523	4.94535	2.48372	3.9308
Gene	ARSE	DOWN	I	early	0.01	0.0975371	0.0149941	1.21649	0.251915	3.82609
Gene	BCHE	DOWN	I	early	0.0182178	6.79723	10.5589	4.82174	5.252	6.47425
Gene	MARCKS	DOWN	I	early	0.2105	106.278	190.258	38.4064	64.737	74.7031
Gene	RALYL	DOWN	I	early	0.0445581	35.1605	45.1874	16.4473	4.4325	15.7254
Gene	RNF150	DOWN	I	early	0.01	1.23574	2.03356	2.82371	3.11706	3.42567
Gene	CD274	DOWN	I	early	0.0128343	0.475651	5.116	1.50784	8.91543	3.9491
Gene	SPI1	DOWN	I	early	0.01	0.674549	1.08744	3.41111	0.467221	2.92034
Gene	GRID2	DOWN	I	early	0.0212415	10.7892	8.6364	7.63187	2.46232	5.7816
Gene	PLD5	DOWN	I	early	0.0551761	10.4315	15.4278	28.6142	20.5484	13.3698
Gene	PCDHB11	DOWN	I	early	0.0216993	0.549718	0.338518	0.676285	1.72155	4.77847
Gene	MBNL3	DOWN	I	early	0.0221563	2.74971	2.79094	1.68093	4.67832	3.90678
Gene	ODZ1	DOWN	I	early	0.0206027	2.98481	3.032	2.19493	5.47596	3.53059
Gene	SYNPR	DOWN	I	early	0.257258	10.3422	59.2308	35.1746	89.9933	40.6105
Gene	PARD3B	DOWN	I	early	0.0702041	6.35282	16.5522	9.66499	15.5275	10.6257
Gene	ADCY1	DOWN	I	early	0.108854	19.0039	8.99356	6.09363	5.9588	15.9204
Gene	KLF9	DOWN	I	early	0.0454573	1.72545	4.1089	2.54177	2.37186	6.13218
Gene	HLA-DQB1	DOWN	I	early	0.0325952	1.66846	1.60899	0.498474	2.31496	4.28405
Gene	MYEF2	DOWN	I	early	0.176918	12.172	24.8062	6.64252	34.4451	22.3879
Gene	NLGN4X	DOWN	I	early	0.0474034	3.70646	3.68716	2.1679	4.58623	5.75744
Gene	CACHD1	DOWN	I	early	0.0980909	3.05904	13.5962	11.125	39.1217	11.6939
Gene	BICC1	DOWN	I	early	0.0233148	1.76364	4.42979	1.62462	5.35341	2.74891
Gene	FREM1	DOWN	I	early	0.0263838	0.919993	3.05122	6.58566	6.16956	3.01624
Gene	NLGN4Y	DOWN	I	early	0.131228	4.49989	10.0324	12.6143	17.6126	12.2263
Gene	LIX1	DOWN	I	early	0.100117	2.75974	3.13412	2.46412	6.46147	9.21703
Gene	VCAN	DOWN	I	early	0.901847	45.4561	51.4656	57.9182	110.931	79.6997
Gene	ST6GALNAC5	DOWN	I	early	0.0917698	11.008	29.8271	23.6837	20.9511	7.87468
Gene	YAP1	DOWN	I	early	0.146063	3.86298	15.7354	10.5821	17.2487	12.1054
Gene	SHC3	DOWN	I	early	0.130222	4.04654	2.99671	6.7362	4.85482	10.6849
Gene	KCNH1	DOWN	I	early	0.0880702	2.78622	3.06495	4.01666	3.22433	6.82289
Gene	HSPA12A	DOWN	I	early	0.279483	6.38005	12.2798	13.5844	10.5477	19.2368

Gene	PLAC8L1	DOWN	I	early	0.103829	2.36199	1.92055	3.92262	10.4614	6.80793
Gene	DDX26B	DOWN	I	early	0.0478164	3.72463	3.24919	1.38817	2.06964	3.12564
Gene	ABCA1	DOWN	I	early	0.160608	4.92941	8.03599	3.59957	13.4696	10.2526
Gene	RERG	DOWN	I	early	0.245957	22.2937	28.1489	14.0851	24.5883	14.4432
Gene	SAMD9L	DOWN	I	early	0.281895	11.1722	11.9333	11.5289	24.3103	15.9527
Gene	SYNPO	DOWN	I	early	0.302843	6.06296	10.9354	27.0055	12.9499	16.7791
Gene	TRPS1	DOWN	I	early	0.627294	23.9342	43.6454	45.5093	27.4369	33.7636
Gene	PARP8	DOWN	I	early	0.533842	36.9645	21.7019	100.99	22.6347	27.9403
Gene	C3orf70	DOWN	I	early	0.27453	5.89281	16.39	14.0149	13.0577	13.4573
Gene	DAPK2	DOWN	I	early	0.101248	1.64892	1.25316	1.2952	1.01806	4.91761
Gene	TUB	DOWN	I	early	0.19871	2.55402	3.57	3.33324	6.59563	8.91369
Gene	FLRT3	DOWN	I	early	0.218783	6.90769	17.7899	3.55049	27.088	9.56801
Gene	C9orf131	DOWN	I	early	0.0880231	0.394346	1.37204	0.606061	0.723304	3.72817
Gene	ASAP2	DOWN	I	early	0.353653	3.98873	11.0869	6.75763	8.69739	14.5356
Gene	MT1F	DOWN	I	early	0.194977	6.14536	3.88046	4.22425	2.06223	7.96158
Gene	ABAT	DOWN	I	early	0.949596	13.1601	18.1887	15.7203	18.3732	37.202
Gene	OLFM2	DOWN	I	early	0.825789	8.24931	17.747	9.00081	10.3407	32.1772
Gene	MAST4	DOWN	I	early	0.557037	7.23179	19.5849	16.6732	33.4948	21.3564
Gene	AIG1	DOWN	I	early	0.775464	24.325	30.6765	23.7309	40.6278	27.9024
Gene	S100A8	DOWN	I	early	0.124429	0.423793	0.344591	1.26119	15.1243	4.46536
Gene	GEM	DOWN	I	early	0.138764	2.66912	13.9923	4.10798	2.55192	4.92059
Gene	SESN3	DOWN	I	early	2.05919	28.4167	73.0975	34.183	68.4601	72.6783
Gene	LEF1	DOWN	I	early	0.606956	11.7937	10.6175	6.46113	47.2402	21.12
Gene	DCLK2	DOWN	I	early	0.466139	4.87593	10.4667	11.6749	12.3147	16.158
Gene	ADCY2	DOWN	I	early	1.12893	16.9709	28.0896	35.7318	42.1515	37.5328
Gene	ARRDC4	DOWN	I	early	0.510382	5.33855	13.9765	7.33427	22.0637	15.5004
Gene	ZNF660	DOWN	I	early	0.228419	6.95816	7.88158	2.98757	8.18816	6.92972
Gene	USP49	DOWN	I	early	1.04278	10.403	23.4252	24.8176	37.7521	31.1789
Gene	KLHL5	DOWN	I	early	1.55144	18.9102	17.3559	12.7262	34.1069	45.6112
Gene	PAM	DOWN	I	early	0.532455	39.1083	45.2865	26.2608	42.637	15.1287
Gene	CTSO	DOWN	I	early	0.374098	6.18183	9.29652	3.08132	6.03929	10.5006
Gene	CXCR4	DOWN	I	early	0.165358	5.40197	5.68223	4.89712	6.45591	4.63953
Gene	NIPAL2	DOWN	I	early	0.916386	8.54783	10.5555	25.2427	15.7448	25.418
Gene	DHRS3	DOWN	I	early	0.139816	1.51881	2.42845	10.6312	7.2728	3.79369
Gene	AXIN2	DOWN	I	early	0.114282	0.903662	2.70851	2.67089	3.88172	2.99251
Gene	IGDCC4	DOWN	I	early	0.168508	1.50274	2.55413	1.23189	4.94648	4.38318

Gene	RNF144B	DOWN	I	early	0.120729	2.25172	9.06818	3.51942	7.2924	3.13822
Gene	MAN1C1	DOWN	I	early	0.207973	1.55593	3.66244	6.97311	4.90294	5.28055
Gene	AKD1	DOWN	I	early	1.54463	20.9715	27.2305	24.2818	53.6112	39.1943
Gene	MSRB3	DOWN	I	early	0.245762	1.79062	9.71892	6.18096	7.73083	6.21261
Gene	PMP22	DOWN	I	early	9.23659	175.021	581.101	417.741	383.903	231.114
Gene	PID1	DOWN	I	early	0.735779	14.7943	15.88	6.54436	11.7185	18.2304
Gene	PRDM5	DOWN	I	early	0.340449	2.80746	8.22451	5.29888	9.55892	8.40773
Gene	ID2	DOWN	I	early	0.851012	6.29706	14.0372	10.4446	11.54	20.545
Gene	LPAR6	DOWN	I	early	0.366074	0.755423	2.80649	2.14683	2.88849	8.70645
Gene	ZFP36L1	DOWN	I	early	1.19659	10.6624	36.8972	33.9433	44.5982	28.3374
Gene	PEG10	DOWN	I	early	2.40814	40.9447	31.9803	29.0504	61.3888	55.6565
Gene	GALNT13	DOWN	I	early	0.507777	26.0117	32.572	19.0947	15.6521	11.2408
Gene	FNDC5	DOWN	I	early	0.169924	1.12345	0.622407	1.8845	1.74548	3.69866
Gene	RAB33A	DOWN	I	early	0.125475	0.545356	0.402497	0.699507	0.355368	2.72679
Gene	TAS2R19	DOWN	I	early	0.258596	1.89204	3.68728	3.23229	2.56356	5.35201
Gene	RASAL2	DOWN	I	early	1.15627	6.75957	7.98008	7.77181	12.4628	23.8788
Gene	NAIP	DOWN	I	early	0.855538	6.10015	11.028	8.48318	11.4837	17.6102
Gene	CHD7	DOWN	I	early	1.88214	23.6268	45.1743	41.3077	82.7954	37.5927
Gene	ALS2CR8	DOWN	I	early	2.06517	11.4519	13.1991	16.4346	17.5676	40.4935
Gene	TIMP2	DOWN	I	early	2.70471	34.2566	90.8985	127.477	149.66	53.0133
Gene	IGFBP5	DOWN	I	early	0.316785	3.68405	1.5981	5.44162	8.06256	6.17439
Gene	ARMCX2	DOWN	I	early	0.417503	3.34819	4.04297	12.0834	10.6734	8.1087
Gene	ADAM15	DOWN	I	early	0.272133	0.607742	1.05582	1.27326	1.07132	5.23493
Gene	MGAT5	DOWN	I	early	0.678123	4.60916	11.7373	8.70038	14.839	12.8308
Gene	GPR162	DOWN	I	early	0.22218	1.03169	2.26934	1.131	1.91253	4.10817
Gene	ERV3-1	DOWN	I	early	0.54822	4.94325	8.13937	7.4579	19.3373	10.1013
Gene	LRRC27	DOWN	I	early	0.339583	2.70443	3.16238	3.37551	4.61563	6.25071
Gene	ST3GAL1	DOWN	I	early	0.263245	2.47438	7.39966	3.43597	2.53345	4.74713
Gene	PLA2G6	DOWN	I	early	0.155422	1.1183	1.2681	1.21557	3.61557	2.76014
Gene	TRIB1	DOWN	I	early	0.503026	11.375	31.4144	6.47742	24.3244	8.91945
Gene	DCBLD1	DOWN	I	early	0.183578	0.352213	1.38029	2.14477	3.15165	3.16141
Gene	NDN	DOWN	I	early	1.65692	8.31417	14.6557	16.9277	30.5013	27.6623
Gene	FRMD3	DOWN	I	early	0.307189	6.59772	18.9369	12.9678	13.2633	5.08855
Gene	MAML2	DOWN	I	early	0.381816	3.48778	9.96584	6.85401	8.93906	6.29603
Gene	GLIPR2	DOWN	I	early	0.445466	4.13961	2.89231	1.95113	4.28364	7.29226

Gene	C3orf58	DOWN	I	early	1.918	15.4239	18.4031	9.52848	10.1152	31.2801
Gene	PDK2	DOWN	I	early	0.791928	3.2605	4.08505	6.32123	4.07713	12.5651
Gene	C1orf54	DOWN	I	early	0.274219	2.28983	1.95283	0.82389	7.24829	4.32469
Gene	PALM3	DOWN	I	early	0.474319	3.05756	3.37879	1.9741	7.63866	7.45217
Gene	SYNGAP1	DOWN	I	early	0.905164	3.43584	4.14235	13.2115	19.5522	14.1323
Gene	TUBA1A	DOWN	I	early	29.125	309.548	575.536	254.379	371.809	450.999
Gene	ZNRF1	DOWN	I	early	0.177873	1.25161	1.48592	1.0251	1.46727	2.7401
Gene	ZNF610	DOWN	I	early	0.385121	1.93196	3.53154	2.41567	9.47761	5.92301
Gene	MGLL	DOWN	I	early	0.653268	2.66563	2.85943	6.27794	3.40366	9.8645
Gene	MYO5C	DOWN	I	early	0.183537	0.976961	2.81749	2.37258	3.01449	2.72108
Gene	SEMA3E	DOWN	I	early	0.241963	11.9788	8.30795	1.00945	2.47693	3.52434
Gene	NKAIN1	DOWN	I	early	0.496706	2.68723	2.29461	2.96399	12.0325	7.23305
Gene	NAV1	DOWN	I	early	1.95099	8.54047	14.2142	15.2545	13.7943	28.2042
Gene	KATNAL1	DOWN	I	early	3.25018	19.0616	18.7157	22.4318	35.8134	46.462
Gene	IQCA1	DOWN	I	early	2.96471	15.2573	32.8011	34.8334	53.8751	42.3241
Gene	JUN	DOWN	I	early	0.598339	9.52782	19.1506	7.14957	21.6001	8.52802
Gene	TAS2R20	DOWN	I	early	0.290701	1.41495	3.52861	5.29011	5.84039	4.08944
Gene	GOLGA8A	DOWN	I	early	0.737616	3.83871	4.06887	5.77566	8.95641	10.3641
Gene	PRKD1	DOWN	I	early	0.650105	7.65227	10.6885	11.7087	5.65879	9.08455
Gene	HDAC9	DOWN	I	early	1.51922	37.8215	25.0161	37.3361	27.9874	21.1489
Gene	ZNF713	DOWN	I	early	1.39609	5.17876	6.17043	11.3268	7.69882	19.3971
Gene	THBS4	DOWN	I	early	0.255858	0.69421	1.00615	4.51247	11.7335	3.53264
Gene	GAB1	DOWN	I	early	14.9643	66.585	109.058	91.6937	120.87	206.007
Gene	NR4A2	DOWN	I	early	0.530011	4.0192	13.3862	1.99516	6.49285	7.29034
Gene	ADRA1A	DOWN	I	early	0.240052	1.74116	1.40984	1.07295	1.29832	3.27822
Gene	LRP1	DOWN	I	early	0.224801	1.02692	2.4361	5.33401	3.65296	3.06104
Gene	SYTL4	DOWN	I	early	0.359334	5.98792	10.0884	3.67323	6.55195	4.81379
Gene	EML1	DOWN	I	early	0.278865	4.10717	5.45622	3.98805	7.38355	3.73434
Gene	SDC3	DOWN	I	early	1.35714	16.6655	23.0498	45.037	15.5419	18.0718
Gene	TRO	DOWN	I	early	1.25556	12.0659	13.6556	23.107	30.5146	16.6876
Gene	ARRDC3	DOWN	I	early	2.31894	10.5156	28.6492	16.1312	36.0645	30.7395
Gene	KLF12	DOWN	I	early	1.9891	10.4908	17.652	14.5924	35.9216	26.1829
Gene	RDH5	DOWN	I	early	0.329469	6.38904	3.25127	0.312951	4.75617	4.32659
Gene	ZSCAN30	DOWN	I	early	0.981179	3.57292	5.27125	3.23438	9.24514	12.75
Gene	GLCCI1	DOWN	I	early	2.65972	18.441	32.254	16.7039	34.7952	34.5254

Gene	PCDHGB7	DOWN	I	early	0.463259	1.99608	2.99129	3.92656	4.35946	6.00938
Gene	SLC30A4	DOWN	I	early	0.415763	1.36369	4.18381	1.85422	3.51003	5.32434
Gene	SLC44A3	DOWN	I	early	0.247373	1.40977	1.19871	0.789217	0.442707	3.16514
Gene	PLN	DOWN	I	early	0.490871	7.82314	8.9928	4.77234	9.17709	6.24438
Gene	TAS2R14	DOWN	I	early	0.609757	3.53473	6.89766	3.38633	7.00802	7.6819
Gene	RCBTB2	DOWN	I	early	0.466526	3.42109	3.42306	2.57527	6.69873	5.83513
Gene	COL4A5	DOWN	I	early	1.24347	16.5992	23.1958	15.7434	11.1976	15.3486
Gene	CROT	DOWN	I	early	0.506213	1.73879	5.73743	2.34596	4.54753	6.24363
Gene	ZMAT4	DOWN	I	early	0.988377	9.73473	15.7067	28.3239	26.7744	12.053
Gene	PKIG	DOWN	I	early	0.418835	1.88136	3.953	6.35845	3.47437	5.06797
Gene	CRMP1	DOWN	I	early	1.00845	8.05425	22.0832	21.3293	30.7652	12.1411
Gene	ZNF345	DOWN	I	early	0.275492	1.45791	3.44589	1.65644	1.79552	3.30831
Gene	FBXL17	DOWN	I	early	1.06019	4.08829	7.35359	3.25971	6.80333	12.6523
Gene	IFI6	DOWN	I	early	1.72739	33.0724	46.8065	20.0654	7.97444	20.5814
Gene	AHDC1	DOWN	I	early	0.601312	4.73181	6.59934	6.36665	10.2962	7.048
Gene	TMEM178	DOWN	I	early	1.81831	14.6016	17.9066	7.1015	10.5919	21.308
Gene	LIMCH1	DOWN	I	early	11.5101	110.536	173.611	164.958	134.556	131.018
Gene	FAM125B	DOWN	I	early	2.11461	6.37583	8.34282	6.68734	6.52317	24.0156
Gene	C1S	DOWN	I	early	0.314728	1.233	2.02215	1.46316	4.67592	3.55006
Gene	ITGA6	DOWN	I	early	2.9185	17.5304	29.336	14.027	88.3522	32.9008
Gene	CHD6	DOWN	I	early	25.1443	82.4391	88.6986	150.798	150.026	281.928
Gene	PER3	DOWN	I	early	1.41125	4.76025	9.42199	8.57856	17.2878	15.5316
Gene	TSPYL2	DOWN	I	early	46.3429	171.682	256.136	131.922	270.535	506.071
Gene	LIMS2	DOWN	I	early	0.416577	0.380037	1.83693	7.37659	3.64498	4.49371
Gene	ZNF596	DOWN	I	early	1.35884	7.21314	9.03506	7.24552	13.0906	14.6436
Gene	CALCOCO1	DOWN	I	early	2.87957	12.3573	15.2451	28.6497	17.4602	30.9945
Gene	FANK1	DOWN	I	early	1.0499	3.00718	8.44986	12.0119	35.0376	11.2465
Gene	FAM117B	DOWN	I	early	0.686725	3.8219	6.5493	3.6347	10.2463	7.25716
Gene	SSBP2	DOWN	I	early	3.49605	26.1987	39.6988	34.3762	72.5032	36.9371
Gene	LPP	DOWN	I	early	2.07491	12.1271	48.8362	68.3685	85.4848	21.8918
Gene	PDE5A	DOWN	I	early	1.52597	6.38448	6.50183	4.09939	6.79613	16.0214
Gene	GNAI1	DOWN	I	early	28.4968	210.145	240.727	105.078	262.959	298.975
Gene	AMT	DOWN	I	early	0.407402	1.6675	1.16859	3.33254	3.14983	4.2736
Gene	ACRC	DOWN	I	early	0.426267	1.39566	2.21699	1.1347	1.45435	4.44949
Gene	DUSP1	DOWN	I	early	0.441873	2.6834	2.99041	1.94263	6.68998	4.60963

Gene	AUTS2	DOWN	I	early	2.25912	6.56604	18.1633	17.9197	39.5627	23.5193
Gene	LRRC4C	DOWN	I	early	5.02036	32.9653	39.7426	33.4749	35.6184	52.1148
Gene	RNPC3	DOWN	I	early	28.0179	82.9751	103.821	118.785	186.699	283.125
Gene	NGFRAP1	DOWN	I	early	17.6781	185.656	276.64	158.775	212.661	177.52
Gene	ZNF285	DOWN	I	early	0.96596	3.12792	4.06831	2.50605	4.05302	9.64818
Gene	FAM135B	DOWN	I	early	1.44363	11.9603	20.3325	46.6234	30.6347	14.3724
Gene	ADARB1	DOWN	I	early	0.407831	1.53468	3.17842	2.19304	3.18016	4.0532
Gene	WDR66	DOWN	I	early	0.2861	1.26367	1.19675	2.06809	1.68125	2.82523
Gene	GPR18	DOWN	I	early	0.536879	1.82659	5.74353	8.84433	6.87987	5.27731
Gene	CHRM3	DOWN	I	early	0.814719	12.5628	18.7434	10.2249	7.09147	8.0005
Gene	DPY19L2	DOWN	I	early	1.18977	4.09827	7.50493	3.69664	6.35032	11.4667
Gene	ATP6AP1L	DOWN	I	early	1.59656	4.48159	5.96788	5.85395	6.14707	15.2592
Gene	PAK3	DOWN	I	early	10.3719	25.3105	33.9689	33.8807	50.8847	97.8872
Gene	PHF21A	DOWN	I	early	49.1833	121.543	268.047	171.22	521.129	452.653
Gene	RTDR1	DOWN	I	early	0.721587	0.370639	0.512641	2.96764	2.24619	6.63082
Gene	SLC12A6	DOWN	I	early	2.56197	9.29742	12.5168	9.7619	22.6076	23.3899
Gene	ATP2B4	DOWN	I	early	4.19408	21.3797	19.5139	13.5208	19.478	38.2899
Gene	AKAP3	DOWN	I	early	0.306288	0.424925	0.939501	0.471162	1.34673	2.76281
Gene	LTBP3	DOWN	I	early	1.35417	4.35348	4.05597	10.4332	5.88499	12.1006
Gene	PEX11A	DOWN	I	early	0.717022	2.02817	3.17291	2.01985	1.71087	6.39653
Gene	CREB3L1	DOWN	I	early	0.319955	1.8794	4.24334	3.27762	2.17065	2.82902
Gene	ZNF577	DOWN	I	early	3.17386	7.91941	11.3883	12.8944	31.8396	27.991
Gene	C15orf38	DOWN	I	early	0.660735	1.7168	2.48002	1.73243	2.50498	5.82142
Gene	CELF2	DOWN	I	early	6.00885	49.7458	82.7845	31.2759	46.7218	51.6307
Gene	SOCS2	DOWN	I	early	0.857129	9.24386	22.6751	5.76686	14.2318	7.34498
Gene	C5orf54	DOWN	I	early	0.321376	0.893471	1.17814	0.743753	1.59238	2.7439
Gene	FOXO1	DOWN	I	early	1.5495	5.56651	14.8671	4.68274	9.00103	13.2167
Gene	MKL1	DOWN	I	early	3.41734	7.32681	23	14.4074	20.8123	28.9028
Gene	WDR52	DOWN	I	early	1.44035	6.53477	10.954	7.64276	11.3184	12.141
Gene	CSRNP3	DOWN	I	early	2.38681	19.4672	18.787	11.7325	11.5048	20.0574
Gene	LMOD1	DOWN	I	early	6.46148	25.891	109.569	21.1543	43.2364	54.2628
Gene	B3GNT4	DOWN	I	early	0.542622	2.39872	0.757352	1.09413	5.44138	4.55609
Gene	ALPK1	DOWN	I	early	0.395198	1.12942	2.76151	2.53937	4.52346	3.30703
Gene	SLC44A2	DOWN	I	early	1.11762	3.16522	7.03186	11.1586	15.9004	9.29104

Gene	CXCL12	DOWN	I	early	2.03127	4.87253	9.13947	13.081	34.6879	16.8583
Gene	NUMBL	DOWN	I	early	0.677693	1.99894	1.42885	6.3873	2.70717	5.61657
Gene	AHI1	DOWN	I	early	29.7142	85.2477	177.129	71.0888	140.46	244.239
Gene	RARRES3	DOWN	I	early	1.70985	4.47943	5.38811	15.3704	11.3314	14.0374
Gene	STX3	DOWN	I	early	0.540274	1.15173	1.91346	2.05363	8.67844	4.43457
Gene	C2orf63	DOWN	I	early	2.20905	8.39856	15.2128	7.96217	6.80721	18.1225
Gene	CAP2	DOWN	I	early	7.64096	60.8767	154.775	245.007	91.5723	62.5868
Gene	NAGK	DOWN	I	early	1.63208	5.88826	8.98033	14.652	12.4563	13.3478
Gene	CCDC13	DOWN	I	early	0.361815	0.01	0.861303	0.474059	1.39643	2.95451
Gene	CLIP2	DOWN	I	early	0.32908	1.8274	0.976245	1.36259	0.711883	2.67308
Gene	FNBP1L	DOWN	I	early	6.28957	43.4477	74.8863	41.0484	126.821	50.9014
Gene	FBXW4	DOWN	I	early	0.692917	1.48526	2.17341	3.17571	2.43703	5.56238
Gene	CYP2R1	DOWN	I	early	0.549472	2.3125	4.11534	1.92517	4.73611	4.40697
Gene	EPB41L5	DOWN	I	early	3.8204	17.7272	18.5295	7.90337	32.144	30.4867
Gene	SH3PXD2A	DOWN	I	early	1.29646	3.02132	4.16873	5.79525	3.00872	10.339
Gene	BTBD9	DOWN	I	early	1.68434	4.83573	5.55223	8.87315	5.54221	13.4196
Gene	RALGDS	DOWN	I	early	0.571383	0.997429	1.87562	4.07058	1.16158	4.52364
Gene	KCNJ13	DOWN	I	early	0.980399	2.96808	4.62942	15.2289	4.67823	7.73594
Gene	STK32A	DOWN	I	early	1.23199	3.4076	5.99075	2.93128	16.0122	9.6935
Gene	FGF9	DOWN	I	early	1.78246	38.6453	16.2227	33.7632	14.1835	13.9644
Gene	RUNX1T1	DOWN	I	early	6.49672	43.959	69.2777	55.5966	41.7929	50.8912
Gene	NOTCH2	DOWN	I	early	7.58098	23.7631	48.254	16.8695	29.6055	59.3148
Gene	POU3F2	DOWN	I	early	1.36219	21.5355	19.4741	4.49074	4.835	10.623
Gene	ZNF780B	DOWN	I	early	1.93408	5.52541	8.89768	8.20503	6.59756	15.0317
Gene	FAM168A	DOWN	I	early	3.00578	6.6664	8.34576	35.0929	17.2794	23.2725
Gene	ATG16L2	DOWN	I	early	0.913517	2.67208	2.74527	3.42877	3.99532	7.06875
Gene	DEAF1	DOWN	I	early	1.24074	5.58444	4.24113	17.6718	6.28747	9.55898
Gene	RANBP17	DOWN	I	early	1.54452	12.7495	19.3489	3.77439	15.3342	11.8924
Gene	KCNIP1	DOWN	I	early	0.885313	3.77731	10.4591	12.4523	10.4941	6.79832
Gene	FREM2	DOWN	I	early	0.428627	3.38157	3.15407	1.7422	8.76852	3.26969
Gene	TAS2R30	DOWN	I	early	0.720092	3.26798	5.24854	3.85313	9.04383	5.49303
Gene	FXYD5	DOWN	I	early	0.44901	0.268846	0.879051	0.263668	6.45008	3.42196
Gene	ZNF763	DOWN	I	early	0.485061	1.03257	2.08994	0.95075	3.14174	3.67158
Gene	FBXL2	DOWN	I	early	2.71652	7.56888	13.4869	19.6826	25.1684	20.4499

Gene	MAB21L2	DOWN	I	early	0.794644	4.55292	6.897	3.19914	2.91247	5.96046
Gene	NELF	DOWN	I	early	0.497156	1.32936	0.496233	1.65782	1.77073	3.72572
Gene	ELK1	DOWN	I	early	0.69809	1.58679	3.3569	2.49082	2.56051	5.18797
Gene	MICAL3	DOWN	I	early	0.603126	1.56296	3.567	2.33578	4.15951	4.4806
Gene	RND2	DOWN	I	early	0.460215	1.19236	0.88478	1.63366	8.65658	3.41632
Gene	NKTR	DOWN	I	early	26.7523	75.1171	108.352	55.9873	106.254	198.57
Gene	AS3MT	DOWN	I	early	0.925058	4.15958	2.56178	4.2866	10.0015	6.86344
Gene	KIAA1109	DOWN	I	early	19.581	43.7023	56.442	46.2699	61.8752	144.546
Gene	MYO9A	DOWN	I	early	2.19935	4.091	9.3525	5.5264	11.1039	15.9626
Gene	PBXIP1	DOWN	I	early	1.06497	3.08132	4.6096	10.2047	7.54974	7.71961
Gene	SLC5A3	DOWN	I	early	2.00466	5.60001	9.90979	4.33245	17.7244	14.5249
Gene	PPFIA2	DOWN	I	early	31.7498	121.326	185.412	96.3868	87.0909	229.783
Gene	SLC40A1	DOWN	I	early	1.30938	5.94686	8.92801	2.61962	8.78562	9.47018
Gene	IKBKB	DOWN	I	early	1.97058	5.84366	5.618	12.6035	10.2596	14.1453
Gene	IFT172	DOWN	I	early	2.51591	5.52006	5.31738	12.2552	10.2396	18.0569
Gene	ZNF71	DOWN	I	early	1.16546	2.46398	3.16704	3.92614	5.58935	8.33389
Gene	KIFAP3	DOWN	I	early	8.29005	20.8681	30.0399	18.9113	39.6382	59.2391
Gene	FOSL2	DOWN	I	early	1.40561	21.0138	35.7925	8.47742	18.019	9.99961
Gene	RHOB	DOWN	I	early	5.6811	27.5063	36.7272	12.3278	45.5967	40.3614
Gene	LRRC48	DOWN	I	early	0.391046	0.417072	1.69448	1.21086	2.92924	2.77222
Gene	FGFR1	DOWN	I	early	0.723699	4.9099	12.2987	12.1624	19.0039	5.12571
Gene	PSEN2	DOWN	I	early	0.396324	1.33846	1.92699	5.82558	3.2037	2.8028
Gene	PTPRS	DOWN	I	early	0.697796	2.55553	3.01128	6.34707	8.59387	4.91303
Gene	DOCK2	DOWN	I	early	0.392599	0.913359	1.09759	1.66093	3.79645	2.75263
Gene	TCEA2	DOWN	I	early	1.41273	5.48232	6.43401	5.42413	5.36968	9.90112
Gene	EPM2AIP1	DOWN	I	early	4.44432	17.8521	19.2462	9.93973	18.4394	31.0998
Gene	JHDM1D	DOWN	I	early	1.02818	2.9894	8.6814	3.32132	8.99446	7.19435
Gene	THNSL2	DOWN	I	early	0.487027	2.76562	2.89507	3.49558	2.94006	3.40035
Gene	ZSCAN16	DOWN	I	early	1.10706	7.72484	9.40459	6.24287	4.02475	7.71049
Gene	ZDHHC21	DOWN	I	early	2.75769	11.2184	17.4343	6.06618	12.6209	19.1478
Gene	CTSF	DOWN	I	early	1.68541	3.66719	8.23768	12.5753	13.2431	11.6973
Gene	EPHA7	DOWN	I	early	0.734707	8.96605	7.77764	4.16774	18.1293	5.08447
Gene	TRAM1L1	DOWN	I	early	0.761404	2.15934	3.69958	1.48133	1.18096	5.24625
Gene	TMEM14A	DOWN	I	early	5.74836	18.9846	26.0821	15.0198	23.2204	39.4493

Gene	SMAD9	DOWN	I	early	0.932835	6.23001	5.47339	1.90475	3.58722	6.39673
Gene	NTN4	DOWN	I	early	1.30208	15.5797	34.632	10.1125	31.786	8.88782
Gene	SELENBP1	DOWN	I	early	0.590416	4.01029	3.55657	6.57737	3.03617	4.01846
Gene	FAM115A	DOWN	I	early	4.79884	23.4175	40.3425	9.48938	15.8069	32.4761
Gene	AMOTL2	DOWN	I	early	0.720271	4.12825	10.5733	8.66318	8.59594	4.86278
Gene	KIDINS220	DOWN	I	early	9.33037	17.8871	20.8656	23.5306	37.7561	62.9003
Gene	SRR	DOWN	I	early	0.839729	4.65413	3.46867	2.81678	8.15423	5.61318
Gene	TSPAN12	DOWN	I	early	1.35087	5.645	15.468	9.40846	25.4653	9.0257
Gene	ZNF793	DOWN	I	early	1.20114	3.19377	7.06745	2.92542	5.29922	8.02143
Gene	COBLL1	DOWN	I	early	4.3529	22.8471	31.7626	20.3055	12.4115	28.9809
Gene	C7orf46	DOWN	I	early	0.525295	1.94187	2.39482	1.3103	2.50133	3.49437
Gene	FAM3A	DOWN	I	early	0.520052	1.3477	1.58789	1.15232	1.81346	3.45598
Gene	ZFP90	DOWN	I	early	0.872766	2.51643	4.90661	2.90429	5.82472	5.78974
Gene	TMEM234	DOWN	I	early	0.855465	4.7836	3.11341	8.34317	4.32414	5.6738
Gene	IFI27	DOWN	I	early	1.90761	35.8316	26.0755	5.9662	3.86662	12.6249
Gene	KLHL22	DOWN	I	early	0.645918	1.10419	1.78839	3.1105	4.76611	4.26852
Gene	PRR4	DOWN	I	early	5.92275	25.9179	30.4736	38.7695	37.2952	39.0683
Gene	TJAP1	DOWN	I	early	1.21182	2.30209	3.12893	3.0955	4.27004	7.98844
Gene	DYNC2H1	DOWN	I	early	1.64932	2.91505	11.0145	5.21235	14.3348	10.8718
Gene	ADCY6	DOWN	I	early	0.622909	2.76187	3.63565	6.71669	4.7323	4.08685
Gene	GTDC1	DOWN	I	early	15.2994	30.7266	46.9134	44.0953	81.5996	100.165
Gene	MLL3	DOWN	I	early	8.98061	21.5618	34.2523	22.7808	32.3304	58.7627
Gene	NLGN2	DOWN	I	early	1.99474	6.13945	8.44432	24.9826	25.5465	12.8902
Gene	ZNF425	DOWN	I	early	3.81204	18.4443	25.4043	12.324	27.0406	24.5881
Gene	ZNF292	DOWN	I	early	19.9162	52.7057	89.5397	68.2141	128.789	128.054
Gene	ARMCX1	DOWN	I	early	1.21887	4.46911	8.98293	3.96834	6.37046	7.83204
Gene	CCDC65	DOWN	I	early	0.70581	1.42121	2.12087	3.06068	2.20555	4.53293
Gene	PDE8A	DOWN	I	early	4.67317	14.2572	19.4257	13.6819	11.3735	29.8285
Gene	STIM1	DOWN	I	early	0.98731	2.60764	2.91527	6.20211	4.34464	6.29185
Gene	MICAL1	DOWN	I	early	0.467605	1.34955	1.28229	2.83896	3.3882	2.97145
Gene	SSBP3	DOWN	I	early	1.57698	3.79503	3.15482	4.75299	7.50337	10.0207
Gene	NT5DC3	DOWN	I	early	1.02741	2.00676	2.76483	2.90862	3.95456	6.52516
Gene	INPP5F	DOWN	I	early	9.30293	28.2149	23.2709	21.3085	26.1631	58.9384
Gene	TRIO	DOWN	I	early	5.51333	11.8722	20.9587	27.3489	38.7256	34.8505
Gene	CNKSR2	DOWN	I	early	7.73693	21.6326	32.8881	16.6936	24.337	48.5357

Gene	PDE7A	DOWN	I	early	4.55547	12.8635	18.5222	10.3628	42.1387	28.5414
Gene	ZNF555	DOWN	I	early	0.898396	1.83757	2.04887	1.84656	3.43324	5.62101
Gene	AKAP13	DOWN	I	early	2.32108	11.1682	24.8552	19.0655	39.8257	14.5145
Gene	PPM1L	DOWN	I	early	1.66524	6.62051	20.3482	10.6133	17.4223	10.3884
Gene	NELL1	DOWN	I	early	1.81296	28.2477	34.1191	13.4478	8.63171	11.2881
Gene	ZMYND11	DOWN	I	early	22.3852	37.1614	42.6197	60.7986	67.2624	139.319
Gene	RRAGB	DOWN	I	early	3.51924	15.1843	17.411	29.4127	34.0381	21.8793
Gene	RNFT2	DOWN	I	early	1.46214	2.29581	4.53773	7.15858	17.6526	9.07732
Gene	FKBP1B	DOWN	I	early	1.49737	3.78649	7.31395	2.66611	7.58772	9.27676
Gene	CYLD	DOWN	I	early	1.43024	2.67236	4.87521	2.22882	6.21322	8.85726
Gene	GRK4	DOWN	I	early	2.04299	6.78218	8.89192	3.58364	5.18327	12.6187
Gene	SERTAD2	DOWN	I	early	1.49056	5.03959	16.0551	14.5015	35.5869	9.18741
Gene	TLE4	DOWN	I	early	18.5224	62.729	86.6721	88.8661	129.486	114.134
Gene	ZNF280D	DOWN	I	early	12.5841	31.0309	44.4775	29.7316	38.5275	77.1541
Gene	HPCAL1	DOWN	I	early	11.7098	42.1712	107.712	181.308	130.397	71.5001
Gene	WWOX	DOWN	I	early	0.652866	1.82301	1.0351	1.96398	2.42957	3.98361
Gene	MED12	DOWN	I	early	2.85556	5.28858	7.62471	16.2904	11.3423	17.4179
Gene	PDE4D	DOWN	I	early	7.23215	20.9728	32.8456	32.5474	39.3389	43.9781
Gene	ARL17A	DOWN	I	early	4.28304	10.2779	16.8632	20.536	30.2766	26.0235
Gene	PGBD1	DOWN	I	early	0.975013	4.05642	3.58476	1.6436	2.97283	5.91681
Gene	TCTN1	DOWN	I	early	1.52448	2.76029	6.53641	7.85683	11.1387	9.24391
Gene	KIAA1267	DOWN	I	early	2.35581	4.48016	4.74005	6.18654	10.778	14.2665
Gene	CDR2L	DOWN	I	early	0.610623	1.12807	1.74808	1.36572	1.21416	3.69441
Gene	TRAPPC6A	DOWN	I	early	0.535561	1.78674	4.53606	5.81316	5.62501	3.22769
Gene	PSTK	DOWN	I	early	2.34936	4.44546	5.24447	5.3361	7.72763	14.139
Gene	GOLGA8B	DOWN	I	early	1.93461	5.63164	8.59111	7.06421	14.6934	11.5819
Gene	ZNF253	DOWN	I	early	2.86883	10.417	14.3508	5.96154	15.1938	17.0579
Gene	PLCG1	DOWN	I	early	3.47782	8.41055	9.5824	18.9764	12.1149	20.6197
Gene	CCDC91	DOWN	I	early	38.5014	80.2691	110.072	152.439	163.992	226.745
Gene	PINK1	DOWN	I	early	7.25525	13.8895	22.8713	34.8544	34.839	42.666
Gene	ZNF585A	DOWN	I	early	2.96572	5.42204	6.57807	6.53029	16.5079	17.4286
Gene	AKTIP	DOWN	I	early	2.11971	6.01812	9.15989	3.16479	5.204	12.3268
Gene	PPP2R3A	DOWN	I	early	1.46762	7.3394	14.9433	8.33035	11.4424	8.48933
Gene	C1orf198	DOWN	I	early	4.78126	11.9192	19.8958	13.0892	24.7219	27.599

Gene	ARMCX3	DOWN	I	early	8.9676	32.834	43.0225	13.1999	31.2408	51.5309
Gene	DDX60L	DOWN	I	early	1.33805	5.34869	6.47861	6.43671	5.05114	7.68655
Gene	PHC2	DOWN	I	early	1.02574	1.73418	4.59218	5.79758	1.65244	5.88121
Gene	MUTYH	DOWN	I	early	0.512557	0.447839	0.781878	1.37166	1.05109	2.932
Gene	TMEM42	DOWN	I	early	0.690983	1.53404	1.2827	3.11122	2.17427	3.94147
Gene	SHPRH	DOWN	I	early	8.62424	12.9966	22.9338	14.0175	28.4724	49.0485
Gene	ZNF638	DOWN	I	early	53.7398	111.198	183.665	89.5903	184.807	303.785
Gene	PJA1	DOWN	I	early	1.04182	1.7839	3.73733	4.07848	3.60125	5.88493
Gene	GNL1	DOWN	I	early	5.06636	7.71468	10.0777	10.3851	11.5631	28.3046
Gene	PRCP	DOWN	I	early	7.22077	15.6182	22.9286	21.1884	38.672	40.0405
Gene	TPP1	DOWN	I	early	19.224	51.3	92.7208	114.402	118.258	106.289
Gene	ZNF70	DOWN	I	early	0.488041	1.37974	2.16004	1.83091	2.3865	2.69625
Gene	ZBTB38	DOWN	I	early	7.81336	18.7069	28.1489	10.8304	28.6321	43.1373
Gene	NRBP2	DOWN	I	early	6.10683	10.2143	17.3034	29.9136	16.9994	33.7115
Gene	IFT27	DOWN	I	early	1.62827	3.23308	4.35877	9.34435	7.60364	8.97769
Gene	AKAP9	DOWN	I	early	64.7174	183.769	381.615	122.5	336.125	354.279
Gene	WNK3	DOWN	I	early	4.22673	9.44867	9.8259	5.78849	31.6267	23.1311
Gene	JAK2	DOWN	I	early	1.48013	2.67546	5.94074	2.51138	4.71473	8.09996
Gene	FUT8	DOWN	I	early	6.08651	17.951	22.0879	19.5599	32.7584	32.994
Gene	FAM160A2	DOWN	I	early	1.24471	3.92103	4.5162	8.93111	6.66283	6.73053
Gene	PHC3	DOWN	I	early	41.6655	69.4066	150.808	122.422	130.882	225.099
Gene	ZFP3	DOWN	I	early	1.84534	5.91478	7.28855	8.53529	5.27806	9.96131
Gene	MLLT11	DOWN	I	early	4.20406	34.419	26.3229	18.4253	25.7684	22.6924
Gene	DPF3	DOWN	I	early	0.87039	3.4023	1.22207	4.21313	1.9418	4.69106
Gene	PAG1	DOWN	I	early	1.28335	3.10189	5.38073	2.23033	2.76014	6.88453
Gene	BCL7A	DOWN	I	early	2.24071	13.9878	8.44875	20.9631	8.34136	11.9883
Gene	MKRN3	DOWN	I	early	0.772737	1.8226	1.74561	1.26137	3.13415	4.13081
Gene	ZNF81	DOWN	I	early	1.58984	3.21977	5.12324	4.86352	5.12099	8.48734
Gene	MOAP1	DOWN	I	early	2.78686	5.13124	9.85348	5.44243	6.93053	14.7734
Gene	URGCP	DOWN	I	early	2.38882	5.5338	6.7248	7.65635	4.13094	12.6552
Gene	PCM1	DOWN	I	early	126.919	333.212	411.307	226.85	501.616	668.114
Gene	ING4	DOWN	I	early	6.58856	28.0554	27.8761	37.4417	35.7894	34.6054
Gene	C11orf54	DOWN	I	early	3.63959	10.8576	17.3381	11.7279	22.0892	19.1135
Gene	MASP2	DOWN	I	early	0.861841	4.50421	4.04565	7.57886	11.4915	4.50766
Gene	FBXL20	DOWN	I	early	3.3747	8.97672	16.1103	15.1715	21.6159	17.5928
Gene	NAB1	DOWN	I	early	1.86118	8.41378	15.3662	7.26035	5.40043	9.67439

Gene	ZNF655	DOWN	I	early	19.4693	58.6339	100.784	37.6521	45.4027	101.173
Gene	TAGLN3	DOWN	I	early	3.255	15.5451	7.90008	9.82285	10.9302	16.8607
Gene	BRAF	DOWN	I	early	7.52769	11.3369	17.5461	15.1968	31.4644	38.8179
Gene	ACAD11	DOWN	I	early	2.7709	8.45074	9.25748	20.08	14.2565	14.2829
Gene	P4HA2	DOWN	I	early	0.703005	1.84461	5.45004	5.07995	6.80494	3.62106
Gene	KIF27	DOWN	I	early	2.77821	4.97348	7.00085	4.9195	15.4559	14.206
Gene	SPIN3	DOWN	I	early	0.554156	1.31885	1.68268	2.61396	3.62106	2.82993
Gene	KLC1	DOWN	I	early	8.42395	15.0816	18.9722	22.4093	32.6538	42.7272
Gene	TFDP2	DOWN	I	early	3.50358	31.5373	27.3753	23.9757	34.8858	17.7267
Gene	KIAA0355	DOWN	I	early	1.13834	2.15282	4.14087	2.96171	4.54702	5.75954
Gene	CDH11	DOWN	I	early	2.16808	11.2034	29.5006	30.6281	33.8688	10.9674
Gene	SAT1	DOWN	I	early	31.175	94.865	162.295	47.9327	170.802	157.479
Gene	HGSNAT	DOWN	I	early	1.8929	7.17058	13.3215	17.0279	13.3894	9.55576
Gene	SPDYA	DOWN	I	early	0.577239	1.41641	3.66543	1.53308	5.08581	2.90857
Gene	ACO1	DOWN	I	early	3.64333	6.2881	10.5728	15.4325	29.1963	18.3547
Gene	ZNF673	DOWN	I	early	2.44841	3.28836	12.3241	4.32995	8.27701	12.3053
Gene	FAM184B	DOWN	I	early	2.24903	4.44792	6.97077	2.89754	5.34055	11.2845
Gene	TTC3	DOWN	I	early	18.0961	49.4306	86.907	42.6284	135.617	90.6231
Gene	HMGCL	DOWN	I	early	0.736362	1.83005	1.25236	4.07001	1.79258	3.68602
Gene	C9orf3	DOWN	I	early	15.5201	23.0485	79.2169	134.309	136.91	77.571
Gene	LRCH4	DOWN	I	early	0.750724	1.43298	2.94517	3.29684	1.88615	3.74738
Gene	KIAA0528	DOWN	I	early	24.9815	41.3427	65.7106	58.0651	65.8801	124.671
Gene	GAS1	DOWN	I	early	0.961821	11.9012	18.3409	6.10575	9.48001	4.79094
Gene	DOCK10	DOWN	I	early	37.5057	195.847	217.275	139.689	67.8095	186.515
Gene	ZMIZ2	DOWN	I	early	0.906837	1.84929	1.36886	5.3235	3.87641	4.50703
Gene	SBF1	DOWN	I	early	0.592211	1.16312	1.04014	1.04496	0.734115	2.94157
Gene	ZHX2	DOWN	I	early	8.24211	19.8619	27.0716	30.8799	22.0682	40.8782
Gene	MLH3	DOWN	I	early	4.49065	7.43557	10.0266	5.88028	9.94581	22.1948
Gene	HIST2H2BE	DOWN	I	early	2.00421	9.08308	6.90055	6.72273	39.0716	9.90432
Gene	ANO10	DOWN	I	early	1.96715	2.43824	4.97423	3.34161	6.83126	9.69819
Gene	SLC38A9	DOWN	I	early	2.57086	5.40967	4.28633	3.84787	7.40644	12.6526
Gene	MED13L	DOWN	I	early	4.23987	11.4368	20.8632	21.1505	28.176	20.8502
Gene	BMPR2	DOWN	I	early	8.9204	23.1869	46.4441	13.5328	46.0722	43.848
Gene	EFR3B	DOWN	I	early	1.71269	4.63524	8.13138	17.5668	10.9223	8.405
Gene	POU2F1	DOWN	I	early	2.59108	8.89064	17.87	11.7801	25.0079	12.6845

Gene	FAM110B	DOWN	I	early	2.5023	16.0868	25.2944	24.444	21.8777	12.2457
Gene	ZBTB25	DOWN	I	early	0.777509	1.79272	2.55609	2.52222	2.84623	3.79801
Gene	SCARB2	DOWN	I	early	13.4199	24.0327	43.0081	18.5508	38.0725	65.5253
Gene	ZNF606	DOWN	I	early	3.43916	6.65423	8.04781	5.70315	13.705	16.7683
Gene	TCF7	DOWN	I	early	0.983714	4.34521	2.93771	4.43295	4.13914	4.76432
Gene	PHF1	DOWN	I	early	1.22177	2.32401	2.38543	6.30114	6.1888	5.91054
Gene	APPL2	DOWN	I	early	7.98294	18.9039	23.3974	21.6907	29.2985	38.6047
Gene	ZNF175	DOWN	I	early	2.14621	4.15627	6.69174	4.7824	5.45332	10.3405
Gene	ARL17B	DOWN	I	early	1.14848	2.83499	3.07984	1.93842	3.41668	5.5244
Gene	FNIP2	DOWN	I	early	3.4813	6.08594	9.08247	6.14481	11.8229	16.743
Gene	TCEAL4	DOWN	I	early	114.125	253.246	518.737	750.622	770.515	548.754
Gene	FAM92A1	DOWN	I	early	4.70457	10.9899	17.7539	8.26704	10.6142	22.5727
Gene	ZNF221	DOWN	I	early	1.32245	1.87446	2.57471	2.852	4.32009	6.34511
Gene	C1orf56	DOWN	I	early	0.914923	2.21137	3.29747	1.54619	1.36586	4.38931
Gene	SDC4	DOWN	I	early	13.8551	40.5613	105.224	75.5113	79.9832	66.3048
Gene	SNX18	DOWN	I	early	2.43172	6.51326	13.5902	4.17528	7.03609	11.6282
Gene	RASGEF1B	DOWN	I	early	2.56772	3.36706	6.66813	6.85958	14.5891	12.2651
Gene	AHNAK	DOWN	I	early	10.3116	28.2494	65.3181	97.9169	98.3114	49.2256
Gene	CLSTN1	DOWN	I	early	11.0962	13.2781	18.0195	22.8081	39.0573	52.9506
Gene	TK2	DOWN	I	early	1.25027	2.44093	3.59253	7.09928	6.49585	5.95002
Gene	NBPF10	DOWN	I	early	3.86027	9.46901	19.9813	7.8328	13.5327	18.3085
Gene	BCAS3	DOWN	I	early	2.82814	5.5564	5.34426	11.6375	11.4571	13.3942
Gene	ANKHD1-EIF4EBP3	DOWN	I	early	0.795967	1.18116	2.59354	3.42115	3.96336	3.76684
Gene	ZNF652	DOWN	I	early	18.2083	21.8553	41.106	23.3589	32.3414	86.0402
Gene	SOX13	DOWN	I	early	0.652235	1.05113	1.76685	4.75269	8.98122	3.0794
Gene	EPHA4	DOWN	I	early	4.25113	9.87382	16.2541	19.337	29.9885	20.0486
Gene	CRELD1	DOWN	I	early	0.653452	1.41695	2.10101	5.46367	3.01568	3.07063
Gene	SEMA3A	DOWN	I	early	0.714969	11.46	8.49618	5.57937	8.00082	3.35093
Gene	NEDD9	DOWN	I	early	1.15562	11.1878	18.9051	15.8654	15.9181	5.40997
Gene	SNURF	DOWN	I	early	23.0668	39.769	34.9466	63.0573	103.484	107.775
Gene	DENND4B	DOWN	I	early	1.57155	1.92718	1.87233	7.90317	3.10052	7.33827
Gene	SLC11A2	DOWN	I	early	12.0188	16.8266	25.9957	29.6403	44.4676	56.0386
Gene	RALGAPA2	DOWN	I	early	3.57095	10.3419	13.4939	7.7553	12.4956	16.6016

Gene	DYNLL2	DOWN	I	early	24.6083	64.5835	62.942	141.653	181.34	114.282
Gene	LHFP	DOWN	I	early	10.2722	29.5347	52.7289	18.593	83.8412	47.6982
Gene	C6orf191	DOWN	I	early	0.903862	5.64693	2.71977	1.95101	2.775	4.19401
Gene	BAZ2B	DOWN	I	early	95.7255	170.321	276.814	232.048	320.277	443.538
Gene	ETS1	DOWN	I	early	1.65847	9.88095	25.3604	8.33019	14.4035	7.67831
Gene	WSB1	DOWN	I	early	22.9981	77.6621	113.338	84.5901	189.967	106.451
Gene	SDC2	DOWN	I	early	12.8015	24.9045	74.0355	98.115	114.556	59.2162
Gene	VPS13B	DOWN	I	early	10.4969	26.6119	37.7536	52.4205	78.9666	48.5255
Gene	RABL2B	DOWN	I	early	2.24861	3.12675	4.09955	11.2876	13.3995	10.374
Gene	LRRC37B	DOWN	I	early	1.89288	2.30357	3.75914	2.20591	3.05161	8.72935
Gene	TMEM220	DOWN	I	early	0.772275	2.02037	4.4703	1.07877	1.75966	3.56133
Gene	DTX3	DOWN	I	early	0.896052	4.52276	3.24998	4.62567	3.17054	4.12974
Gene	ATRN	DOWN	I	early	5.14725	19.6126	29.5865	15.1798	15.8204	23.7225
Gene	SATB1	DOWN	I	early	9.19224	30.6938	18.4496	24.1848	33.5935	42.2641
Gene	ZNF470	DOWN	I	early	1.60278	2.07756	4.38693	2.49603	5.48446	7.35914
Gene	PTK2	DOWN	I	early	61.4305	86.1235	111.453	99.9093	102.593	281.805
Gene	C10orf58	DOWN	I	early	9.71479	14.2786	25.0745	18.4857	28.5198	44.5598
Gene	C22orf25	DOWN	I	early	1.02687	0.631602	1.2194	3.27225	2.47465	4.70952
Gene	MGMT	DOWN	I	early	0.674889	0.410261	2.09643	2.35298	1.30653	3.09135
Gene	TCEAL3	DOWN	I	early	23.1898	41.7239	59.5866	104.247	55.3508	106.108
Gene	TIAM2	DOWN	I	early	3.36818	13.1557	20.606	22.9868	30.8713	15.411
Gene	ZNF34	DOWN	I	early	0.59678	0.776417	1.85981	1.05004	1.89697	2.72625
Gene	SALL2	DOWN	I	early	1.69027	3.65045	3.45505	3.20691	18.6799	7.68952
Gene	MAN2A2	DOWN	I	early	4.90125	7.40383	10.9772	7.30886	13.9689	22.2436
Gene	FER	DOWN	I	early	31.168	114.981	147.358	42.6111	63.3172	140.856
Gene	ZNF605	DOWN	I	early	4.66543	9.87841	14.1803	6.83876	13.4282	21.0469
Gene	LRRC37A2	DOWN	I	early	1.88567	2.57809	5.08664	4.82721	6.35778	8.50451
Gene	ZNF224	DOWN	I	early	1.7944	2.79543	2.7454	4.42455	8.73607	8.087
Gene	PRDM2	DOWN	I	early	17.6923	37.8238	54.3266	39.57	72.0423	79.52
Gene	IL6ST	DOWN	I	early	58.1309	107.672	163.787	76.634	168.849	260.872
Gene	NUMA1	DOWN	I	early	4.96355	7.14945	10.5516	16.3079	15.0618	22.2397
Gene	ZKSCAN1	DOWN	I	early	9.64292	16.8717	25.6086	25.3846	36.0699	43.181
Gene	TAPT1	DOWN	I	early	3.67112	6.90508	8.47656	10.9814	12.8811	16.3712
Gene	ZNF84	DOWN	I	early	4.29831	15.0944	15.6868	7.30866	19.328	19.1497
Gene	BSDC1	DOWN	I	early	2.94406	5.27585	6.02869	4.43408	4.46056	13.0474

Gene	DNAJC27	DOWN	I	early	1.1524	1.69298	2.98833	1.72334	1.60321	5.10091
Gene	ATG2B	DOWN	I	early	3.03701	4.22959	5.88299	3.68227	6.61117	13.4273
Gene	PHKA2	DOWN	I	early	12.6391	25.5654	41.3484	77.913	44.9664	55.8645
Gene	JMY	DOWN	I	early	3.55906	10.0749	16.4692	6.36238	13.7268	15.6907
Gene	CSAD	DOWN	I	early	1.8661	3.33281	3.52386	6.47262	6.1866	8.21774
Gene	GABARAPL1	DOWN	I	early	20.675	39.4288	62.2723	51.2891	107.942	90.9097
Gene	CDK9	DOWN	I	early	1.83409	4.90723	2.99647	5.10112	10.5269	8.05484
Gene	ANKZF1	DOWN	I	early	3.71846	8.00353	9.43743	17.9219	24.7371	16.3269
Gene	CLK4	DOWN	I	early	18.4279	34.654	54.0639	25.2279	63.9896	80.8622
Gene	FRS2	DOWN	I	early	104.2	248.786	309.521	242.3	414.885	456.453
Gene	UTY	DOWN	I	early	5.42104	10.5827	15.8716	8.52147	13.729	23.6945
Gene	GPHN	DOWN	I	early	3.12353	5.09961	8.59783	8.80382	12.9538	13.6412
Gene	ZNF658	DOWN	I	early	0.620385	0.972511	2.1527	0.804305	1.04718	2.70597
Gene	N6AMT1	DOWN	I	early	0.992797	1.76395	1.79728	1.93227	3.61586	4.32688
Gene	KLHL24	DOWN	I	early	21.1141	69.0096	86.0859	57.9193	115.811	91.9406
Gene	ZNF184	DOWN	I	early	13.1455	48.388	26.8423	66.1039	21.6821	57.1852
Gene	OSCP1	DOWN	I	early	2.40751	4.62317	2.94777	5.57868	3.45021	10.4667
Gene	ASAH1	DOWN	I	early	9.32445	13.9765	31.0839	22.6905	46.0625	40.5077
Gene	NICN1	DOWN	I	early	0.807931	2.13419	1.59383	3.06329	3.19283	3.50914
Gene	ARMC9	DOWN	I	early	8.32736	10.7585	29.5694	22.7922	30.5907	36.0645
Gene	DBNL	DOWN	I	early	3.75893	5.75452	10.4446	8.61946	6.32142	16.2554
Gene	SEC62	DOWN	I	early	89.7485	116.095	165.249	114.64	203.024	388.112
Gene	CLN8	DOWN	I	early	0.757329	1.34356	1.79428	1.99794	1.26608	3.27406
Gene	DBC1	DOWN	I	early	1.17792	6.86048	8.21921	15.4665	4.75295	5.09129
Gene	NUDT16	DOWN	I	early	8.85396	10.5004	14.4722	13.9997	25.4358	38.2114
Gene	ACVR2A	DOWN	I	early	4.02774	10.8964	19.6809	6.74386	20.6485	17.3678
Gene	C6orf170	DOWN	I	early	3.82781	8.64746	11.3708	6.70121	4.78067	16.4949
Gene	POLI	DOWN	I	early	2.68757	7.77587	9.54459	3.88982	10.7172	11.5813
Gene	SPTBN1	DOWN	I	early	47.6917	110.499	213.393	398.251	224.866	205.454
Gene	PDP1	DOWN	I	early	9.48865	32.069	53.0929	20.2324	27.4543	40.814
Gene	NISCH	DOWN	I	early	2.52641	5.96684	4.73244	14.658	9.30714	10.8532
Gene	TMEM106A	DOWN	I	early	0.813489	1.529	3.05596	5.39184	2.35112	3.49305
Gene	ZFYVE9	DOWN	I	early	4.50156	7.3141	9.21852	5.05419	8.00206	19.3003
Gene	MAP3K3	DOWN	I	early	0.838405	0.915162	2.74449	4.7514	3.57442	3.59113
Gene	NEXN	DOWN	I	early	2.04038	17.858	33.711	5.43319	20.2024	8.69744

Gene	RAPGEF2	DOWN	I	early	22.788	75.6534	98.6856	91.0321	86.0544	97.0204
Gene	C8orf37	DOWN	I	early	1.00452	1.54402	2.07294	1.16741	1.67526	4.27165
Gene	ZNF397	DOWN	I	early	1.98076	3.70748	4.33642	2.78388	7.6199	8.41367
Gene	SOCS7	DOWN	I	early	6.00078	7.11689	11.5901	10.9154	11.1472	25.4635
Gene	IL1RAP	DOWN	I	early	2.15258	13.5062	5.84801	13.079	5.02519	9.11814
Gene	ARHGAP6	DOWN	I	early	1.01736	1.42068	3.15426	1.9384	2.96288	4.30221
Gene	MEF2C	DOWN	I	early	48.8358	64.8001	67.3241	61.9437	62.443	206.494
Gene	ZMYND8	DOWN	I	early	7.46023	21.4394	12.1415	20.8001	75.3998	31.5152
Gene	USP47	DOWN	I	early	25.4415	53.1709	75.471	36.9775	64.1162	107.429
Gene	TXNIP	DOWN	I	early	19.1947	51.48	97.6549	111.79	161.833	81.032
Gene	ZNF417	DOWN	I	early	3.00609	3.94289	5.25611	4.28534	10.7822	12.6877
Gene	ZNF461	DOWN	I	early	1.83131	3.16143	6.33774	3.28144	9.24568	7.71886
Gene	RBM41	DOWN	I	early	12.6196	22.1069	38.2498	14.1718	31.7752	53.1835
Gene	LRCH3	DOWN	I	early	30.8179	41.5614	103.295	66.4463	79.7601	129.813
Gene	AGER	DOWN	I	early	2.58522	5.90463	19.0507	14.6018	22.6685	10.8515
Gene	FXC1	DOWN	I	early	18.5	23.9181	36.199	32.0589	87.0805	77.5139
Gene	WHSC1L1	DOWN	I	early	45.8695	66.3497	87.0144	58.6664	101.761	192.12
Gene	KCND2	DOWN	I	early	1.84602	6.24323	7.25829	2.70641	3.26374	7.73125
Gene	ARNTL	DOWN	I	early	2.60381	6.9919	11.8337	11.4655	11.1765	10.8963
Gene	INPP5A	DOWN	I	early	1.11586	1.56179	2.59741	6.71946	2.9534	4.66507
Gene	MAML3	DOWN	I	early	1.29948	2.73621	5.56224	4.50622	10.3863	5.43218
Gene	ZNF548	DOWN	I	early	2.54728	8.1292	10.8528	3.43323	6.60586	10.6433
Gene	EFNB3	DOWN	I	early	1.30409	4.35955	3.44643	6.19328	10.1346	5.43944
Gene	ASH1L	DOWN	I	early	18.917	30.9374	49.2683	36.6664	64.1426	78.8402
Gene	SEC14L1	DOWN	I	early	17.0147	46.4967	44.5102	44.6954	77.9927	70.8561
Gene	CXorf23	DOWN	I	early	13.5778	18.165	26.2577	29.6802	76.769	56.4772
Gene	ZNF83	DOWN	I	early	2.28133	5.02375	6.18391	3.53646	11.6251	9.48883
Gene	ZNF283	DOWN	I	early	2.07395	4.19591	3.80348	6.48557	11.1402	8.62552
Gene	STARD9	DOWN	I	early	1.0586	1.82058	2.59088	2.34676	2.10591	4.3949
Gene	ZNF211	DOWN	I	early	2.19054	2.49978	5.75618	5.04035	6.02771	9.09148
Gene	ZNF585B	DOWN	I	early	1.63884	2.54915	3.78916	2.9077	4.3278	6.78918
Gene	FAM122A	DOWN	I	early	1.91269	4.65346	7.06514	3.20937	6.69868	7.92044
Gene	FBXL4	DOWN	I	early	2.55066	3.87204	6.58824	4.9181	10.8998	10.5514
Gene	SASH1	DOWN	I	early	10.7908	18.6637	22.9476	11.7038	23.0528	44.5173
Gene	ITGA1	DOWN	I	early	1.74533	8.62499	15.2545	5.08589	13.8169	7.20029

Gene	NPHP3	DOWN	I	early	6.8715	15.1313	26.7995	19.1459	20.1552	28.3172
Gene	ZNF334	DOWN	I	early	1.40538	3.54859	2.80375	2.10337	2.41494	5.7829
Gene	USP11	DOWN	I	early	4.07709	9.20326	11.1416	19.8073	18.5316	16.7709
Gene	MSI2	DOWN	I	early	6.68426	12.1595	21.8488	25.0595	23.0646	27.4951
Gene	TCTN2	DOWN	I	early	0.934992	1.67708	2.6596	4.75866	2.97094	3.83949
Gene	ASTN2	DOWN	I	early	1.15592	1.20039	2.53218	4.80849	4.49347	4.73534
Gene	CCDC84	DOWN	I	early	5.01174	5.26662	9.10508	11.8785	14.849	20.5172
Gene	GYPC	DOWN	I	early	1.12525	5.59174	7.20431	13.9742	3.38556	4.60631
Gene	AGAP4	DOWN	I	early	0.86493	1.48955	2.08863	2.84152	3.68184	3.53975
Gene	FAM63A	DOWN	I	early	1.03821	1.73863	1.81473	2.40437	2.71791	4.24566
Gene	AGAP3	DOWN	I	early	2.53217	3.5409	2.80602	4.85425	3.13828	10.3512
Gene	CRTC3	DOWN	I	early	2.06487	4.48777	9.99657	17.3298	11.3787	8.42012
Gene	FAM193A	DOWN	I	early	4.70589	7.47017	11.137	14.179	18.943	19.1554
Gene	ZMYM5	DOWN	I	early	10.2884	17.1029	29.8714	11.5787	19.2097	41.7878
Gene	AHSA2	DOWN	I	early	8.15342	19.6149	22.4747	11.393	19.6138	33.1038
Gene	FAM164A	DOWN	I	early	8.70666	12.3724	22.3858	13.5224	31.4179	35.2777
Gene	GBP3	DOWN	I	early	3.11701	3.23152	9.06137	12.6739	33.7147	12.628
Gene	UBE2D4	DOWN	I	early	0.838471	2.14823	1.91647	3.37028	3.37963	3.39646
Gene	SMPD1	DOWN	I	early	1.06248	1.86379	3.45387	9.87847	7.6026	4.29752
Gene	HOMEZ	DOWN	I	early	1.88686	4.15353	5.20689	8.90002	15.4187	7.62994
Gene	TSGA10	DOWN	I	early	9.0206	10.9582	12.0679	11.6355	15.622	36.4474
Gene	BID	DOWN	I	early	1.30941	2.97454	2.99574	2.16925	2.61881	5.27646
Gene	KIAA0240	DOWN	I	early	3.31017	6.60564	7.89954	6.99918	9.89834	13.3046
Gene	STK17A	DOWN	I	early	2.53278	4.4469	12.0587	3.2163	7.97998	10.1767
Gene	C11orf71	DOWN	I	early	7.89459	17.6225	12.2653	9.68775	38.9882	31.69
Gene	SEC14L2	DOWN	I	early	0.868915	1.13039	2.11602	2.33599	2.79413	3.48253
Gene	ZNF154	DOWN	I	early	1.26631	2.18962	3.93271	2.30274	3.88353	5.06897
Gene	C11orf80	DOWN	I	early	0.980514	1.72105	1.84883	0.984358	1.94856	3.92368
Gene	DMTF1	DOWN	I	early	44.5772	118.84	148.72	102.508	242.309	178.344
Gene	LRRC7	DOWN	II	early-mid	0.0166697	5.43688	18.9051	11.4396	19.7951	43.267
Gene	SLC4A4	DOWN	II	early-mid	0.0247963	5.58985	29.855	36.7092	43.7684	57.8893
Gene	PCSK2	DOWN	II	early-mid	0.01	1.46601	15.4233	18.7116	28.129	10.077
Gene	PDGFA	DOWN	II	early-mid	0.0655948	11.2327	38.7967	29.44	58.6463	46.7031
Gene	KCND3	DOWN	II	early-mid	0.0184061	1.57787	5.28594	5.90857	8.75133	12.8361

Gene	LRRN1	DOWN	II	early-mid	0.0365075	1.08551	8.01371	9.04604	94.7039	24.7237
Gene	NT5E	DOWN	II	early-mid	0.01	0.272259	10.059	3.78542	21.896	6.54429
Gene	FHOD3	DOWN	II	early-mid	0.01	0.57585	5.01348	13.2979	20.3648	5.9564
Gene	MPDZ	DOWN	II	early-mid	0.318977	39.0037	87.1101	74.2105	133.95	165.024
Gene	GREB1	DOWN	II	early-mid	0.0119639	1.34064	3.80635	2.22262	5.94535	5.73616
Gene	THBS2	DOWN	II	early-mid	0.01	0.202653	2.12561	2.89265	4.93372	4.64352
Gene	ERG	DOWN	II	early-mid	0.0228353	1.10886	12.0647	22.3601	32.725	10.0593
Gene	LARGE	DOWN	II	early-mid	0.01	0.258495	1.59239	1.40091	1.29287	4.38752
Gene	CHST3	DOWN	II	early-mid	0.01	0.482523	1.51457	2.50275	1.64476	4.08001
Gene	GSG1L	DOWN	II	early-mid	0.01	0.328862	0.982077	1.8508	3.22741	3.65356
Gene	TCP10L	DOWN	II	early-mid	0.01	0.01	0.05754	0.0670704	1.4983	3.56947
Gene	C2orf84	DOWN	II	early-mid	0.01	0.01	0.187008	1.56004	0.661829	3.44285
Gene	GRIK4	DOWN	II	early-mid	0.01	0.216938	1.64187	1.25837	2.32807	3.43052
Gene	ARHGEF10L	DOWN	II	early-mid	0.01	0.112128	0.934219	1.14786	0.90523	3.38133
Gene	DUSP8	DOWN	II	early-mid	0.01	0.0951071	0.11831	0.475796	1.29339	3.10365
Gene	SOX5	DOWN	II	early-mid	0.132776	8.03319	19.8727	13.8433	16.8779	40.7592
Gene	SSTR1	DOWN	II	early-mid	0.01	0.641013	1.01628	2.08856	2.09016	2.89548
Gene	MAPK4	DOWN	II	early-mid	0.0603255	2.40085	10.3357	11.3864	15.3376	14.7579
Gene	NAV2	DOWN	II	early-mid	0.099957	1.97275	13.0443	13.138	20.8319	19.8637
Gene	SPEF2	DOWN	II	early-mid	0.0627556	1.01956	3.19873	4.89513	5.70854	11.897
Gene	PMEPA1	DOWN	II	early-mid	0.0535875	0.845194	9.49858	9.39049	9.77829	9.12984
Gene	FBXO32	DOWN	II	early-mid	0.136486	1.91417	8.264	6.31918	21.7687	22.5163
Gene	PPAP2A	DOWN	II	early-mid	0.118333	3.25396	9.47184	8.812	16.0368	17.8146
Gene	PLXDC2	DOWN	II	early-mid	0.136932	4.31221	10.2732	8.8447	10.0538	19.1634
Gene	TNS3	DOWN	II	early-mid	0.107385	1.68144	3.49898	12.8209	10.4472	13.1975
Gene	GFRA1	DOWN	II	early-mid	0.0735189	1.03547	3.78279	8.40508	18.4533	7.34401
Gene	MYOM1	DOWN	II	early-mid	0.0386638	0.803997	1.7894	1.92945	2.30284	3.4999
Gene	DIP2C	DOWN	II	early-mid	0.129439	0.962078	4.03547	4.0258	4.14059	11.5669

Gene	SERPING1	DOWN	II	early-mid	0.145507	1.69395	5.54278	5.79137	33.1493	12.231
Gene	LRRC70	DOWN	II	early-mid	0.0371246	0.589423	0.927306	1.02757	4.28907	2.86628
Gene	TTN	DOWN	II	early-mid	0.232792	3.0435	19.3719	7.51255	15.818	17.9505
Gene	DKK3	DOWN	II	early-mid	2.91751	18.1739	54.6339	126.784	154.728	210.819
Gene	PDZD2	DOWN	II	early-mid	0.762727	7.14716	22.444	21.6146	30.2238	51.2368
Gene	AGPAT4	DOWN	II	early-mid	0.330153	2.62152	6.82831	6.87303	13.8959	21.6254
Gene	GRB10	DOWN	II	early-mid	0.159173	1.30384	4.60192	4.59875	13.1103	10.395
Gene	C18orf1	DOWN	II	early-mid	0.201495	0.510849	7.547	6.31484	14.0579	12.3616
Gene	BGN	DOWN	II	early-mid	0.381616	2.72862	11.3852	20.5097	6.91237	15.9964
Gene	PPAPDC1A	DOWN	II	early-mid	0.104899	0.552785	1.47986	1.70063	2.21906	4.09902
Gene	SLC41A2	DOWN	II	early-mid	1.05845	3.35136	17.3956	14.7216	15.8489	38.7456
Gene	GRAMD3	DOWN	II	early-mid	2.8478	15.8942	33.6661	50.8809	55.8133	104.242
Gene	GPR183	DOWN	II	early-mid	0.157337	0.3975	1.45884	2.36939	2.43219	5.66313
Gene	CTSS	DOWN	II	early-mid	0.193659	0.442142	2.14177	2.79882	4.0753	6.86886
Gene	SLC2A11	DOWN	II	early-mid	9.24191	75.5515	190.914	122.557	144.91	318.002
Gene	PDE4DIP	DOWN	II	early-mid	11.9185	57.4881	120.008	127.246	113.559	408.105
Gene	CXXC5	DOWN	II	early-mid	0.246065	1.85866	4.66918	2.38592	3.06168	7.74522
Gene	C17orf57	DOWN	II	early-mid	0.192336	1.41451	5.82453	1.96454	6.18542	6.00473
Gene	YPEL2	DOWN	II	early-mid	0.40247	1.79814	3.66511	3.22746	4.64055	12.2782
Gene	ERRFI1	DOWN	II	early-mid	0.534212	3.24293	11.6315	4.95617	20.0073	15.8862
Gene	ITGA9	DOWN	II	early-mid	0.265897	1.12071	6.27296	17.4709	8.0348	7.70001
Gene	MITF	DOWN	II	early-mid	0.416261	0.920256	3.0248	5.66234	7.42687	11.2191
Gene	DFNA5	DOWN	II	early-mid	0.331906	1.88441	5.25708	4.3941	9.22669	8.93577
Gene	WWC1	DOWN	II	early-mid	2.71172	12.9419	23.4635	42.1015	43.3518	68.7123
Gene	MUC6	DOWN	II	early-mid	0.179829	0.575959	5.46005	2.84024	2.32512	4.53659
Gene	INA	DOWN	II	early-mid	1.06888	6.15397	14.9442	7.0136	17.3661	26.9478
Gene	RNF130	DOWN	II	early-mid	1.42581	6.65599	12.2143	11.7978	27.0149	34.7612
Gene	ARHGEF17	DOWN	II	early-mid	0.216589	1.15818	2.04916	4.12986	2.61547	5.25712

Gene	GFPT2	DOWN	II	early-mid	0.17755	0.293074	0.807477	1.81855	6.7217	4.08283
Gene	SORBS1	DOWN	II	early-mid	2.99635	12.5663	22.1171	22.135	34.925	68.2219
Gene	PLEKHH2	DOWN	II	early-mid	0.386578	1.06904	3.76193	2.15741	7.42782	8.43389
Gene	NCF2	DOWN	II	early-mid	0.138198	0.249701	1.01039	1.04456	1.31129	2.90988
Gene	CCDC92	DOWN	II	early-mid	1.67266	6.47128	15.4961	23.5823	21.1797	35.1289
Gene	NR1D1	DOWN	II	early-mid	0.400914	0.706182	2.91851	6.35625	4.5094	8.39511
Gene	CRTC1	DOWN	II	early-mid	0.14755	0.371326	0.859146	1.49369	2.4937	3.08435
Gene	THRA	DOWN	II	early-mid	0.854673	4.16644	4.87839	15.8307	5.57789	17.0998
Gene	SLC15A2	DOWN	II	early-mid	0.64899	2.16021	7.5113	3.95846	9.165	12.9786
Gene	FAM114A1	DOWN	II	early-mid	0.531179	1.57971	4.89274	4.26154	9.16236	9.96331
Gene	AXL	DOWN	II	early-mid	0.337147	1.06749	3.0854	4.30124	2.96944	6.23774
Gene	GSDMB	DOWN	II	early-mid	0.423706	1.54482	2.0413	3.06912	7.10247	7.32886
Gene	C20orf112	DOWN	II	early-mid	0.924939	3.50459	6.57971	5.46857	8.62434	15.3879
Gene	PPP1R12B	DOWN	II	early-mid	3.77254	14.6752	29.9523	26.9265	27.0379	62.5697
Gene	C1orf51	DOWN	II	early-mid	0.691617	1.8935	6.2769	8.43669	25.088	11.2422
Gene	IGF1R	DOWN	II	early-mid	0.587887	1.1348	2.49216	4.0602	12.272	9.09449
Gene	EVL	DOWN	II	early-mid	0.434359	1.46736	2.46841	3.84576	3.77262	6.70341
Gene	CCDC113	DOWN	II	early-mid	0.201317	0.379851	1.11575	1.57754	2.87327	3.09594
Gene	C11orf49	DOWN	II	early-mid	0.890474	2.38119	5.74634	5.75056	6.74085	13.6076
Gene	DCLK1	DOWN	II	early-mid	3.11716	11.717	22.7721	19.288	25.482	47.0243
Gene	PPAP2B	DOWN	II	early-mid	1.66996	6.12871	11.9806	11.1996	11.879	25.0406
Gene	ZER1	DOWN	II	early-mid	0.423653	1.17623	1.85126	4.86701	3.28998	6.238
Gene	ARHGAP31	DOWN	II	early-mid	0.290456	0.525877	2.07072	1.7473	1.53417	4.19518
Gene	CCDC149	DOWN	II	early-mid	0.879072	2.15467	4.22894	3.48803	4.12062	12.6734
Gene	MATN2	DOWN	II	early-mid	1.37227	2.29743	5.76721	9.83419	13.3397	19.1361
Gene	TMEM14E	DOWN	II	early-mid	0.822302	2.80484	6.14189	3.762	12.5364	11.3314
Gene	RAB15	DOWN	II	early-mid	0.323941	1.02294	1.16177	1.29161	2.58093	4.28316
Gene	NPIP	DOWN	II	early-mid	2.33607	3.97104	8.21193	10.3042	17.0198	30.2917

Gene	FRMD4A	DOWN	II	early-mid	1.75234	3.59638	7.67583	14.7938	18.6814	22.3511
Gene	KIAA1328	DOWN	II	early-mid	1.66614	4.2258	8.31064	7.68821	6.26213	20.9599
Gene	TANC2	DOWN	II	early-mid	1.05132	2.89259	4.49874	9.07023	11.4854	13.0507
Gene	LPHN1	DOWN	II	early-mid	0.457814	1.08005	1.38509	3.31548	4.51406	5.34274
Gene	TMEM175	DOWN	II	early-mid	0.47715	0.414121	0.844813	5.85428	1.69695	5.44924
Gene	HEG1	DOWN	II	early-mid	1.22522	3.14029	17.3865	13.4478	25.7545	13.8311
Gene	SEC61A2	DOWN	II	early-mid	18.962	51.3365	73.8119	117.062	263.184	211.722
Gene	CSRP1	DOWN	II	early-mid	2.68189	5.65762	8.76861	14.6975	14.6928	29.5032
Gene	KCNMA1	DOWN	II	early-mid	2.05601	1.85733	7.43167	7.92321	15.7759	22.0628
Gene	TOM1L2	DOWN	II	early-mid	1.06775	1.78628	2.9761	6.28701	10.3602	11.2186
Gene	TMEM140	DOWN	II	early-mid	0.506293	0.33507	1.37192	1.4757	1.4728	5.29641
Gene	LMLN	DOWN	II	early-mid	1.28973	2.83129	12.8135	14.3331	15.504	13.4518
Gene	TECPR2	DOWN	II	early-mid	0.782202	1.20725	2.66949	6.05038	4.52107	8.01794
Gene	COTL1	DOWN	II	early-mid	0.465766	1.02011	5.5214	6.40686	8.78339	4.77107
Gene	SPG20	DOWN	II	early-mid	9.01044	21.0629	38.6032	26.8861	51.7539	91.8692
Gene	MAK	DOWN	II	early-mid	0.32988	0.695888	1.86964	4.82018	1.25647	3.34478
Gene	ZNF594	DOWN	II	early-mid	0.791639	1.74201	2.06838	2.45931	3.24136	8.01672
Gene	SIRT2	DOWN	II	early-mid	2.03544	4.3044	6.54022	8.70805	7.81288	20.4088
Gene	SDCCAG8	DOWN	II	early-mid	8.03821	11.7251	24.7203	31.7492	23.6059	80.2678
Gene	KANK1	DOWN	II	early-mid	1.28996	2.42306	6.21304	10.7317	17.9009	12.8503
Gene	ALOX12	DOWN	II	early-mid	0.930308	1.81371	4.93668	2.6007	3.64899	9.16518
Gene	EFHD1	DOWN	II	early-mid	6.53997	9.74275	19.8472	76.9836	35.9229	63.9561
Gene	ZNF841	DOWN	II	early-mid	0.991188	2.17389	5.3017	4.42363	6.80201	9.47595
Gene	NRIP3	DOWN	II	early-mid	0.947307	2.0952	3.59586	2.90129	2.98963	8.99832
Gene	LHFPL2	DOWN	II	early-mid	1.41225	1.73904	4.95403	4.60526	16.2785	13.2976
Gene	ZBTB4	DOWN	II	early-mid	3.80857	6.99138	12.3913	25.9446	24.9013	35.3132
Gene	ZDHHC14	DOWN	II	early-mid	3.61049	3.11413	17.4271	8.72253	14.6153	33.1047
Gene	FAM131A	DOWN	II	early-mid	0.452322	0.608306	1.13664	1.18327	1.11754	4.11187

Gene	PODN	DOWN	II	early-mid	0.539627	0.922954	4.75411	9.84426	4.91924	4.81984
Gene	ZNF528	DOWN	II	early-mid	1.70495	3.68601	5.85256	7.78987	13.5066	15.0953
Gene	ZNF782	DOWN	II	early-mid	1.95071	4.00402	7.53549	4.68784	9.20532	17.1695
Gene	TMEM116	DOWN	II	early-mid	0.714329	1.01193	1.64835	2.20161	2.16553	6.23786
Gene	SPATA7	DOWN	II	early-mid	0.661595	1.08461	1.85337	2.07905	6.629	5.77571
Gene	WDR91	DOWN	II	early-mid	0.373305	0.486308	1.2479	1.80917	2.19833	3.21982
Gene	FAM171A1	DOWN	II	early-mid	4.11368	4.95249	11.3289	13.35	18.7132	35.0114
Gene	CLSTN3	DOWN	II	early-mid	0.824886	0.713414	2.90379	5.05779	6.06417	6.97647
Gene	RGS12	DOWN	II	early-mid	1.52058	2.66508	6.25208	4.59342	3.99926	12.7775
Gene	HDAC4	DOWN	II	early-mid	0.959829	2.00422	3.8729	2.61878	3.4116	8.05457
Gene	MKL2	DOWN	II	early-mid	5.2627	9.50955	14.6863	12.197	18.3955	43.5232
Gene	FHIT	DOWN	II	early-mid	1.50812	2.69711	6.5341	7.57867	9.92576	12.4266
Gene	ALMS1	DOWN	II	early-mid	4.3885	7.25565	9.22255	14.3077	19.635	35.8165
Gene	SFI1	DOWN	II	early-mid	0.749345	1.11092	2.62961	2.45487	5.49889	6.08065
Gene	MORN4	DOWN	II	early-mid	0.740544	0.849223	1.55612	2.23246	2.02548	5.93771
Gene	PKD2	DOWN	II	early-mid	2.57348	4.43368	12.8265	5.73349	13.497	20.1581
Gene	FAM22D	DOWN	II	early-mid	0.523123	0.817623	1.12122	0.89411	1.41782	4.01733
Gene	ZNF790	DOWN	II	early-mid	2.41425	4.53742	10.0272	7.26493	11.1013	18.4632
Gene	HYI	DOWN	II	early-mid	2.13984	3.66875	8.76668	7.17992	4.86242	16.3586
Gene	SRPK2	DOWN	II	early-mid	16.0759	26.1622	58.8082	52.3323	83.0957	121.973
Gene	MACF1	DOWN	II	early-mid	91.4055	131.807	271.999	268.163	406.275	688.397
Gene	ZNF25	DOWN	II	early-mid	1.99203	3.72216	5.52215	4.20207	4.22418	14.9412
Gene	FCHSD2	DOWN	II	early-mid	12.4282	17.672	38.1282	32.2649	75.7098	92.9736
Gene	RSPH3	DOWN	II	early-mid	1.94838	2.54088	5.16174	5.69678	7.62024	14.4107
Gene	CD99L2	DOWN	II	early-mid	1.39974	2.10413	4.43521	3.4421	6.12232	10.1575
Gene	PPFIBP2	DOWN	II	early-mid	2.63168	2.19914	7.13472	17.3945	17.6069	18.8517
Gene	GPX3	DOWN	II	early-mid	1.82134	1.84576	11.3479	13.4665	26.5576	12.9638
Gene	LRRC37A	DOWN	II	early-mid	1.39281	1.96438	4.02536	3.28287	4.24898	9.87216

Gene	ZHX3	DOWN	II	early-mid	2.37637	2.4657	4.60412	8.43387	7.03381	16.6328
Gene	UBE2L6	DOWN	II	early-mid	1.44689	1.00502	3.25975	7.0815	17.162	9.96605
Gene	DOCK5	DOWN	II	early-mid	7.06485	6.13953	20.8072	24.0229	39.8165	48.1068
Gene	RABL2A	DOWN	II	early-mid	1.3162	1.80374	3.67137	7.89324	5.54327	8.76047
Gene	CHKA	DOWN	II	early-mid	2.54649	3.08286	4.9598	4.54397	6.55398	16.5942
Gene	SNX24	DOWN	II	early-mid	2.15163	3.45163	7.17909	4.22999	3.90375	13.9473
Gene	NUPR1	DOWN	II	early-mid	3.35356	4.9388	30.9172	66.3343	67.4496	21.7246
Gene	PACS2	DOWN	II	early-mid	0.945437	0.876013	1.55369	4.8557	5.57866	6.07423
Gene	USP31	DOWN	II	early-mid	2.16859	3.21482	4.7673	4.11821	5.56776	13.9149
Gene	HERC1	DOWN	II	early-mid	4.90759	6.63005	9.62038	10.3539	13.6759	31.17
Gene	DNHD1	DOWN	II	early-mid	1.95499	2.23691	4.37323	5.13077	5.04083	12.2675
Gene	NFIA	DOWN	II	early-mid	8.05755	11.2589	18.6913	22.0639	24.2549	49.8813
Gene	SIRT3	DOWN	II	early-mid	2.47977	3.185	4.79491	7.8502	8.933	15.3472
Gene	PTPRA	DOWN	II	early-mid	16.464	21.3291	32.4051	33.6281	46.3156	101.893
Gene	GSN	DOWN	II	early-mid	1.72372	2.36352	5.49445	9.9277	7.39274	10.5326
Gene	TOLLIP	DOWN	II	early-mid	0.79693	0.728338	3.32567	1.40455	1.95382	4.86955
Gene	KIF16B	DOWN	II	early-mid	8.55828	8.63831	20.0534	29.0855	23.4471	51.9681
Gene	MAGI1	DOWN	II	early-mid	4.75063	4.23091	24.9196	31.2788	57.5415	28.7697
Gene	ARHGAP21	DOWN	II	early-mid	56.4859	71.3063	111.167	117.7	104.646	336.834
Gene	PTPN21	DOWN	II	early-mid	1.28861	1.80253	6.24579	3.72705	10.4211	7.68224
Gene	RAB4B	DOWN	II	early-mid	1.1384	0.952481	5.30906	9.70651	2.78433	6.72142
Gene	PLD3	DOWN	II	early-mid	2.05753	2.60571	4.77086	9.63393	7.4197	12.0479
Gene	ARHGEF1	DOWN	II	early-mid	0.828	0.860696	2.50591	4.37809	2.94413	4.81907
Gene	ATP9A	DOWN	II	early-mid	11.869	16.0982	31.3745	25.6307	31.9429	66.6287
Gene	ZDHHC9	DOWN	II	early-mid	8.40727	9.40823	12.5204	28.0304	32.1126	45.3039
Gene	RFTN1	DOWN	II	early-mid	0.704149	0.645425	1.01738	1.34729	2.05757	3.70571
Gene	UBR3	DOWN	II	early-mid	14.2442	17.828	36.9218	19.3355	37.6049	74.9058
Gene	NBPF3	DOWN	II	early-mid	0.613797	0.721236	2.64737	3.57986	1.69272	3.22129

Gene	ST6GALNAC6	DOWN	II	early-mid	3.64163	2.95052	5.0866	10.345	5.76684	19.0232
Gene	RBMS3	DOWN	II	early-mid	4.65356	3.04483	12.3155	13.497	37.6336	24.1597
Gene	SGMS1	DOWN	II	early-mid	3.15946	3.34224	4.64322	6.48397	9.46484	16.2406
Gene	FNDC3B	DOWN	II	early-mid	33.2309	40.2286	137.042	168.061	197.766	169.007
Gene	CBFA2T2	DOWN	II	early-mid	1.99413	1.5471	3.15218	3.83171	5.46857	9.84635
Gene	ZNF438	DOWN	II	early-mid	0.851194	0.931342	1.35881	1.44134	2.42373	4.18671
Gene	VPS13D	DOWN	II	early-mid	3.87488	4.13834	6.27473	8.32337	8.57514	18.6871
Gene	CAMKK2	DOWN	II	early-mid	1.89792	1.88508	2.3672	4.55406	2.51149	8.80454
Gene	BICD1	DOWN	II	early-mid	9.77116	10.4812	15.3231	20.1789	62.4573	45.0914
Gene	ABR	DOWN	II	early-mid	7.87195	6.17226	12.1431	28.8423	37.7798	36.1517
Gene	MINK1	DOWN	II	early-mid	1.70088	1.71812	4.85687	8.65999	5.22119	7.73772
Gene	PIK3C2B	DOWN	II	early-mid	1.22394	1.1534	2.04474	2.52768	5.07452	5.46361
Gene	ZSCAN18	DOWN	II	early-mid	1.83581	1.69391	2.80896	3.23084	6.55092	7.9723
Gene	AP1G2	DOWN	II	early-mid	2.21342	1.23829	2.21697	3.48261	3.72056	9.61074
Gene	CDC14A	DOWN	II	early-mid	5.25893	5.26134	6.34243	7.9737	24.3898	22.5327
Gene	PPP1R13B	DOWN	II	early-mid	1.66915	0.899056	3.88923	3.53811	2.25223	7.059
Gene	AAK1	DOWN	II	early-mid	12.6119	10.737	19.2008	23.4758	28.5371	52.5722
Gene	ZNF674	DOWN	II	early-mid	1.22767	0.862744	4.45416	1.33048	2.2989	5.08944
Gene	CSRP2	DOWN	II	early-mid	1.60696	1.20229	3.53673	4.00008	19.1719	6.57438
Gene	PHLDA1	DOWN	II	early-mid	0.877649	0.79113	4.98908	2.03034	3.78985	3.57574
Gene	TMTC2	DOWN	II	early-mid	12.7997	8.11151	24.5386	18.6875	33.4901	51.371
Gene	PDE1C	DOWN	III	mid-late	0.00446751	9.18624	12.5943	46.6136	52.8288	95.6967
Gene	CADM3	DOWN	III	mid-late	0.01	1.36694	1.13004	29.4744	35.3384	48.4246
Gene	CTNNA2	DOWN	III	mid-late	0.01	1.25031	3.80085	13.7877	16.6682	39.9649
Gene	CHI3L1	DOWN	III	mid-late	0.01	0.892828	1.20059	8.96919	15.3893	31.3867
Gene	CNTN3	DOWN	III	mid-late	0.01	3.88169	3.65512	8.98761	8.9162	17.1416
Gene	PCDHB5	DOWN	III	mid-late	0.01	0.268537	2.63433	8.44462	10.5777	16.0138
Gene	FAM177B	DOWN	III	mid-late	0.01	1.52271	1.27056	11.2865	11.5847	15.621
Gene	KCNN3	DOWN	III	mid-late	0.01	0.432775	1.99368	6.43746	5.47912	9.38239

Gene	SETBP1	DOWN	III	mid-late	0.01	0.236965	0.991785	2.69466	3.50843	8.85131
Gene	TSTD1	DOWN	III	mid-late	0.01	0.01	0.01	0.12326	0.187953	7.01829
Gene	PCDHB7	DOWN	III	mid-late	0.01	0.367527	0.109045	1.98926	1.54941	6.60179
Gene	ADAMTS9	DOWN	III	mid-late	0.01	0.0582848	0.366369	4.15084	6.59678	6.17265
Gene	C5	DOWN	III	mid-late	0.0136069	0.702079	0.640651	1.66119	0.641353	6.83895
Gene	NOS1AP	DOWN	III	mid-late	0.01	0.275412	0.954785	1.53156	1.56178	4.78905
Gene	IFFO2	DOWN	III	mid-late	0.00923388	0.312703	0.6029	1.50838	1.13397	3.81958
Gene	FNDC9	DOWN	III	mid-late	0.01	0.01	0.0929292	2.62937	0.916736	4.03956
Gene	C20orf26	DOWN	III	mid-late	0.01	0.01	0.01	0.18005	0.799601	4.03561
Gene	TMEM196	DOWN	III	mid-late	0.01	0.01	0.0415291	0.10066	0.26328	3.98528
Gene	KLF8	DOWN	III	mid-late	0.01	0.0967823	0.323602	2.28708	2.20325	3.67299
Gene	CUX2	DOWN	III	mid-late	0.0104544	0.665131	0.713116	1.70969	4.69633	3.77406
Gene	EPHX2	DOWN	III	mid-late	0.01	0.519967	0.20947	1.09876	1.62734	3.60317
Gene	SLC24A3	DOWN	III	mid-late	0.01	0.0452318	0.443455	2.04688	1.26934	3.50976
Gene	ARHGAP25	DOWN	III	mid-late	0.01	0.0900672	0.179722	0.787741	1.16363	3.14829
Gene	LRRTM1	DOWN	III	mid-late	0.01	0.142695	0.182869	1.03877	0.760625	3.11192
Gene	FAM19A5	DOWN	III	mid-late	0.01	0.01	0.01	0.226761	0.674851	2.98411
Gene	CLDN1	DOWN	III	mid-late	0.01	0.01	0.01	0.705481	4.69477	2.87871
Gene	PDZRN4	DOWN	III	mid-late	0.0190071	0.368182	0.508297	0.963374	0.884996	3.98415
Gene	HSPB8	DOWN	III	mid-late	0.170297	2.47573	2.21077	17.8081	15.2996	35.4909
Gene	SYT2	DOWN	III	mid-late	0.0277645	0.500898	0.458662	2.79597	2.65348	5.68726
Gene	FAM129A	DOWN	III	mid-late	0.0158095	0.125773	0.291266	0.840843	1.9862	3.23404
Gene	SRGAP3	DOWN	III	mid-late	0.529238	5.62085	14.3723	28.4507	50.4046	92.2894
Gene	ZIM2	DOWN	III	mid-late	0.431263	12.6723	10.1748	22.6292	54.5947	69.5051
Gene	LRRC4	DOWN	III	mid-late	0.0836376	2.23328	2.76135	6.08326	6.25039	12.8557
Gene	CDH8	DOWN	III	mid-late	0.0284355	0.918685	0.775575	1.09473	1.78674	3.81703
Gene	CRYAB	DOWN	III	mid-late	8.63532	38.0428	210.018	391.986	320.286	1091.49
Gene	C2CD2	DOWN	III	mid-late	0.237935	3.06359	6.47651	10.9457	20.6729	27.0202
Gene	THY1	DOWN	III	mid-late	0.206658	3.35371	5.17978	11.0377	13.234	22.7125
Gene	EPHB1	DOWN	III	mid-late	0.0353721	0.01	0.0949765	0.604089	2.18243	3.41761
Gene	ZBTB20	DOWN	III	mid-late	2.45906	25.085	55.2674	64.4909	126.908	235.585

Gene	NOTCH4	DOWN	III	mid-late	0.0411875	0.0332294	0.139027	0.932529	0.624416	2.79204
Gene	TSPAN5	DOWN	III	mid-late	0.276106	0.632694	3.88329	5.35586	8.45527	17.3911
Gene	BHMT2	DOWN	III	mid-late	0.380535	2.79241	2.69436	14.4809	42.6195	23.3741
Gene	GRM1	DOWN	III	mid-late	0.136766	0.540603	1.59284	4.0434	6.37634	8.33096
Gene	GAB2	DOWN	III	mid-late	0.881091	2.10903	5.67827	12.89	13.8513	47.704
Gene	INSR	DOWN	III	mid-late	0.182385	0.684903	1.45402	2.51082	5.20145	9.41679
Gene	PTGDS	DOWN	III	mid-late	2.21209	8.19892	8.94478	47.279	32.0293	95.5388
Gene	PADI2	DOWN	III	mid-late	0.83222	2.00452	8.22945	12.0282	10.3319	33.5303
Gene	IGFBP3	DOWN	III	mid-late	0.116029	0.01	0.01	0.472074	1.76687	4.39233
Gene	VAMP2	DOWN	III	mid-late	33.4482	229.548	270.772	424.973	333.892	1138.59
Gene	TAS2R4	DOWN	III	mid-late	0.116304	0.179845	0.595353	1.26577	2.11058	3.72059
Gene	WBSCR17	DOWN	III	mid-late	0.167116	0.384141	1.14954	3.03369	7.16773	4.97513
Gene	C5orf4	DOWN	III	mid-late	2.24948	8.00869	14.605	17.5459	22.3206	63.915
Gene	KIAA1671	DOWN	III	mid-late	0.354996	0.806556	1.84177	2.64228	10.0944	9.59431
Gene	FMNL3	DOWN	III	mid-late	0.363118	1.73314	2.10727	3.32572	6.73434	9.74345
Gene	PCDHGB6	DOWN	III	mid-late	0.142809	0.298489	0.77088	1.76428	5.65159	3.71856
Gene	TTC21A	DOWN	III	mid-late	0.178406	0.510978	0.288872	1.51994	1.19696	4.28745
Gene	KIAA0513	DOWN	III	mid-late	0.234121	0.721763	0.931607	1.97954	1.43124	5.37089
Gene	ZNF135	DOWN	III	mid-late	0.851408	2.33694	4.24288	14.5572	10.7467	19.1033
Gene	KIFC2	DOWN	III	mid-late	0.142499	0.343492	0.476182	0.449548	0.619275	2.9482
Gene	LDOC1	DOWN	III	mid-late	0.600529	2.07637	2.49027	7.65711	8.04744	11.126
Gene	C6orf105	DOWN	III	mid-late	0.200306	0.01	0.439828	0.120355	0.553724	3.51091
Gene	PCDHGC3	DOWN	III	mid-late	0.492015	1.05123	1.24099	2.21663	3.53148	8.50114
Gene	ADHFE1	DOWN	III	mid-late	0.836761	2.12109	1.37536	6.10496	5.23945	14.3172
Gene	ZFHX2	DOWN	III	mid-late	0.323154	0.944776	1.25763	2.54846	3.33018	5.45355
Gene	DNAJB2	DOWN	III	mid-late	1.33243	1.03952	4.04316	6.84328	8.65737	22.4487
Gene	SNX32	DOWN	III	mid-late	0.180614	0.195349	0.269358	0.903644	1.38884	2.85539
Gene	SLC48A1	DOWN	III	mid-late	2.15478	5.13264	5.85081	12.4044	10.823	33.7899
Gene	DUSP18	DOWN	III	mid-late	0.625057	0.524662	0.952156	2.76319	3.15597	9.36431
Gene	AMIGO1	DOWN	III	mid-late	0.391868	0.680401	1.22444	2.36036	2.50601	5.73342
Gene	APOL3	DOWN	III	mid-late	0.581346	0.904414	1.07195	3.17309	3.8105	8.2159

Gene	MRAS	DOWN	III	mid-late	15.6208	21.6623	31.9781	56.0949	91.4615	210.621
Gene	SHISA4	DOWN	III	mid-late	0.345273	0.593317	0.221482	3.3408	2.43455	4.64863
Gene	ZCCHC24	DOWN	III	mid-late	0.902865	1.26199	1.76167	2.98996	3.145	11.8555
Gene	PHC1	DOWN	III	mid-late	1.91753	2.53975	2.76724	13.8747	38.2383	24.8447
Gene	ANKRD6	DOWN	III	mid-late	0.413163	0.82252	1.12349	2.91493	4.82019	5.12067
Gene	MAPRE3	DOWN	III	mid-late	0.59547	0.236593	1.26107	1.79072	2.81953	7.11185
Gene	LAT2	DOWN	III	mid-late	0.364655	0.545559	0.612591	0.933915	0.735225	4.18508
Gene	SPRYD3	DOWN	III	mid-late	0.515752	0.604298	0.477995	2.3857	1.72967	5.84388
Gene	BIN1	DOWN	III	mid-late	0.982687	1.02766	1.90298	10.2965	8.2301	10.872
Gene	CLSTN2	DOWN	III	mid-late	0.670613	0.290485	0.885106	2.08408	2.61379	7.00031
Gene	MXI1	DOWN	III	mid-late	15.5394	28.2665	28.0402	46.364	77.2198	161.845
Gene	ROGDI	DOWN	III	mid-late	0.413398	0.519153	0.625062	3.42083	1.74483	4.17307
Gene	DUSP22	DOWN	III	mid-late	1.07095	1.43105	1.51866	2.76901	8.65581	10.1477
Gene	BBS1	DOWN	III	mid-late	1.14285	2.05362	1.43637	7.00078	5.18248	10.7609
Gene	SH3GLB2	DOWN	III	mid-late	0.557312	0.558476	0.521364	1.59089	1.98799	5.23903
Gene	PCDHA3	DOWN	III	mid-late	0.285005	0.182669	0.291746	0.825501	0.459683	2.6738
Gene	KIF3C	DOWN	III	mid-late	1.88234	2.75064	2.67879	6.31732	5.6842	16.8544
Gene	AKR1E2	DOWN	III	mid-late	0.759466	0.977093	0.935051	3.51585	5.5111	6.73079
Gene	YPEL3	DOWN	III	mid-late	0.90373	0.92219	1.20464	5.48787	3.25586	7.92864
Gene	RNF24	DOWN	III	mid-late	0.586794	0.902093	1.23064	1.83019	4.08296	4.97744
Gene	GM2A	DOWN	III	mid-late	2.49662	3.26473	3.93761	6.15579	6.94992	21.1757
Gene	VAMP1	DOWN	III	mid-late	3.04967	4.43286	3.21001	25.1197	9.48561	24.7402
Gene	RERE	DOWN	III	mid-late	23.7109	29.2464	47.2909	61.1704	71.9	189.211
Gene	TEF	DOWN	III	mid-late	0.455962	0.23838	0.744982	0.973469	1.04081	3.5819
Gene	CRY2	DOWN	III	mid-late	1.13604	1.79567	2.17375	3.4392	3.05754	8.9031
Gene	TRIM3	DOWN	III	mid-late	0.738384	0.83406	1.26277	2.177	2.17048	5.67314
Gene	NCS1	DOWN	III	mid-late	1.16939	1.44016	1.25351	2.76071	2.42996	8.86207
Gene	RAD52	DOWN	III	mid-late	4.71064	5.64937	4.66798	28.3067	19.0876	35.3485
Gene	EZH1	DOWN	III	mid-late	2.67136	4.10572	3.71204	6.84524	10.9992	18.2905
Gene	SFXN3	DOWN	III	mid-late	1.88958	0.940387	1.88559	8.956	5.01915	12.2904
Gene	PRPF40B	DOWN	III	mid-late	2.11734	1.61906	2.482	10.9405	4.10313	13.5807
Gene	ZNRF3	DOWN	III	mid-late	0.796661	0.913154	0.815922	1.2961	1.41576	5.08253

Gene	WDR60	DOWN	III	mid-late	22.6058	31.0957	34.9373	40.0964	49.7371	141.564
Gene	C9orf25	DOWN	III	mid-late	1.88749	2.23815	2.25339	3.41335	4.05209	11.6908
Gene	CNIH3	DOWN	III	mid-late	1.23905	0.99797	1.78843	2.03816	3.14705	7.59142
Gene	DENND3	DOWN	III	mid-late	1.78578	1.18754	1.73988	2.72768	2.7147	10.8235
Gene	RAB3A	DOWN	III	mid-late	1.84676	1.57898	0.929774	7.63533	5.26326	9.91159
Gene	MPP1	DOWN	III	mid-late	1.94718	1.8513	2.3791	3.75963	5.8036	10.1242
Gene	SYNJ1	DOWN	III	mid-late	7.9068	9.30234	6.06825	16.8934	15.2933	40.977
Gene	CD160	DOWN	III	mid-late	0.587141	0.523579	0.706953	1.29921	1.31788	2.90427
Gene	ECE2	DOWN	III	mid-late	0.622062	0.229684	0.467479	0.746791	0.438954	2.87198
Gene	IQCE	DOWN	III	mid-late	0.722779	0.484603	0.78811	2.28429	2.73798	3.31748
Gene	CPNE2	DOWN	III	mid-late	0.767781	0.656357	0.815407	2.02081	1.33156	3.47582
Gene	GCNT1	DOWN	III	mid-late	1.29677	0.345224	0.864336	0.794258	5.14541	5.68135
Gene	RAB3B	DOWN	III	mid-late	1.60474	0.338327	0.403377	1.88105	12.7145	6.93825
Gene	DDRGK1	DOWN	III	mid-late	5.34055	5.05852	5.06621	8.09989	8.34966	22.8607
Gene	CAMK2B	DOWN	III	mid-late	3.53198	3.03184	3.30208	7.88123	4.84124	15.0421
Gene	HSPA1L	DOWN	III	mid-late	0.846076	0.749744	0.772684	1.30885	1.77508	3.52619
Gene	CACNA1C	DOWN	III	mid-late	2.09597	0.745916	1.98091	2.45031	7.53611	8.71739
Gene	VASH1	DOWN	III	mid-late	0.704599	0.455243	0.645822	1.46519	1.9906	2.90574
Gene	SH3D19	DOWN	IV	late	0.00925732	0.345858	5.27738	25.2381	112.142	162.14
Gene	GAP43	DOWN	IV	late	0.01	0.365633	0.284645	2.27546	71.3796	153.875
Gene	MAPK10	DOWN	IV	late	0.01	0.138849	0.550277	0.01	25.8985	99.8518
Gene	PTPRD	DOWN	IV	late	0.0112903	14.0147	7.93112	7.36984	35.2754	100.757
Gene	CPNE8	DOWN	IV	late	0.01	0.7626	0.01	0.358679	23.9828	76.9657
Gene	NMNAT2	DOWN	IV	late	0.00916796	0.633892	0.863147	2.79502	18.9918	68.7209
Gene	NEGR1	DOWN	IV	late	0.01	2.88244	10.0378	2.24212	24.2646	72.9833
Gene	LRRTM4	DOWN	IV	late	0.01	2.34728	4.49842	5.62541	50.1696	50.2879
Gene	NELL2	DOWN	IV	late	0.0563069	26.3118	38.7786	6.16877	111.591	262.376
Gene	STMN2	DOWN	IV	late	0.01	0.209051	0.255367	0.831551	34.5501	41.192
Gene	C9orf4	DOWN	IV	late	0.01	0.0692595	0.382995	0.01	8.91721	32.8248
Gene	PTPN13	DOWN	IV	late	0.01	0.0885463	0.0288563	0.0368781	34.1888	30.5599
Gene	LGI1	DOWN	IV	late	0.01	0.942492	2.11842	0.481633	14.5116	28.1772
Gene	TTLL7	DOWN	IV	late	0.294215	5.64971	2.04449	6.83917	47.8979	798.464
Gene	HDX	DOWN	IV	late	0.01	2.06885	0.728915	0.256784	12.1111	23.1477

Gene	SH3BGRL	DOWN	IV	late	0.0472391	9.41492	18.6064	15.6247	38.0396	107.036
Gene	ADD2	DOWN	IV	late	0.01	0.01	0.0803461	0.01	42.2011	21.5166
Gene	CDH9	DOWN	IV	late	0.01	0.0984899	0.01	0.87094	39.2692	19.2831
Gene	CD200	DOWN	IV	late	0.01	0.460136	0.143034	0.960682	10.584	18.1667
Gene	FAM131B	DOWN	IV	late	0.01	0.0613441	0.153929	0.102343	7.74492	17.9322
Gene	CDH2	DOWN	IV	late	0.01	0.259487	0.532287	2.62069	24.7019	17.7893
Gene	ST6GALNAC3	DOWN	IV	late	0.00585721	0.0545745	0.16486	0.189045	6.52373	10.1607
Gene	NCALD	DOWN	IV	late	0.01	3.48723	3.31424	3.00726	5.20181	17.1063
Gene	NAP1L3	DOWN	IV	late	0.0166782	4.53379	0.84787	1.64248	9.34718	28.1134
Gene	PTPRZ1	DOWN	IV	late	0.0856027	0.279653	0.0065426	0.0629194	63.5671	136.723
Gene	PHKA1	DOWN	IV	late	0.00814829	0.25944	0.649278	2.1796	6.38728	12.7231
Gene	CA8	DOWN	IV	late	0.01	1.04156	0.53321	0.182687	7.44443	13.9786
Gene	NEK10	DOWN	IV	late	0.01	0.682492	1.96508	2.9694	4.43629	13.3367
Gene	KLHL4	DOWN	IV	late	0.01	0.01	0.01	0.01	7.36445	13.2375
Gene	ST6GAL1	DOWN	IV	late	0.0126504	1.4941	0.0781711	0.042184	23.9503	14.6864
Gene	BEX1	DOWN	IV	late	0.0674912	1.33124	0.0682625	0.0866021	19.7413	77.8326
Gene	RAMP2	DOWN	IV	late	0.01	1.84366	0.0731007	0.73148	5.57418	11.4403
Gene	DPYSL5	DOWN	IV	late	0.01	0.494936	0.557593	0.113016	10.2156	11.2193
Gene	PCDH11X	DOWN	IV	late	0.01	0.0340529	0.00452103	0.01	4.56508	10.9065
Gene	SRRM4	DOWN	IV	late	0.01	0.01	0.00630704	0.01	4.33591	10.0937
Gene	SYT4	DOWN	IV	late	0.01	0.296762	0.0453333	0.250839	4.53741	9.95681
Gene	C8orf34	DOWN	IV	late	0.01	0.351685	1.05117	0.653102	3.03337	9.62189
Gene	ZC4H2	DOWN	IV	late	0.01	0.01	0.746509	0.01	11.5656	9.59559
Gene	PARM1	DOWN	IV	late	0.01	0.187829	0.101992	0.0574943	6.4912	9.45864
Gene	TRPM3	DOWN	IV	late	0.01	0.135877	0.16635	1.0422	4.84499	9.15793
Gene	MRAP2	DOWN	IV	late	0.01	0.14821	2.08621	1.48372	5.8442	8.96142
Gene	MIPOL1	DOWN	IV	late	0.01	0.772193	1.14282	0.988992	2.16252	8.83737
Gene	LPL	DOWN	IV	late	0.01	0.618024	0.0838625	0.41537	4.20692	8.39142
Gene	MAP6	DOWN	IV	late	0.0147671	0.993719	0.01	0.170569	5.95057	12.3892
Gene	MBOAT2	DOWN	IV	late	0.0361627	1.77747	4.11118	6.35873	8.84765	29.6176
Gene	SCG2	DOWN	IV	late	0.0179878	0.01	0.239735	0.142888	3.16448	14.5845
Gene	CSF1R	DOWN	IV	late	0.01	0.01	0.01	0.0538512	0.0401761	8.01687
Gene	GRM3	DOWN	IV	late	0.029708	0.227633	0.109362	0.137528	5.93295	23.0911
Gene	RASA3	DOWN	IV	late	0.01	0.105877	1.2961	0.29387	2.53029	7.75604
Gene	LST1	DOWN	IV	late	0.01	0.506461	0.199756	0.273475	1.65582	7.68187

Gene	PLA2G7	DOWN	IV	late	0.01	0.107361	0.01	0.0562912	3.89224	7.40549
Gene	C1orf21	DOWN	IV	late	0.279531	0.924778	2.63946	11.4494	122.415	206.553
Gene	PCDHB14	DOWN	IV	late	0.01	0.515208	0.775093	0.901289	3.14986	7.36779
Gene	TMEM150C	DOWN	IV	late	0.01	0.01	0.690464	0.267364	3.94748	7.14044
Gene	DLEU7	DOWN	IV	late	0.01	0.381051	0.233675	0.87638	1.36162	7.10144
Gene	RHOJ	DOWN	IV	late	0.01	0.211923	0.713923	0.805233	1.95847	6.91452
Gene	C7orf62	DOWN	IV	late	0.01	0.01	0.01	0.01	1.83892	6.86594
Gene	C12orf53	DOWN	IV	late	0.01	0.337835	0.369282	0.549844	1.7564	6.81225
Gene	ELAVL3	DOWN	IV	late	0.01	0.01	0.0299732	0.01	1.78913	6.6285
Gene	GIMAP5	DOWN	IV	late	0.01	0.01	0.01	0.01	2.79443	6.62007
Gene	CDH13	DOWN	IV	late	0.01	0.658615	0.470379	0.870604	1.70498	6.30237
Gene	KCNMB2	DOWN	IV	late	0.01	0.01	0.0479974	0.01	0.281919	6.23644
Gene	C3orf15	DOWN	IV	late	0.01	0.01	0.01	0.271895	6.36578	5.9829
Gene	UNC5D	DOWN	IV	late	0.01	0.112001	0.137971	0.01	3.48067	5.73907
Gene	SOX21	DOWN	IV	late	0.01	0.01	0.01	0.01	2.8846	5.7187
Gene	PRKAA2	DOWN	IV	late	0.0110757	0.193946	0.125467	0.134777	3.02017	6.00335
Gene	FLI1	DOWN	IV	late	0.01	0.01	0.01	0.0612866	1.82783	5.37745
Gene	SYT16	DOWN	IV	late	0.01	0.01	0.190141	0.331771	1.02014	5.30799
Gene	RSPO3	DOWN	IV	late	0.01	0.0217163	0.01	0.128452	1.29891	5.27573
Gene	XKR4	DOWN	IV	late	0.01	0.0450636	0.0795328	0.01	3.63548	5.19504
Gene	BMP7	DOWN	IV	late	0.01	0.01	0.01	0.01	2.08459	5.19482
Gene	SPINK7	DOWN	IV	late	0.01	0.151463	0.660697	0.251025	0.926336	5.10616
Gene	MAP2	DOWN	IV	late	0.445874	7.75035	8.03997	7.8645	75.8441	226.647
Gene	SULT1C4	DOWN	IV	late	0.01	1.08403	1.1738	0.497918	3.41469	5.02005
Gene	RIC3	DOWN	IV	late	0.0659801	1.37011	1.66024	1.14969	17.8246	32.7278
Gene	CAMK1G	DOWN	IV	late	0.01	0.01	0.01	0.125285	6.29721	4.70622
Gene	SLITRK5	DOWN	IV	late	0.01	0.186644	0.658906	0.305287	1.14276	4.66759
Gene	CALN1	DOWN	IV	late	0.01	0.391519	0.256153	1.02702	1.30634	4.59614
Gene	C6orf138	DOWN	IV	late	0.01	0.166809	0.246863	0.0748185	1.08108	4.52589
Gene	RPS6KA6	DOWN	IV	late	0.01	0.01	0.01	0.01	1.48896	4.47725
Gene	HEPH	DOWN	IV	late	0.0120109	0.0477284	0.172522	0.368172	1.92158	5.34427
Gene	ZNF462	DOWN	IV	late	0.053184	0.856764	1.84655	4.91365	47.5149	23.5596
Gene	FABP7	DOWN	IV	late	0.0578476	0.228998	0.181451	0.01	16.0914	24.8315
Gene	HIF3A	DOWN	IV	late	0.04254	0.937567	0.314334	0.0869139	10.7981	18.2161

Gene	CEND1	DOWN	IV	late	0.01	0.01	0.137937	0.108072	1.23632	4.28171
Gene	HPSE2	DOWN	IV	late	0.01	0.01	0.134092	0.181344	2.11417	4.1594
Gene	PCP4L1	DOWN	IV	late	0.01	0.139609	0.162726	0.2526	3.12179	4.03481
Gene	ZIC5	DOWN	IV	late	0.01	0.208098	0.01	0.0856756	2.35105	4.02817
Gene	KCNH5	DOWN	IV	late	0.01	0.01	0.01	0.020636	1.13411	3.92785
Gene	SNCB	DOWN	IV	late	0.01	0.01	0.01	0.01	0.340048	3.88215
Gene	ZNF521	DOWN	IV	late	0.01	0.233959	0.0261061	0.191956	8.56884	3.87568
Gene	EHD3	DOWN	IV	late	0.0267477	0.40841	0.924669	1.00076	2.8541	10.2334
Gene	ANGPTL2	DOWN	IV	late	0.01	0.0888583	0.193499	0.912344	1.87856	3.7836
Gene	KBTBD12	DOWN	IV	late	0.01	0.368517	0.466978	0.065267	0.164704	3.71152
Gene	PKNOX2	DOWN	IV	late	0.0123444	0.213826	0.149412	0.41622	1.79605	4.55379
Gene	INSM1	DOWN	IV	late	0.01	0.158698	0.17362	0.13303	10.3435	3.62908
Gene	KLHL34	DOWN	IV	late	0.01	0.357743	0.869537	0.863485	0.842483	3.62528
Gene	GABRB3	DOWN	IV	late	0.0562726	0.122463	0.01	0.471614	41.9501	20.2607
Gene	PATE3	DOWN	IV	late	0.01	0.01	0.01	0.01	0.897825	3.52928
Gene	ST6GAL2	DOWN	IV	late	0.01	0.0756277	0.422074	0.0279047	1.09682	3.46837
Gene	FXYD6	DOWN	IV	late	0.199915	0.401572	0.0663032	0.01	33.9098	69.1084
Gene	ZDHHC15	DOWN	IV	late	0.01	0.0449183	0.0710175	0.0600654	1.34475	3.44619
Gene	GABRG3	DOWN	IV	late	0.01	0.01	0.01	0.01	1.16928	3.41324
Gene	LINGO1	DOWN	IV	late	0.01	0.153138	0.42259	0.664187	1.46471	3.41112
Gene	PTPRN	DOWN	IV	late	0.01	0.01	0.01	0.01	0.478871	3.34488
Gene	KIF21B	DOWN	IV	late	0.01	0.01	0.0315972	0.254134	1.18009	3.28437
Gene	CADPS	DOWN	IV	late	0.173818	1.32305	4.68074	3.29281	16.5603	56.2849
Gene	PCDHB13	DOWN	IV	late	0.01	0.412542	0.765433	0.617662	0.950777	3.2015
Gene	CELF5	DOWN	IV	late	0.0116075	0.030407	0.0695789	0.0148721	2.38127	3.70184
Gene	GDPD2	DOWN	IV	late	0.01	0.01	0.01	0.01	6.38023	3.1424
Gene	ERVW-1	DOWN	IV	late	0.01	0.0545925	0.036207	0.0466982	0.572047	3.07909
Gene	PRMT8	DOWN	IV	late	0.01	0.01	0.01	0.0740259	5.24975	3.03022
Gene	SLC19A3	DOWN	IV	late	0.01	0.01	0.01	0.0523696	0.65651	3.02805
Gene	C11orf63	DOWN	IV	late	0.01	0.01	0.169452	0.11989	0.709922	3.00085
Gene	TMEM132B	DOWN	IV	late	0.14224	3.11051	1.96131	4.64299	16.3416	42.6773
Gene	PPP1R1C	DOWN	IV	late	0.01	0.01	0.01	0.01	2.7165	2.86813
Gene	PZP	DOWN	IV	late	0.01	0.01	0.215298	0.0155177	0.399599	2.84923
Gene	CELF3	DOWN	IV	late	0.01	0.01	0.01	0.01	2.81784	2.84292

Gene	TMEM133	DOWN	IV	late	0.01	0.120279	0.275448	0.121374	3.76581	2.81846
Gene	DMRTC1	DOWN	IV	late	0.01	0.01	0.01	0.01	0.43406	2.72349
Gene	DMRTC1B	DOWN	IV	late	0.01	0.01	0.01	0.01	0.434116	2.72349
Gene	PABPC5	DOWN	IV	late	0.01	0.28738	0.288065	0.0984371	0.651943	2.7188
Gene	HSD3B1	DOWN	IV	late	0.01	0.01	0.01	0.01	0.116866	2.66984
Gene	CACNG7	DOWN	IV	late	0.0184822	0.0662031	0.01	0.01	3.399	4.73105
Gene	RFX4	DOWN	IV	late	0.0844138	0.655707	0.222477	0.0348014	12.2764	21.0216
Gene	BAALC	DOWN	IV	late	0.118801	0.334326	1.69486	1.03052	1.96635	29.1901
Gene	JAM2	DOWN	IV	late	0.263768	1.38828	2.75104	5.0912	23.9054	63.7923
Gene	TMEM35	DOWN	IV	late	0.0207181	0.107945	0.0251204	0.0680135	2.21593	4.96183
Gene	FILIP1	DOWN	IV	late	0.0480318	0.351933	0.518369	0.168553	34.1492	11.4989
Gene	CDK14	DOWN	IV	late	0.0908935	0.608602	2.701	2.57073	10.5433	21.7542
Gene	AMY1C	DOWN	IV	late	0.0570266	0.317871	1.80556	0.878193	5.16303	13.3158
Gene	CNTNAP4	DOWN	IV	late	0.0800496	0.767997	0.285609	1.17925	4.86525	18.5595
Gene	TOX	DOWN	IV	late	0.0418742	0.795577	0.77652	0.476026	3.85338	9.51013
Gene	FYN	DOWN	IV	late	0.357841	6.21776	10.7841	11.3515	32.3131	79.184
Gene	ARHGEF6	DOWN	IV	late	0.123642	0.815958	1.71618	4.06876	14.3266	27.0965
Gene	GNG2	DOWN	IV	late	0.0434282	0.356896	0.228431	0.0991951	3.2076	9.14808
Gene	GABRA5	DOWN	IV	late	0.0278852	0.01	0.01	0.01	3.14934	5.80847
Gene	IGF2	DOWN	IV	late	0.0516671	0.207361	0.51665	0.212963	10.7905	10.5934
Gene	RNF152	DOWN	IV	late	0.0437547	1.17261	0.887211	1.6167	4.95651	8.10319
Gene	PCDHB10	DOWN	IV	late	0.0166205	0.174024	0.110352	0.328964	0.421154	2.91217
Gene	RCAN2	DOWN	IV	late	0.220291	0.0305187	0.0533787	0.240414	8.73426	38.5548
Gene	TRIM36	DOWN	IV	late	0.0491443	0.94958	0.29516	0.268143	5.36908	8.02817
Gene	C1orf114	DOWN	IV	late	0.118238	0.756168	1.36468	0.694705	5.02203	19.1393
Gene	ZNF280B	DOWN	IV	late	0.0529789	0.116204	0.0383928	0.0673123	5.54707	8.57004
Gene	GKAP1	DOWN	IV	late	0.21408	1.66767	3.42871	2.28386	11.9076	33.5636
Gene	MARK1	DOWN	IV	late	0.141817	1.10456	0.100338	0.0167072	5.05919	21.044
Gene	GPR85	DOWN	IV	late	0.0623674	1.5359	1.65889	0.881306	4.94171	9.00181
Gene	SMOC1	DOWN	IV	late	0.0817114	1.26041	0.893083	2.25666	3.01174	11.5582
Gene	LHFPL1	DOWN	IV	late	0.0288943	0.01	0.01	0.01	1.60817	3.9653
Gene	UTRN	DOWN	IV	late	0.361474	10.6937	6.53313	7.22714	53.987	47.6525
Gene	WIPF3	DOWN	IV	late	0.112265	0.039593	0.1504	0.0430686	4.60801	14.7754
Gene	CNTNAP2	DOWN	IV	late	0.313954	0.30733	1.44957	0.0282076	52.0791	39.3576

Gene	FAM171A2	DOWN	IV	late	0.0223328	0.373132	0.654905	0.493345	1.44388	2.70401
Gene	PCDHGB1	DOWN	IV	late	0.0644568	0.0249066	0.427785	0.133159	2.91265	7.72801
Gene	DDX25	DOWN	IV	late	0.12036	0.662631	0.547855	0.261644	3.85746	14.2566
Gene	LRRTM2	DOWN	IV	late	0.249677	0.754214	3.66439	3.03474	8.3016	27.8413
Gene	FZD3	DOWN	IV	late	0.105479	0.793403	0.710636	0.599862	22.2298	10.5375
Gene	CCDC102B	DOWN	IV	late	0.0857873	0.381209	0.947008	0.592302	4.08645	8.21364
Gene	ZNF423	DOWN	IV	late	0.02975	0.112337	0.118299	0.607752	2.78799	2.84487
Gene	NBEA	DOWN	IV	late	0.232693	1.26702	2.90473	1.29859	12.2074	22.2306
Gene	PDE1B	DOWN	IV	late	0.0513237	0.993828	0.513303	0.352976	4.29432	4.87083
Gene	KLHDC1	DOWN	IV	late	0.183355	1.46086	1.97212	0.438128	4.18902	16.8207
Gene	KCNIP2	DOWN	IV	late	0.160819	0.242376	0.592157	1.09189	4.32108	14.3053
Gene	APLF	DOWN	IV	late	0.0922344	0.339951	0.797439	0.488592	3.13578	8.08951
Gene	ARL4C	DOWN	IV	late	0.130468	0.44532	0.725674	0.144769	10.1123	11.3845
Gene	CPEB4	DOWN	IV	late	0.875228	4.10781	7.27864	6.48035	22.8725	75.639
Gene	TUBB2B	DOWN	IV	late	1.56317	19.725	16.1086	9.03876	193.767	134.936
Gene	ESYT3	DOWN	IV	late	0.0688385	0.129489	1.1436	0.584494	2.08525	5.44348
Gene	TM4SF1	DOWN	IV	late	0.0982392	0.01	0.01	0.127047	2.42287	7.5436
Gene	PLA2G4C	DOWN	IV	late	0.0415231	0.148997	0.114886	0.300497	1.38509	3.18185
Gene	ELAVL2	DOWN	IV	late	0.163924	0.367227	0.0989722	1.56126	4.81669	12.4602
Gene	RAB39B	DOWN	IV	late	0.10044	0.193295	0.122332	0.0817835	1.56239	7.47075
Gene	KIAA1257	DOWN	IV	late	0.0468941	0.01	0.01	0.01	1.72031	3.42163
Gene	SGCE	DOWN	IV	late	0.725162	9.89206	11.5409	4.89098	45.7768	51.6253
Gene	C14orf38	DOWN	IV	late	0.0390499	0.0662236	0.0183872	0.01	0.0263406	2.77544
Gene	FGF1	DOWN	IV	late	3.19305	17.8177	31.8767	47.2866	80.1613	218.853
Gene	SORCS1	DOWN	IV	late	0.20023	0.959377	0.909686	0.334783	4.44066	13.5776
Gene	NUDT10	DOWN	IV	late	0.137015	0.0694671	0.763605	0.0634931	3.77755	9.10784
Gene	CCDC136	DOWN	IV	late	0.147603	0.676677	1.19915	0.244713	14.0091	9.79044
Gene	ENO2	DOWN	IV	late	1.9482	5.4185	2.50994	14.7744	86.4161	127.725
Gene	PCNXL2	DOWN	IV	late	2.23332	2.18444	7.63487	12.073	35.8902	140.077
Gene	OPHN1	DOWN	IV	late	0.432135	1.72411	4.34436	2.88981	9.00183	26.7992
Gene	TBC1D4	DOWN	IV	late	0.167561	0.599819	0.210988	0.359528	5.76888	10.1809
Gene	FAM190A	DOWN	IV	late	0.117185	0.980941	0.87386	0.366971	1.99287	6.95998
Gene	MANBA	DOWN	IV	late	0.262216	1.01523	1.7585	1.80383	11.4112	14.73
Gene	TMEM232	DOWN	IV	late	0.237617	1.39149	1.64463	0.884714	6.16241	13.3289

Gene	KIAA1324L	DOWN	IV	late	0.609032	5.35573	6.30577	3.94022	19.5977	31.374
Gene	OCLN	DOWN	IV	late	0.29839	1.98381	3.17762	1.58387	5.85468	15.2479
Gene	EPB41L4A	DOWN	IV	late	0.446928	0.92797	1.06617	0.342396	6.28593	22.7307
Gene	PNMA2	DOWN	IV	late	0.669762	2.48919	3.61325	1.14484	15.9443	33.8495
Gene	FAM78B	DOWN	IV	late	0.0816521	0.338997	0.275902	0.420192	1.35398	4.08036
Gene	BHLHB9	DOWN	IV	late	0.251085	1.34569	2.47546	0.684216	3.1837	12.5029
Gene	LPCAT2	DOWN	IV	late	0.165411	0.629041	0.258647	0.302611	2.6656	8.02035
Gene	ZNF454	DOWN	IV	late	0.0881047	0.520832	0.769186	0.820005	2.51721	4.20206
Gene	CCDC144A	DOWN	IV	late	3.4279	16.0853	27.8123	12.7904	49.2194	161.887
Gene	ARHGEF9	DOWN	IV	late	3.44396	5.70368	18.2166	28.0388	47.4435	162.6
Gene	ZSWIM5	DOWN	IV	late	0.080921	0.331317	0.192037	0.519805	3.34624	3.80291
Gene	GPR98	DOWN	IV	late	1.21966	2.63123	5.34955	0.604557	22.9085	56.9209
Gene	SCN4B	DOWN	IV	late	0.128558	0.209911	0.282802	0.285996	2.08153	5.97423
Gene	DCX	DOWN	IV	late	0.103766	0.168064	0.0880604	0.0750542	15.9933	4.73536
Gene	ATP8A2	DOWN	IV	late	0.201501	0.745973	0.612899	0.127045	2.08524	9.15003
Gene	DEPTOR	DOWN	IV	late	0.248664	0.354998	0.854359	2.21718	3.58369	11.2159
Gene	ICA1	DOWN	IV	late	0.636203	1.86731	4.87451	3.26359	14.3243	28.4616
Gene	PPIL6	DOWN	IV	late	0.0943958	0.620909	0.621761	0.96461	1.21699	4.1618
Gene	ARNTL2	DOWN	IV	late	0.252369	1.53432	0.80876	0.699954	3.7906	11.078
Gene	UNC5B	DOWN	IV	late	0.0613038	0.311146	0.118249	0.421776	1.08709	2.69059
Gene	AIF1L	DOWN	IV	late	1.43536	0.351105	0.71589	0.591306	31.2967	62.6762
Gene	CLIP3	DOWN	IV	late	10.074	71.4939	101.548	67.4948	226.392	438.964
Gene	TNFSF4	DOWN	IV	late	0.0851085	0.0852443	0.32413	0.499479	1.64428	3.67344
Gene	HCLS1	DOWN	IV	late	0.170472	0.824225	0.327865	0.146218	1.88889	7.19832
Gene	TMEM98	DOWN	IV	late	0.173692	0.01	0.539075	0.43672	2.69718	7.21942
Gene	PRELID2	DOWN	IV	late	0.171988	0.482691	0.575356	0.149501	1.41895	7.14162
Gene	RAP1GAP2	DOWN	IV	late	0.0704788	0.01	0.0278108	0.01	0.76236	2.92091
Gene	PCDHGB2	DOWN	IV	late	0.195719	0.39186	1.89309	2.00714	2.88096	8.07599
Gene	GCNT4	DOWN	IV	late	0.121466	0.179905	0.882829	0.0197377	1.11079	4.993
Gene	ZFP2	DOWN	IV	late	0.157539	0.645889	0.807309	0.303406	2.80766	6.4744
Gene	CCDC160	DOWN	IV	late	0.0878405	0.01	0.01	0.01	1.05443	3.58416
Gene	KRT222	DOWN	IV	late	0.198895	1.17859	0.720376	0.120278	0.0248212	8.06346
Gene	TMEM169	DOWN	IV	late	0.106967	0.220954	0.239194	0.139291	2.52714	4.27494
Gene	MYO10	DOWN	IV	late	1.30276	3.12423	1.10709	2.05021	68.6846	51.4125

Gene	SLC4A8	DOWN	IV	late	0.975788	2.19715	4.26777	4.52351	12.7831	37.5772
Gene	ANO4	DOWN	IV	late	0.510184	2.36521	1.34798	0.661375	4.93567	19.3561
Gene	ZNF483	DOWN	IV	late	2.3458	4.46869	4.02767	3.6316	23.9139	88.1629
Gene	CP	DOWN	IV	late	0.343102	1.8902	1.5113	0.365606	8.82543	12.6412
Gene	STXBP1	DOWN	IV	late	6.85209	11.5763	26.5746	29.6044	79.2726	249.443
Gene	ST18	DOWN	IV	late	7.79585	3.1416	1.74222	1.52414	8.72382	282.985
Gene	PPP1R3F	DOWN	IV	late	0.412191	1.77342	1.76353	1.75233	4.01731	13.8974
Gene	C12orf68	DOWN	IV	late	0.235436	0.292814	0.322071	0.01	15.9911	7.91992
Gene	FAM18A	DOWN	IV	late	0.111515	0.156259	0.114462	0.123551	1.33228	3.6774
Gene	CDKN1C	DOWN	IV	late	0.174372	1.15468	0.969581	1.24353	5.36829	5.60903
Gene	NTM	DOWN	IV	late	3.8511	20.6797	19.6662	24.0146	34.8931	119.72
Gene	STAG3	DOWN	IV	late	0.585942	2.38286	3.03073	3.03404	7.19266	18.0801
Gene	C16orf45	DOWN	IV	late	0.47928	0.744533	2.57358	3.36489	8.55855	14.7244
Gene	FAM188B	DOWN	IV	late	0.12778	0.414786	0.900865	0.86287	1.4456	3.8158
Gene	ZNF471	DOWN	IV	late	0.323268	1.03292	1.82202	0.99606	2.48388	9.1709
Gene	FAM102B	DOWN	IV	late	0.21166	0.28134	0.232774	0.0668433	3.07656	5.84922
Gene	BEX2	DOWN	IV	late	3.17375	13.9409	21.2958	6.28698	50.2903	86.4236
Gene	TESK2	DOWN	IV	late	0.620333	0.719283	0.527332	1.43728	4.73637	16.8263
Gene	HS3ST4	DOWN	IV	late	0.223813	0.62025	0.0165038	0.01	0.939765	5.91028
Gene	TTC18	DOWN	IV	late	0.216547	0.258905	0.444066	0.957064	2.94947	5.70206
Gene	RALGPS2	DOWN	IV	late	0.309785	0.633597	0.219884	0.0470877	8.83569	8.15674
Gene	GOLM1	DOWN	IV	late	2.76452	9.94107	16.0009	12.782	51.7764	70.8761
Gene	FAM70A	DOWN	IV	late	0.187892	0.213429	0.570428	0.05491	1.0763	4.63049
Gene	SERP2	DOWN	IV	late	0.411177	1.00835	0.636334	1.61927	4.07193	10.0641
Gene	MMD	DOWN	IV	late	0.850764	2.45727	4.48317	0.974311	7.90229	20.7991
Gene	YPEL4	DOWN	IV	late	0.264356	0.275052	0.19905	0.328443	1.59388	6.45111
Gene	DGKG	DOWN	IV	late	1.5738	0.0784835	1.29862	0.01	1.38156	38.0513
Gene	HSD17B6	DOWN	IV	late	0.313261	0.301952	0.669358	0.419833	2.33093	7.49981
Gene	SEMA5B	DOWN	IV	late	0.326451	0.01	0.01	0.01	23.4194	7.6776
Gene	TMOD1	DOWN	IV	late	0.964713	3.19664	3.12378	2.49969	8.46139	22.1351
Gene	ABCA10	DOWN	IV	late	0.292953	0.791329	0.922329	1.61782	2.62244	6.70873
Gene	RNF175	DOWN	IV	late	0.121575	0.01	0.0999975	0.01	1.50107	2.78212
Gene	COL16A1	DOWN	IV	late	0.157135	0.143151	0.0191333	0.01	0.660367	3.46774
Gene	LRRN3	DOWN	IV	late	0.361748	0.680586	1.45208	1.19103	4.05579	7.97422

Gene	C7orf63	DOWN	IV	late	0.332424	1.10002	0.81069	0.463483	1.84246	7.26316
Gene	HS3ST2	DOWN	IV	late	0.138561	0.01	0.083399	0.0473649	1.28656	3.02145
Gene	FAM169A	DOWN	IV	late	1.01839	2.23566	4.79277	3.56108	6.95483	22.1479
Gene	FEZ1	DOWN	IV	late	4.85692	15.9027	8.96576	9.83336	33.3355	102.262
Gene	ABHD6	DOWN	IV	late	0.265469	0.293108	0.651791	0.468901	1.28012	5.57554
Gene	SESTD1	DOWN	IV	late	2.31779	5.67715	8.40306	8.00451	27.934	48.248
Gene	APC	DOWN	IV	late	10.9914	22.2943	35.038	22.3102	47.1369	224.345
Gene	F8	DOWN	IV	late	0.177823	0.341748	0.592482	0.286262	0.99176	3.57728
Gene	CYP4V2	DOWN	IV	late	3.10731	3.16799	3.4856	7.41871	20.6174	61.5608
Gene	SLCO3A1	DOWN	IV	late	0.463147	0.270649	0.929583	0.429525	2.61249	8.97478
Gene	PDE4B	DOWN	IV	late	8.30903	22.0894	32.9136	12.7269	47.0872	159.255
Gene	SNN	DOWN	IV	late	0.714527	1.22123	1.88331	2.09793	4.7864	13.5928
Gene	CDKL5	DOWN	IV	late	1.46007	1.68289	3.73925	4.27281	11.0035	27.0416
Gene	RUFY3	DOWN	IV	late	4.16336	6.43848	12.4438	10.5781	28.4853	76.6655
Gene	ZNF323	DOWN	IV	late	0.589349	1.67209	1.87581	2.38943	3.41905	10.8405
Gene	BCL6	DOWN	IV	late	0.87956	1.65677	3.4224	1.42049	8.41473	16.1148
Gene	DYX1C1	DOWN	IV	late	6.75868	9.10477	24.1896	10.8553	49.1022	122.996
Gene	PDGFRA	DOWN	IV	late	1.44698	1.05957	1.65005	1.71283	18.4757	25.9386
Gene	DNM1	DOWN	IV	late	0.820525	0.593631	0.454472	0.609278	3.88401	14.5788
Gene	SLC26A4	DOWN	IV	late	0.315565	0.01	0.0558972	0.174452	2.8426	5.56543
Gene	DLG4	DOWN	IV	late	1.24763	2.34925	2.59639	5.19626	8.80814	21.1528
Gene	CELSR2	DOWN	IV	late	1.14125	3.20727	2.20932	4.36906	11.3285	18.6923
Gene	PHACTR2	DOWN	IV	late	2.22534	0.739637	0.598034	0.804627	32.5319	36.1239
Gene	ZNF177	DOWN	IV	late	0.337531	0.916551	0.875411	1.35825	3.65703	5.44952
Gene	ADAM22	DOWN	IV	late	1.40401	4.53349	2.37586	0.614486	6.4348	22.3348
Gene	ANKDD1A	DOWN	IV	late	1.308	2.26778	3.90378	3.18448	5.88567	20.7188
Gene	PDE10A	DOWN	IV	late	0.20954	0.607483	0.0572934	0.0374885	3.43169	3.24603
Gene	ZNF613	DOWN	IV	late	0.37546	0.773516	1.27822	1.05709	1.7926	5.81347
Gene	EPB41L1	DOWN	IV	late	4.02186	3.07059	4.88653	9.37025	24.528	60.3557
Gene	GDPD1	DOWN	IV	late	0.335707	0.655949	0.421637	0.153205	1.70771	4.89627
Gene	HLA-DMA	DOWN	IV	late	0.277675	0.231336	0.361973	0.51987	1.0785	4.00159
Gene	SCAMP5	DOWN	IV	late	0.349834	0.290053	0.292824	0.89304	1.20501	5.03957
Gene	AGAP1	DOWN	IV	late	3.27902	2.47923	4.94982	5.23656	12.8738	46.0238
Gene	FAM167A	DOWN	IV	late	0.33132	0.492027	0.396309	0.131233	1.8489	4.61191

Gene	LRRC6	DOWN	IV	late	5.85917	4.57952	4.90265	7.15982	20.4634	81.5485
Gene	CALB1	DOWN	IV	late	0.294839	0.354143	0.543815	0.032163	0.63669	4.10097
Gene	ZNF565	DOWN	IV	late	0.629533	1.01865	1.7587	1.12823	2.64814	8.64275
Gene	FN3K	DOWN	IV	late	0.660721	0.897354	1.68109	1.81326	2.36715	8.95561
Gene	BLNK	DOWN	IV	late	0.679877	0.551311	0.961668	1.39519	7.03136	8.98582
Gene	MCART6	DOWN	IV	late	0.676754	0.990398	2.11637	1.05496	5.52279	8.88977
Gene	AGTPBP1	DOWN	IV	late	4.94126	7.67097	9.14724	4.62555	20.44	60.7697
Gene	RABGAP1L	DOWN	IV	late	8.99237	16.4283	23.8474	15.0995	43.8821	108.064
Gene	C20orf118	DOWN	IV	late	0.325059	0.431135	0.172476	0.182303	1.11106	3.83328
Gene	CDH26	DOWN	IV	late	0.248175	0.508059	0.238561	0.0674881	0.583236	2.89767
Gene	KIAA1407	DOWN	IV	late	0.929739	1.39196	2.12644	1.68138	3.32095	10.7693
Gene	RNF157	DOWN	IV	late	1.6637	0.675787	1.89415	1.14792	7.07873	18.9798
Gene	LEPR	DOWN	IV	late	0.719816	0.666139	1.18687	1.14716	4.64073	8.20743
Gene	NEFM	DOWN	IV	late	50.2096	99.9103	108.694	65.0197	452.288	568.566
Gene	SH3BGR	DOWN	IV	late	1.97512	2.50621	1.38262	2.83957	17.118	22.1993
Gene	LRRC49	DOWN	IV	late	0.79353	0.705059	1.14764	0.469786	2.45095	8.58349
Gene	C12orf76	DOWN	IV	late	4.9322	4.61789	7.93205	4.99774	14.8701	51.287
Gene	RNASET2	DOWN	IV	late	1.21949	1.69415	1.89927	2.83814	3.41415	12.486
Gene	CDO1	DOWN	IV	late	1.42412	1.74283	2.22516	2.90969	5.77377	14.5295
Gene	STK33	DOWN	IV	late	1.33732	1.67813	0.731799	0.0285424	8.64241	13.5051
Gene	TRANK1	DOWN	IV	late	1.26366	1.88191	1.13043	2.67076	4.6247	12.258
Gene	ZNF418	DOWN	IV	late	0.989175	1.18781	1.2114	1.97526	4.83193	9.43477
Gene	EPHX1	DOWN	IV	late	2.00283	1.32085	0.757704	2.61134	6.1701	18.7648
Gene	TNFRSF21	DOWN	IV	late	6.60338	11.2985	8.74971	3.67528	21.2051	60.8798
Gene	NIPAL3	DOWN	IV	late	2.90928	3.23742	5.19685	5.08999	15.1447	26.0857
Gene	BBS2	DOWN	IV	late	4.19895	5.61507	6.71589	5.82809	15.5481	36.7501
Gene	ADORA1	DOWN	IV	late	1.25759	1.24945	1.07793	1.64208	7.56269	10.8102
Gene	NRIP1	DOWN	IV	late	3.46291	2.87976	6.65152	1.94025	13.1705	29.5806
Gene	SLC22A23	DOWN	IV	late	2.01552	2.41619	4.22731	3.45456	5.60389	17.0084
Gene	MCTP1	DOWN	IV	late	7.3328	3.39095	7.90863	11.4715	30.9979	61.0644
Gene	WDR7	DOWN	IV	late	2.97007	3.95262	6.07077	4.49406	8.42373	24.4139
Gene	SLC1A1	DOWN	IV	late	0.623155	0.304813	0.408726	0.512802	1.88496	4.94199
Gene	ZEB1	DOWN	IV	late	37.2996	21.1679	54.6123	45.6845	201.275	290.756

Gene	SLC35F1	DOWN	IV	late	2.12098	3.17184	1.55248	0.973248	9.05078	16.2436
Gene	BCL2L2	DOWN	IV	late	2.08468	3.15053	3.35321	2.53288	5.43098	15.852
Gene	SCN8A	DOWN	IV	late	2.35517	0.507631	1.19951	0.875548	6.40072	17.8904
Gene	PTPRJ	DOWN	IV	late	1.55169	0.912045	1.34982	1.89982	4.35938	11.7125
Gene	MECOM	DOWN	IV	late	0.65246	0.0694173	0.04237	0.0125989	2.61942	4.91673
Gene	DST	DOWN	IV	late	135.666	133.466	192.391	128.628	378.25	991.423
Gene	SPRY1	DOWN	IV	late	1.76613	0.428865	0.15202	0.0149633	6.28559	12.9054
Gene	CAMKV	DOWN	IV	late	0.873733	0.0525307	0.01	0.938212	5.24705	6.35685
Gene	PRKCH	DOWN	IV	late	2.32342	1.13998	0.288112	0.358585	7.33233	16.8471
Gene	ALAD	DOWN	IV	late	12.2402	15.52	12.8514	12.5031	27.6661	88.1478
Gene	STON2	DOWN	IV	late	0.849766	0.787482	0.885331	1.23268	2.71932	6.09326
Gene	ZDHHC23	DOWN	IV	late	1.13467	1.49428	0.760698	0.29537	2.01091	8.11393
Gene	C16orf46	DOWN	IV	late	1.49359	1.04506	1.74162	1.74708	16.1683	10.0653
Gene	ITM2C	DOWN	IV	late	7.44268	5.08134	7.77934	9.10283	17.1542	49.6784
Gene	PRNP	DOWN	IV	late	20.7731	5.08676	22.6329	15.9619	44.3919	136.861
Gene	MYOM2	DOWN	IV	late	1.07169	0.640675	0.698325	0.817568	2.37932	6.99938
Gene	SNTG1	DOWN	IV	late	5.42362	0.106606	0.167345	0.13358	20.6385	34.2881
Gene	GLIS3	DOWN	IV	late	1.38982	0.199645	1.70868	1.04151	3.49403	8.47841
Gene	FLRT2	DOWN	IV	late	2.67812	0.914107	0.725625	1.56943	8.57996	16.2079
Gene	DFNB31	DOWN	IV	late	1.40176	1.0128	0.347925	0.676451	3.93076	8.41409
Gene	HIP1	DOWN	IV	late	1.65469	0.561558	0.945606	1.28656	5.13486	9.88095
Gene	PCYT1B	DOWN	IV	late	1.83127	1.87836	1.06341	0.0959551	8.86741	10.06
Gene	IL18	DOWN	IV	late	0.701071	0.339995	0.814664	0.617186	1.10421	3.66331
Gene	FAM19A1	DOWN	IV	late	0.865892	0.370669	0.52018	0.348015	1.42748	4.52443
Gene	CCDC85A	DOWN	IV	late	2.24476	0.632188	1.91097	0.5282	1.73773	11.5676
Gene	AMN1	DOWN	IV	late	9.57888	8.58133	7.04927	5.96293	14.0962	48.3834
Gene	PVRL1	DOWN	IV	late	1.04713	0.42033	1.27078	1.13973	5.62639	5.27329
Gene	SMAP2	DOWN	IV	late	8.16935	6.59075	8.06103	9.40994	12.5519	40.461
Gene	PTP4A2	DOWN	IV	late	107.489	83.2055	126.821	49.7358	150.807	530.27
Gene	LRRC8D	DOWN	IV	late	2.86222	1.59421	3.28989	2.43444	8.66254	14.0589
Gene	STAT4	DOWN	IV	late	2.24503	1.07906	1.5458	0.930363	4.43725	10.5605
Gene	APBB1	DOWN	IV	late	2.03257	1.25361	0.462028	0.641965	2.42126	9.46411
Gene	PRKAG2	DOWN	IV	late	3.68739	1.39148	3.51664	2.44601	5.23827	17.0467
Gene	C6orf168	DOWN	IV	late	1.40962	0.958622	0.957294	0.330007	1.47463	6.43633
Gene	KIF13B	DOWN	IV	late	5.54225	1.7952	2.47851	4.15066	9.14529	25.0665

Gene	BMPER	DOWN	IV	late	2.55041	0.240648	0.238974	0.0119807	1.62063	11.292
Gene	LXN	DOWN	IV	late	1.29337	0.38507	0.619633	0.516714	5.68076	5.6188
Gene	CDR1	DOWN	V	In Vivo-sp.	0.01	38.5898	117.343	43.9403	113.736	1927.78
Gene	PLP1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	8.62912	1533.3
Gene	SLC1A2	DOWN	V	In Vivo-sp.	0.01	0.0375852	0.0688913	0.108075	1.10085	657.196
Gene	GFAP	DOWN	V	In Vivo-sp.	0.01	0.308152	0.0185167	0.477843	0.813259	586.482
Gene	SLC1A3	DOWN	V	In Vivo-sp.	0.01	1.63646	5.14523	4.40897	21.4104	563.952
Gene	PMP2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0115297	0.01	532.188
Gene	GPM6A	DOWN	V	In Vivo-sp.	0.0131527	1.46734	0.429569	1.2681	12.5344	594.278
Gene	AQP4	DOWN	V	In Vivo-sp.	0.01	0.100082	0.0950262	0.0430224	0.104339	428.854
Gene	HLF	DOWN	V	In Vivo-sp.	0.00777692	0.381639	0.500099	8.82279	1.9105	310.686
Gene	ERMN	DOWN	V	In Vivo-sp.	0.01	1.44388	0.193721	0.0764418	1.20873	319.028
Gene	RTN1	DOWN	V	In Vivo-sp.	0.01	0.475294	2.64597	2.4459	18.6181	213.845
Gene	MOBP	DOWN	V	In Vivo-sp.	0.033777	0.01	0.120985	0.227604	0.162754	662.573
Gene	RIMS2	DOWN	V	In Vivo-sp.	0.01	0.532115	0.01	0.0843213	5.40512	190.31
Gene	MT3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	176.356
Gene	SNAP25	DOWN	V	In Vivo-sp.	0.0238689	4.01882	9.60783	0.775376	4.81647	387.542
Gene	PHYHIPL	DOWN	V	In Vivo-sp.	0.01	0.01	0.24552	2.02554	9.20485	157.283
Gene	SPP1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.18978	146.777
Gene	FAM123A	DOWN	V	In Vivo-sp.	0.00386953	0.132014	0.0858445	0.0260942	0.692891	52.8251
Gene	NCAM2	DOWN	V	In Vivo-sp.	0.01	3.3108	1.9337	1.80732	3.26101	126.432
Gene	PTN	DOWN	V	In Vivo-sp.	0.01	0.90485	2.97239	10.6838	9.28291	126.146
Gene	SLC4A10	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.024921	123.001

Gene	SGIP1	DOWN	V	In Vivo-sp.	0.0109429	0.777815	0.411724	1.09297	3.65071	126.428
Gene	FAM107A	DOWN	V	In Vivo-sp.	0.0183694	0.0524882	0.112449	0.0973284	0.117232	195.707
Gene	SLCO1A2	DOWN	V	In Vivo-sp.	0.0103415	0.0241588	0.0849567	0.01	1.71344	93.9894
Gene	ATP1A2	DOWN	V	In Vivo-sp.	0.0677795	1.23661	0.149171	0.01	20.1539	582.124
Gene	JPH4	DOWN	V	In Vivo-sp.	0.01	6.57419	8.77292	3.2684	12.8797	84.9445
Gene	RNASE1	DOWN	V	In Vivo-sp.	0.01	0.273266	0.01	0.745888	0.01	83.1509
Gene	OPALIN	DOWN	V	In Vivo-sp.	0.01	0.0501297	0.203238	0.01	0.01	82.2278
Gene	NOVA1	DOWN	V	In Vivo-sp.	0.0116114	0.01	0.742484	0.01	10.0308	93.0329
Gene	UNC80	DOWN	V	In Vivo-sp.	0.00354255	0.324176	0.373902	0.0215296	0.410533	27.8857
Gene	CDH10	DOWN	V	In Vivo-sp.	0.01	7.20357	1.58189	1.01548	1.80746	76.6057
Gene	SCD5	DOWN	V	In Vivo-sp.	0.0705504	13.0395	26.9833	9.09664	30.5949	536.162
Gene	EMX2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.251706	72.6138
Gene	CADM2	DOWN	V	In Vivo-sp.	0.01	3.70916	2.2413	1.83351	0.885011	72.1605
Gene	CAMK2A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.743023	71.9684
Gene	SPOCK3	DOWN	V	In Vivo-sp.	0.01	0.0568437	0.0466367	0.15848	0.01	70.804
Gene	HEPN1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	69.6652
Gene	SORBS2	DOWN	V	In Vivo-sp.	0.01	1.65825	0.0378221	12.4329	1.67092	64.6785
Gene	NCKAP5	DOWN	V	In Vivo-sp.	0.01	2.97821	8.87341	8.37249	14.3371	64.3961
Gene	GABRG1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.00288733	0.01	60.6412
Gene	HEPACAM	DOWN	V	In Vivo-sp.	0.01	0.01	0.0150593	0.01	0.044817	59.3524
Gene	ASPA	DOWN	V	In Vivo-sp.	0.01	0.0607316	0.564053	0.87065	1.81371	59.0211
Gene	RSPO2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0208963	0.332845	58.2031

Gene	SPOCK2	DOWN	V	In Vivo-sp.	0.01	0.134452	0.073977	0.273818	2.42787	58.171
Gene	C1orf61	DOWN	V	In Vivo-sp.	0.01	2.20576	1.63329	4.28179	0.464372	57.8551
Gene	TCEAL5	DOWN	V	In Vivo-sp.	0.01	8.13765	0.01	0.01	0.01	51.3175
Gene	FCGR2A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	4.63012	50.42
Gene	CNDP1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.317147	0.01	48.8878
Gene	PLCL1	DOWN	V	In Vivo-sp.	0.0161475	4.2824	11.3385	3.11016	9.09523	78.7583
Gene	A2M	DOWN	V	In Vivo-sp.	0.01	1.5442	0.0180863	0.253022	0.01	48.4821
Gene	ZMAT1	DOWN	V	In Vivo-sp.	0.01	4.33085	11.6459	4.26638	9.18985	46.9607
Gene	FMN2	DOWN	V	In Vivo-sp.	0.01	0.291918	0.197547	0.01	0.59294	42.7886
Gene	PLA2G16	DOWN	V	In Vivo-sp.	0.0204373	0.275238	0.910635	1.59334	4.94698	86.0868
Gene	MYT1L	DOWN	V	In Vivo-sp.	0.0119885	0.106064	0.315196	0.230698	1.04531	49.9103
Gene	KCNJ10	DOWN	V	In Vivo-sp.	0.0466162	0.200283	0.178064	0.242128	0.189979	190.52
Gene	SCN2A	DOWN	V	In Vivo-sp.	0.00784926	0.0575477	0.138868	0.101504	0.295434	31.7284
Gene	DPP10	DOWN	V	In Vivo-sp.	0.01	2.89404	3.51328	4.70513	8.75665	40.3881
Gene	TBR1	DOWN	V	In Vivo-sp.	0.01	0.0454548	0.12378	0.01	0.01	40.2939
Gene	FRMD4B	DOWN	V	In Vivo-sp.	0.01	0.74011	1.4584	0.427986	5.8516	39.2313
Gene	SCN3B	DOWN	V	In Vivo-sp.	0.0100017	0.01	0.01	0.01	1.91181	37.7869
Gene	PPP1R9A	DOWN	V	In Vivo-sp.	0.01	0.11122	0.0189122	0.0431538	5.75253	37.3727
Gene	DLG2	DOWN	V	In Vivo-sp.	0.116383	5.47192	2.91379	4.33789	13.6965	432.354
Gene	STMN4	DOWN	V	In Vivo-sp.	0.01	0.282532	0.247243	0.01	7.94903	36.9584
Gene	SCG3	DOWN	V	In Vivo-sp.	0.0280869	0.0417413	0.0573275	0.162712	3.2516	103.468
Gene	FAIM2	DOWN	V	In Vivo-sp.	0.01	0.124985	0.153789	0.01	1.97265	35.8254

Gene	LRP2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	7.13855	35.2253
Gene	RGS7	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	4.63353	35.0865
Gene	FUT9	DOWN	V	In Vivo-sp.	0.01	0.01	0.21949	0.0326399	0.01	34.7227
Gene	CDH20	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.572674	34.6095
Gene	RHOU	DOWN	V	In Vivo-sp.	0.01	0.375843	1.24907	0.445266	3.65231	34.5914
Gene	MAOB	DOWN	V	In Vivo-sp.	0.0199975	0.993695	1.83943	10.2127	1.60329	69.1344
Gene	SGMS2	DOWN	V	In Vivo-sp.	0.0188008	0.369525	3.32474	0.760734	3.49758	64.2812
Gene	ITM2A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	34.0843
Gene	EFEMP1	DOWN	V	In Vivo-sp.	0.01	0.195989	1.65988	2.7161	4.05283	33.9041
Gene	TF	DOWN	V	In Vivo-sp.	0.0889421	0.180716	0.227036	0.114534	1.12264	301.4
Gene	BMPR1B	DOWN	V	In Vivo-sp.	0.01	0.177202	0.226635	0.119257	4.15338	33.7549
Gene	TNS1	DOWN	V	In Vivo-sp.	0.01	0.251974	0.869529	3.64204	3.54297	33.3581
Gene	ID4	DOWN	V	In Vivo-sp.	0.0196954	5.49991	7.16232	0.405553	1.16723	65.1268
Gene	NTRK2	DOWN	V	In Vivo-sp.	0.151866	1.05688	12.34	13.3782	20.28	500.862
Gene	ACVRL1	DOWN	V	In Vivo-sp.	0.01	0.739525	2.45232	3.25874	0.0492196	32.6736
Gene	SLCO1C1	DOWN	V	In Vivo-sp.	0.01	0.364907	4.00771	0.268477	4.40312	31.3717
Gene	KHDRBS2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.06565	31.339
Gene	VSTM2A	DOWN	V	In Vivo-sp.	0.01	0.409671	0.0553026	0.40211	2.86871	30.9369
Gene	GIMAP4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.84068	30.7848
Gene	PRKCB	DOWN	V	In Vivo-sp.	0.01	0.208388	0.318103	0.0901686	4.27383	28.7913
Gene	ABLIM2	DOWN	V	In Vivo-sp.	0.01	0.01	0.131778	0.141908	1.09291	28.4879
Gene	CHD5	DOWN	V	In Vivo-sp.	0.01	0.0847273	0.0441219	0.429988	0.398644	28.2083

Gene	P2RX7	DOWN	V	In Vivo-sp.	0.01	0.01	0.781941	0.58118	1.54247	28.0727
Gene	PLEKHB1	DOWN	V	In Vivo-sp.	0.036582	0.694297	0.143018	1.46364	5.96073	102.099
Gene	KIF1A	DOWN	V	In Vivo-sp.	0.01	1.02892	0.753701	0.291347	0.812183	27.0906
Gene	ERC2	DOWN	V	In Vivo-sp.	0.140644	7.0932	6.46892	6.56813	18.281	379.7
Gene	FAM69C	DOWN	V	In Vivo-sp.	0.01	0.599058	0.01	0.01	0.01	26.9587
Gene	SLITRK1	DOWN	V	In Vivo-sp.	0.01	0.0531094	0.0844514	0.340942	1.29423	26.8505
Gene	CD74	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.655514	26.3667
Gene	RPH3A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.45463	26.2198
Gene	TCEAL7	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.412692	25.9855
Gene	UNC13C	DOWN	V	In Vivo-sp.	0.01	0.0213768	0.160434	0.0833161	0.431861	25.7994
Gene	HHIP	DOWN	V	In Vivo-sp.	0.01	0.086605	0.261266	0.132596	0.100567	25.3148
Gene	HBB	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	25.1571
Gene	CDH18	DOWN	V	In Vivo-sp.	0.01	0.01	0.271587	0.01	0.0510784	25.1093
Gene	IL1RAPL1	DOWN	V	In Vivo-sp.	0.01	0.270726	0.165903	0.952513	0.486344	24.9901
Gene	FAM49A	DOWN	V	In Vivo-sp.	0.0092199	0.333251	0.488961	0.100811	1.25754	22.9125
Gene	AGAP2	DOWN	V	In Vivo-sp.	0.01	0.0301858	0.161662	0.0552835	0.156662	24.7407
Gene	TMEM235	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.0808795	24.6191
Gene	GABRG2	DOWN	V	In Vivo-sp.	0.01	0.0632948	0.01	0.01	0.940155	24.3791
Gene	AKT3	DOWN	V	In Vivo-sp.	0.350707	1.6265	3.20416	0.632656	10.8656	845.93
Gene	SYNE1	DOWN	V	In Vivo-sp.	0.102744	0.990565	6.38288	4.51975	10.1453	238.224
Gene	VSNL1	DOWN	V	In Vivo-sp.	0.311834	6.61811	2.74522	10.4873	30.1386	714.851
Gene	LRP1B	DOWN	V	In Vivo-sp.	0.0146631	0.596408	1.512	3.10599	3.63144	33.4506

Gene	ATP13A4	DOWN	V	In Vivo-sp.	0.01	0.01	0.0487813	0.01	0.01	22.567
Gene	GABRA4	DOWN	V	In Vivo-sp.	0.01	0.0543849	1.00153	0.0521498	0.630016	22.4478
Gene	PSD2	DOWN	V	In Vivo-sp.	0.01	0.111281	0.01	0.0767276	1.63102	22.1739
Gene	CDK5R2	DOWN	V	In Vivo-sp.	0.01	0.01	0.0219425	0.01	0.326508	22.1084
Gene	ATP10B	DOWN	V	In Vivo-sp.	0.01	0.381512	0.024916	0.01	0.253601	21.9429
Gene	NRG3	DOWN	V	In Vivo-sp.	0.01	0.263461	0.0135096	0.72156	3.0561	21.891
Gene	SLITRK2	DOWN	V	In Vivo-sp.	0.01	1.04377	0.23732	0.374671	2.62756	21.6552
Gene	WIPF1	DOWN	V	In Vivo-sp.	0.01	0.206687	0.293778	0.0228758	2.19679	20.9605
Gene	C1orf173	DOWN	V	In Vivo-sp.	0.00944342	0.01	0.01	0.01	0.705604	19.6749
Gene	CHRDL1	DOWN	V	In Vivo-sp.	0.0106334	0.0445585	0.391154	0.0851135	0.520216	22.1221
Gene	NLGN3	DOWN	V	In Vivo-sp.	0.01	0.207246	0.361509	0.344625	3.94862	20.541
Gene	CLU	DOWN	V	In Vivo-sp.	1.39823	18.3223	114.714	617.431	610.859	2871.16
Gene	SLC38A11	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	20.4808
Gene	GABRB1	DOWN	V	In Vivo-sp.	0.01	0.0406147	0.0689455	0.342935	0.01	20.4679
Gene	GPM6B	DOWN	V	In Vivo-sp.	0.208092	6.88325	5.22263	3.7787	23.9088	423.806
Gene	STXBP6	DOWN	V	In Vivo-sp.	0.01	0.01	0.677084	0.253144	0.28443	20.3499
Gene	NPTX1	DOWN	V	In Vivo-sp.	0.01	0.356667	1.23774	0.0896006	0.162797	20.3478
Gene	DIO2	DOWN	V	In Vivo-sp.	0.01	0.202632	0.419052	0.924722	1.93838	20.1585
Gene	KCNC2	DOWN	V	In Vivo-sp.	0.01	1.37987	0.01	0.0366952	0.01	20.0571
Gene	MYOT	DOWN	V	In Vivo-sp.	0.01	0.308455	0.217157	0.01	0.251306	19.8027
Gene	S1PR5	DOWN	V	In Vivo-sp.	0.01	0.380159	0.150464	0.517617	0.322297	19.7857
Gene	MBP	DOWN	V	In Vivo-sp.	3.62687	0.59959	2.01738	0.714722	1.25033	7121.93

Gene	CCDC164	DOWN	V	In Vivo-sp.	0.01	0.01	0.364482	0.01	2.72106	18.6127
Gene	NTRK3	DOWN	V	In Vivo-sp.	0.01	0.01	0.201522	0.145583	0.762292	18.5433
Gene	NXPH1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	3.53554	18.5033
Gene	CLDN10	DOWN	V	In Vivo-sp.	0.01	0.01	0.0700623	0.066738	0.320216	18.2475
Gene	SIRPA	DOWN	V	In Vivo-sp.	0.01	0.01	0.0879027	0.0202647	0.523902	17.8509
Gene	GPR37	DOWN	V	In Vivo-sp.	0.01	0.405061	0.523765	0.382995	0.01	17.7937
Gene	SIDT1	DOWN	V	In Vivo-sp.	0.01	0.01	0.108409	0.392964	1.02143	17.6792
Gene	TMEM130	DOWN	V	In Vivo-sp.	0.0213412	0.0830212	0.01	0.877658	1.79218	37.7089
Gene	DIRAS2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.260612	17.5687
Gene	LCP2	DOWN	V	In Vivo-sp.	0.01	0.471633	0.328833	0.399252	4.19172	17.3723
Gene	CDH19	DOWN	V	In Vivo-sp.	0.00664343	0.792886	1.66918	0.298651	0.16382	11.5244
Gene	SPINK13	DOWN	V	In Vivo-sp.	0.01	0.01	0.114624	0.01	2.36394	17.0224
Gene	OLIG2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.063255	17.0202
Gene	ST8SIA3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	3.02324	16.956
Gene	SYT17	DOWN	V	In Vivo-sp.	0.0189484	0.116558	0.05915	0.451247	2.14414	31.8079
Gene	HOPX	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	16.6598
Gene	WIF1	DOWN	V	In Vivo-sp.	0.01	0.01	0.210642	0.01	0.01	16.6199
Gene	RNF182	DOWN	V	In Vivo-sp.	0.01	0.218524	0.384081	0.0367919	2.7168	16.553
Gene	ZNF365	DOWN	V	In Vivo-sp.	0.01	0.01	0.0679714	0.01	0.01	16.4754
Gene	CD22	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.246677	16.4389
Gene	TNNT2	DOWN	V	In Vivo-sp.	0.01	1.38718	0.01	0.0228087	0.332746	16.3723
Gene	S100B	DOWN	V	In Vivo-sp.	0.32252	10.423	4.36989	2.60082	4.69851	523.435

Gene	ANKRD30B	DOWN	V	In Vivo-sp.	0.01	0.0971552	0.0209097	0.01	0.01	15.7608
Gene	ASTN1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.25713	15.7256
Gene	BEX4	DOWN	V	In Vivo-sp.	0.0446412	2.68999	2.17939	0.531884	13.9274	69.6259
Gene	AGBL4	DOWN	V	In Vivo-sp.	0.01	0.139596	0.437136	0.121185	0.01	15.3746
Gene	SLC39A12	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	15.2824
Gene	CREG2	DOWN	V	In Vivo-sp.	0.01	0.01	0.0468746	0.01	0.0508206	15.1561
Gene	MAOA	DOWN	V	In Vivo-sp.	0.01	1.50017	2.42356	0.0231259	1.30268	15.0832
Gene	SEZ6L	DOWN	V	In Vivo-sp.	0.01	0.309571	0.0574508	0.01	1.9676	14.947
Gene	P2RY12	DOWN	V	In Vivo-sp.	0.01	0.0360401	0.01	0.0827164	0.0796774	14.9
Gene	ST8SIA1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.653221	14.8917
Gene	ADORA3	DOWN	V	In Vivo-sp.	0.01	0.01	0.0841762	0.01	0.01	14.8331
Gene	PABPC1L2A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	2.30932	14.7266
Gene	HPCAL4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	14.5359
Gene	BCAS1	DOWN	V	In Vivo-sp.	0.546904	2.73669	3.42978	5.79427	6.10873	784.314
Gene	RFTN2	DOWN	V	In Vivo-sp.	0.256052	0.589364	0.951678	0.749749	8.66314	367.136
Gene	MS4A6A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	14.0758
Gene	CRHBP	DOWN	V	In Vivo-sp.	0.01	0.01	0.347233	0.0225907	1.63178	14.005
Gene	CCK	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	13.8888
Gene	TCEAL2	DOWN	V	In Vivo-sp.	0.187695	0.879575	0.0877752	0.401501	0.363374	255.843
Gene	GAD1	DOWN	V	In Vivo-sp.	0.01	0.369803	1.80453	0.528514	2.9907	13.5096
Gene	OLIG1	DOWN	V	In Vivo-sp.	0.01	0.01	0.600996	0.01	0.01	13.4375
Gene	PCDH19	DOWN	V	In Vivo-sp.	0.00544938	1.682	1.43887	0.998643	1.68758	7.3073

Gene	TAS2R40	DOWN	V	In Vivo-sp.	0.01	0.699466	0.39081	0.209354	0.333564	13.3227
Gene	TDRD6	DOWN	V	In Vivo-sp.	0.01	0.0509803	0.01	0.01	0.0719826	13.3192
Gene	CX3CR1	DOWN	V	In Vivo-sp.	0.01	0.01	0.0179264	0.01	0.01	13.2924
Gene	PPP1R14A	DOWN	V	In Vivo-sp.	0.01	0.74546	0.392834	1.35874	0.815519	13.2179
Gene	SAMD12	DOWN	V	In Vivo-sp.	0.0227668	0.216165	0.740042	0.0338979	0.83927	29.8677
Gene	SCRG1	DOWN	V	In Vivo-sp.	0.01	0.483486	0.530282	0.831882	2.35723	13.0539
Gene	EIF4E1B	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	12.7887
Gene	KIF5A	DOWN	V	In Vivo-sp.	0.447051	0.502844	1.21679	0.68299	7.68419	564.917
Gene	AP3B2	DOWN	V	In Vivo-sp.	0.01	0.595193	0.021332	0.0176947	0.64701	12.0224
Gene	HLA-DRA	DOWN	V	In Vivo-sp.	0.01	0.975574	1.08404	0.468623	0.728898	11.9419
Gene	RGS22	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0161161	0.01	11.9157
Gene	LGI4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.513571	11.7958
Gene	ZBBX	DOWN	V	In Vivo-sp.	0.01	0.185235	0.0191674	0.0736422	0.405647	11.7731
Gene	EYA2	DOWN	V	In Vivo-sp.	0.01	0.0499027	0.445533	0.0247172	1.67136	11.6722
Gene	CYP2J2	DOWN	V	In Vivo-sp.	0.01	0.01	0.0789604	0.0363535	0.01	11.6602
Gene	TNR	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.199613	11.6414
Gene	HSPB6	DOWN	V	In Vivo-sp.	0.01	0.13215	0.0406316	1.85605	0.241845	11.5635
Gene	GIMAP7	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	11.2935
Gene	PCDH11Y	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.07733	11.1249
Gene	PAQR6	DOWN	V	In Vivo-sp.	0.446011	2.00125	1.38235	9.49676	11.9086	484.099
Gene	GPC5	DOWN	V	In Vivo-sp.	0.01	0.01	1.65435	0.0601944	0.337376	10.8212
Gene	FCGR3A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	10.7672

Gene	SLC6A11	DOWN	V	In Vivo-sp.	0.01	0.116161	0.01	0.01	0.0462472	10.7665
Gene	PLA1A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.28891	10.6704
Gene	FAM5B	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0522423	0.01	10.6466
Gene	MPEG1	DOWN	V	In Vivo-sp.	0.01	0.193036	0.17961	0.165254	0.285639	10.5429
Gene	SNAP91	DOWN	V	In Vivo-sp.	0.050396	0.350767	0.01	0.01	1.39142	52.3545
Gene	ITGB2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.22124	0.01	10.3878
Gene	CACNA1D	DOWN	V	In Vivo-sp.	0.0112699	0.19997	0.283141	0.167174	0.272109	11.687
Gene	NEUROD2	DOWN	V	In Vivo-sp.	0.01	0.01	0.155448	0.01	0.01	10.1812
Gene	NRXN1	DOWN	V	In Vivo-sp.	0.263223	1.25494	1.2934	0.613997	4.57509	266.632
Gene	NHS	DOWN	V	In Vivo-sp.	0.01	0.476669	0.43589	0.0368582	2.203	10.1191
Gene	RIMS1	DOWN	V	In Vivo-sp.	0.0786976	3.06149	0.807931	0.606408	4.59355	78.7017
Gene	TTYH1	DOWN	V	In Vivo-sp.	0.0182832	0.0489355	0.0507886	0.177319	4.48054	18.2336
Gene	ATCAY	DOWN	V	In Vivo-sp.	0.01	0.01	0.191988	0.01	1.5855	9.81683
Gene	ALOX5AP	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.194854	9.72745
Gene	CPLX2	DOWN	V	In Vivo-sp.	0.0761536	0.0675746	0.0195259	0.431609	1.0358	74.0229
Gene	SLITRK3	DOWN	V	In Vivo-sp.	0.01	0.01	0.0341224	0.01	0.113578	9.66097
Gene	HAPLN2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	9.6046
Gene	IKZF2	DOWN	V	In Vivo-sp.	0.01	0.315684	0.331651	0.0843047	0.616694	9.52041
Gene	ABLIM3	DOWN	V	In Vivo-sp.	0.0143445	0.0296728	0.0597927	0.0314968	0.534448	13.5056
Gene	KCNH7	DOWN	V	In Vivo-sp.	0.01	0.442854	0.0681432	1.0059	0.0297819	9.39697
Gene	GRM5	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	9.33821
Gene	STX1B	DOWN	V	In Vivo-sp.	0.01	0.01	0.0860278	0.0511986	0.687581	9.27704

Gene	ABCB1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.40543	9.22666
Gene	KCNA4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.14818	9.2159
Gene	LAYN	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.121736	0.150466	9.20992
Gene	TMEM59L	DOWN	V	In Vivo-sp.	0.01	0.01	0.0347592	0.01	0.940402	9.20109
Gene	NETO1	DOWN	V	In Vivo-sp.	0.01	0.10355	0.01	0.01	0.421908	9.1813
Gene	CLEC14A	DOWN	V	In Vivo-sp.	0.01	0.626816	0.596707	0.477466	0.119995	9.17852
Gene	HCN1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.0592333	9.15618
Gene	CYP2C8	DOWN	V	In Vivo-sp.	0.01	0.01	0.28018	1.80839	0.412979	9.10128
Gene	GRM7	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.413653	9.09627
Gene	ITPKB	DOWN	V	In Vivo-sp.	0.01	0.194097	0.589378	1.01365	0.57185	9.09319
Gene	HPGDS	DOWN	V	In Vivo-sp.	0.01	0.0777407	0.260808	0.196807	0.528953	9.08266
Gene	IL33	DOWN	V	In Vivo-sp.	0.01	0.01	0.301702	0.00970048	0.01	8.93248
Gene	FAAH2	DOWN	V	In Vivo-sp.	0.01	0.440189	1.28593	0.211672	0.811855	8.80475
Gene	HECW1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	2.13437	8.7754
Gene	DGKB	DOWN	V	In Vivo-sp.	0.0411897	0.348186	0.999536	0.208885	2.36829	35.9906
Gene	GABBR2	DOWN	V	In Vivo-sp.	0.0227766	0.0290237	0.0105167	0.0073147	0.125038	19.7154
Gene	SYCE1	DOWN	V	In Vivo-sp.	0.01	0.137633	0.01	0.01	0.01	8.65006
Gene	AK4	DOWN	V	In Vivo-sp.	0.0349852	0.850839	2.74525	1.87562	5.94509	30.2081
Gene	APBB1IP	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	8.58568
Gene	GUCY1A3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.797836	8.58199
Gene	NECAB1	DOWN	V	In Vivo-sp.	0.0484153	0.0908762	0.162209	0.0355424	0.18438	41.4739
Gene	AMOT	DOWN	V	In Vivo-sp.	0.026535	2.36399	2.83112	1.48982	3.14932	22.3376

Gene	KIAA0748	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	8.1785
Gene	PAQR8	DOWN	V	In Vivo-sp.	0.0553226	0.148041	0.50145	0.484522	1.70678	44.7884
Gene	RYR2	DOWN	V	In Vivo-sp.	0.0435185	0.515256	2.35965	2.12404	5.59639	35.1888
Gene	EGFR	DOWN	V	In Vivo-sp.	0.0124648	0.0646716	0.250079	0.764107	0.597008	10.0218
Gene	PTPRB	DOWN	V	In Vivo-sp.	0.01	0.0434377	0.0325316	0.01	0.399188	8.03291
Gene	BTNL9	DOWN	V	In Vivo-sp.	0.01	0.0390279	0.01	0.01	0.01	7.99589
Gene	ENPP5	DOWN	V	In Vivo-sp.	0.01	0.01	0.133382	0.01	0.774153	7.95051
Gene	GPR158	DOWN	V	In Vivo-sp.	0.00946454	0.380167	1.40706	0.950798	1.56343	7.47509
Gene	GABRA1	DOWN	V	In Vivo-sp.	0.0301611	0.721373	0.243605	0.382005	0.318709	23.773
Gene	SOX10	DOWN	V	In Vivo-sp.	0.01	0.213832	0.01	0.025143	0.130499	7.86062
Gene	MPZL2	DOWN	V	In Vivo-sp.	0.01	0.0679817	0.01	0.01	1.13074	7.83955
Gene	EPAS1	DOWN	V	In Vivo-sp.	0.0157974	0.01	0.479023	0.01	0.448702	12.3581
Gene	CC2D2B	DOWN	V	In Vivo-sp.	0.0179002	0.523353	0.648548	0.0704055	0.235224	13.9818
Gene	BZRAP1	DOWN	V	In Vivo-sp.	0.01	0.01	0.0605611	0.01	1.08165	7.81028
Gene	HYDIN	DOWN	V	In Vivo-sp.	0.0380265	0.761065	0.855481	0.456399	1.07927	29.6357
Gene	CACNA1A	DOWN	V	In Vivo-sp.	0.01	0.0563414	0.0195127	0.0334028	0.178047	7.77145
Gene	STXBP5L	DOWN	V	In Vivo-sp.	0.041471	0.188284	0.160885	2.57718	1.16511	32.02
Gene	POU6F2	DOWN	V	In Vivo-sp.	0.01	0.837504	0.0807039	1.08326	0.738707	7.70438
Gene	CCR1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.059592	7.64531
Gene	C7orf41	DOWN	V	In Vivo-sp.	1.11836	13.6844	17.1692	10.4757	16.1781	853.915
Gene	CACNA1E	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.792964	7.62972
Gene	EPHX4	DOWN	V	In Vivo-sp.	0.01	0.18103	0.263957	0.0775404	1.1777	7.58526

Gene	CARTPT	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0571319	0.01	7.56926
Gene	ZBTB16	DOWN	V	In Vivo-sp.	0.0115145	0.01	0.01	0.01	0.403915	8.67022
Gene	TEK	DOWN	V	In Vivo-sp.	0.01	0.0318122	0.01	0.0121261	0.01	7.50229
Gene	NAP1L2	DOWN	V	In Vivo-sp.	0.0806048	2.48719	1.31349	1.33173	3.46652	60.3335
Gene	ANO5	DOWN	V	In Vivo-sp.	0.0111563	0.500057	0.24516	0.0981203	0.570013	8.066
Gene	MEPE	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	7.21035
Gene	GPR56	DOWN	V	In Vivo-sp.	0.01	0.0557734	0.0350996	0.0986597	0.52386	7.19452
Gene	SHC4	DOWN	V	In Vivo-sp.	0.0494332	0.024009	0.127053	0.115144	0.703182	35.1896
Gene	OR14I1	DOWN	V	In Vivo-sp.	0.01	0.01	0.210534	0.01	0.01	7.11816
Gene	MLC1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	7.07767
Gene	LRRK2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.00941251	0.01	7.07141
Gene	AKAP6	DOWN	V	In Vivo-sp.	0.0824899	0.249263	0.199324	0.29522	6.82489	58.2594
Gene	PITPNM3	DOWN	V	In Vivo-sp.	0.01	0.0253212	0.193975	0.0896746	0.218583	6.99599
Gene	GPR116	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.05323	6.90523
Gene	GPR12	DOWN	V	In Vivo-sp.	0.01	0.01	0.0602039	0.177128	0.84347	6.87916
Gene	SLC25A48	DOWN	V	In Vivo-sp.	0.01	0.01	0.675488	0.470626	0.01	6.86547
Gene	GJB1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	6.76581
Gene	NPTXR	DOWN	V	In Vivo-sp.	0.0116592	0.01	0.0283383	0.01	0.251324	7.87009
Gene	TGFB2	DOWN	V	In Vivo-sp.	0.0595737	0.516121	2.35726	0.780896	7.1109	39.5714
Gene	ASCL1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.27909	6.61165
Gene	ST8SIA5	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.242884	0.160122	6.59891
Gene	GALNTL2	DOWN	V	In Vivo-sp.	0.01	0.01	0.0694615	0.0122417	0.01	6.59212

Gene	SYT9	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0168019	0.146585	6.57123
Gene	HMGCLL1	DOWN	V	In Vivo-sp.	0.01	0.01	0.0224527	0.105737	1.21228	6.51505
Gene	STOX2	DOWN	V	In Vivo-sp.	0.0196603	0.01	0.01	0.01	1.52717	12.7118
Gene	PCDHB4	DOWN	V	In Vivo-sp.	0.01	0.0487151	0.158209	0.0625108	0.244915	6.4363
Gene	LAPTM5	DOWN	V	In Vivo-sp.	0.01	0.01	0.0756264	0.0332451	0.01	6.43215
Gene	PPP1R16B	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.0277428	6.43089
Gene	ERBB4	DOWN	V	In Vivo-sp.	0.0358801	0.634718	3.11839	0.256737	0.964568	22.8852
Gene	KCNA1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.304889	6.34772
Gene	DGKI	DOWN	V	In Vivo-sp.	0.01	0.01	0.0231982	0.245685	0.837612	6.30107
Gene	PDC	DOWN	V	In Vivo-sp.	0.01	0.608563	0.272169	0.369692	0.542648	6.26157
Gene	CLCA4	DOWN	V	In Vivo-sp.	0.01	0.0328691	0.0490856	0.0348727	0.160697	6.21935
Gene	SCN2B	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	6.19652
Gene	CACNG3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0267812	0.37332	6.16519
Gene	HEATR8	DOWN	V	In Vivo-sp.	0.00785386	0.01	0.01	0.01	0.113732	4.7968
Gene	CPEB1	DOWN	V	In Vivo-sp.	0.01	0.01	0.0489368	0.01	0.750142	6.08671
Gene	LYVE1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	6.02784
Gene	APLNR	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.01404	6.00002
Gene	KIAA0319	DOWN	V	In Vivo-sp.	0.01	0.0597289	0.0164386	0.01	0.0915922	5.99823
Gene	C21orf63	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.190414	5.93804
Gene	RASGRF1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.165006	5.92583
Gene	C10orf128	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	5.91708
Gene	CNTNAP5	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.551027	5.90632

Gene	AJAP1	DOWN	V	In Vivo-sp.	0.01	0.310764	0.140869	0.714734	0.459709	5.8955
Gene	SCN3A	DOWN	V	In Vivo-sp.	0.057792	1.1605	0.432445	0.362332	7.48143	33.906
Gene	NEUROD6	DOWN	V	In Vivo-sp.	0.01	0.01	0.164653	0.0434671	0.01	5.79475
Gene	GRIN2B	DOWN	V	In Vivo-sp.	0.01	0.01	0.0265832	0.01	1.10054	5.78149
Gene	COBL	DOWN	V	In Vivo-sp.	0.0366091	0.0376406	0.0767774	0.113989	0.790166	21.0543
Gene	RUNDC3A	DOWN	V	In Vivo-sp.	0.01	0.01	0.325035	0.01	0.0909019	5.70545
Gene	TMEM132D	DOWN	V	In Vivo-sp.	0.01	0.01	0.0519472	0.01	0.371745	5.70267
Gene	ENPP4	DOWN	V	In Vivo-sp.	0.0401613	0.01	0.0277258	0.00414771	0.91026	22.8219
Gene	HAVCR2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0122755	0.179691	5.65614
Gene	SLC16A14	DOWN	V	In Vivo-sp.	0.0105829	0.419186	0.345153	0.302395	0.444511	5.98129
Gene	GPR37L1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.0308711	5.62301
Gene	MCHR2	DOWN	V	In Vivo-sp.	0.01	0.270416	0.124115	0.01	0.356871	5.61353
Gene	SLC25A27	DOWN	V	In Vivo-sp.	0.0877782	0.225438	0.257998	0.410188	6.8076	49.2106
Gene	SLC35F3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.0576565	0.790511	5.59612
Gene	SYP	DOWN	V	In Vivo-sp.	1.46894	2.39932	7.92998	1.52036	21.3263	820.118
Gene	PDZD4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.133879	5.50128
Gene	BHLHE41	DOWN	V	In Vivo-sp.	0.915624	0.982124	0.595273	0.392487	3.04283	500.899
Gene	PI16	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	5.45406
Gene	CD34	DOWN	V	In Vivo-sp.	0.0237755	0.01	0.01	0.206475	0.382198	12.9256
Gene	GPRC5B	DOWN	V	In Vivo-sp.	1.36456	57.4104	96.4527	131.837	107.425	735.013
Gene	PLXDC1	DOWN	V	In Vivo-sp.	0.00944056	0.242886	0.295283	0.01	0.302259	5.03127
Gene	ST8SIA4	DOWN	V	In Vivo-sp.	0.01	1.21138	1.13626	0.380008	0.624844	5.18876

Gene	KCNA3	DOWN	V	In Vivo-sp.	0.01	0.01	0.110236	0.01	0.241698	5.18616
Gene	CELF6	DOWN	V	In Vivo-sp.	0.01	0.118666	0.700193	0.402842	0.433875	5.146
Gene	SYT13	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	1.07665	5.13859
Gene	ABCD2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	5.12586
Gene	GRIK1	DOWN	V	In Vivo-sp.	0.01	0.740717	0.896035	0.903741	0.122785	5.08002
Gene	KCTD8	DOWN	V	In Vivo-sp.	0.01	0.01	0.0211783	0.01	0.01	5.07596
Gene	MS4A7	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	5.04816
Gene	MS4A14	DOWN	V	In Vivo-sp.	0.01	0.01	0.245705	0.01	0.01	5.03951
Gene	OPRM1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	5.02453
Gene	CAPN13	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	4.97803
Gene	CNTN2	DOWN	V	In Vivo-sp.	0.0402226	0.0213688	0.186586	0.0686912	0.531973	19.999
Gene	RBP4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	4.94833
Gene	FOXQ1	DOWN	V	In Vivo-sp.	0.01	0.01	0.0237342	0.01	0.141267	4.92261
Gene	HVCN1	DOWN	V	In Vivo-sp.	0.01	0.0952256	0.611244	0.0681692	0.648126	4.87265
Gene	LMO3	DOWN	V	In Vivo-sp.	0.872413	23.6482	12.5574	13.2213	50.354	422.754
Gene	PCDHB15	DOWN	V	In Vivo-sp.	0.01	0.343367	0.26686	0.124254	0.75221	4.78447
Gene	GNA14	DOWN	V	In Vivo-sp.	0.01	0.01	0.034328	0.0152094	0.0657928	4.75918
Gene	ABCG1	DOWN	V	In Vivo-sp.	0.01	0.0290789	0.0812769	0.136583	0.0730623	4.72282
Gene	SIRPB1	DOWN	V	In Vivo-sp.	0.01	0.01	0.220248	0.01	0.0652293	4.64785
Gene	SOX8	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.14548	0.01	4.64493
Gene	RAB27B	DOWN	V	In Vivo-sp.	0.01	0.01	0.0323281	0.01	0.368898	4.64046
Gene	LGI3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	4.63171

Gene	RBFOX3	DOWN	V	In Vivo-sp.	0.01	0.01	0.0204337	0.01	0.01	4.63019
Gene	C5orf64	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.117003	0.334722	4.58742
Gene	RAB9B	DOWN	V	In Vivo-sp.	0.01	0.182265	0.11021	0.0294499	0.348533	4.55534
Gene	SRGN	DOWN	V	In Vivo-sp.	0.0323576	0.155385	0.487058	0.01	0.01	14.7395
Gene	TAS2R39	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.363504	0.01	4.53402
Gene	SLC30A10	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.09232	0.68059	4.50522
Gene	MLIP	DOWN	V	In Vivo-sp.	0.104942	0.01	0.277653	0.01	0.01	47.0509
Gene	C6orf10	DOWN	V	In Vivo-sp.	0.035091	0.01	0.163724	0.01	1.87427	15.5013
Gene	SLC2A2	DOWN	V	In Vivo-sp.	0.01	0.0329542	0.109353	0.00937108	0.01	4.3398
Gene	PHYHIP	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.054175	0.104787	4.27594
Gene	KIAA1755	DOWN	V	In Vivo-sp.	0.01	0.01	0.0590265	1.00696	0.0889161	4.16435
Gene	PROX1	DOWN	V	In Vivo-sp.	0.0440889	0.208122	0.121445	0.169336	4.24552	18.3196
Gene	CELF4	DOWN	V	In Vivo-sp.	0.0910557	3.34058	4.02445	3.24927	1.23556	37.3978
Gene	PTPN5	DOWN	V	In Vivo-sp.	0.01	0.106151	0.0778368	0.01	0.282408	4.08389
Gene	CLVS1	DOWN	V	In Vivo-sp.	0.0157598	0.0271545	0.118937	0.192064	0.394788	6.41409
Gene	SULT4A1	DOWN	V	In Vivo-sp.	0.158197	2.24574	2.13004	5.67419	15.0781	64.0115
Gene	ANKRD45	DOWN	V	In Vivo-sp.	0.01	0.126796	0.116331	0.0439436	0.448174	4.04377
Gene	RIT2	DOWN	V	In Vivo-sp.	0.01	0.01	0.386888	0.0943398	0.156971	4.01648
Gene	CLIC2	DOWN	V	In Vivo-sp.	0.0146095	0.173111	0.486732	0.107254	0.108593	5.82487
Gene	DLGAP2	DOWN	V	In Vivo-sp.	0.022237	0.01	0.01	0.01	0.808803	8.82032
Gene	PTCHD1	DOWN	V	In Vivo-sp.	0.01	0.0134043	0.02902	0.0103286	0.311411	3.96486
Gene	PCDH9	DOWN	V	In Vivo-sp.	0.551648	16.0039	25.9825	16.7681	4.80806	218.589

Gene	RYR3	DOWN	V	In Vivo-sp.	0.0264673	0.0270661	0.0761567	0.0244682	0.13797	10.4847
Gene	NRXN3	DOWN	V	In Vivo-sp.	0.0381807	0.406159	1.15395	0.320889	1.63929	15.0528
Gene	SHE	DOWN	V	In Vivo-sp.	0.00726071	0.01	0.01	0.0567055	0.413522	2.85696
Gene	TCTEX1D1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.9264
Gene	DDIT4L	DOWN	V	In Vivo-sp.	0.01	0.01	0.0313675	0.01	0.183039	3.88522
Gene	TM4SF18	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.8732
Gene	SYT11	DOWN	V	In Vivo-sp.	0.208121	1.89726	0.649926	1.7602	14.6136	80.344
Gene	VIP	DOWN	V	In Vivo-sp.	0.01	0.120524	0.113291	0.01	0.01	3.85982
Gene	NKX2-2	DOWN	V	In Vivo-sp.	0.01	0.01	0.117734	0.01	0.01	3.83011
Gene	FEZF2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.82974
Gene	CD86	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.79509
Gene	OLFM1	DOWN	V	In Vivo-sp.	0.3351	0.01	0.0220149	0.165152	1.74289	126.979
Gene	RGS7BP	DOWN	V	In Vivo-sp.	0.0219707	0.01	0.01	0.01	0.171282	8.28519
Gene	KIAA1045	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.7483
Gene	PATE4	DOWN	V	In Vivo-sp.	0.01	0.0601025	0.234618	0.01	0.01	3.74311
Gene	SLC24A4	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.115257	3.73196
Gene	APOD	DOWN	V	In Vivo-sp.	1.19137	5.88702	17.3367	33.743	35.3318	444.491
Gene	PATE2	DOWN	V	In Vivo-sp.	0.01	0.01	0.139796	0.202797	0.200819	3.706
Gene	GRIK2	DOWN	V	In Vivo-sp.	0.0539543	1.62776	2.56282	2.1598	2.39832	19.9833
Gene	PRELP	DOWN	V	In Vivo-sp.	0.0121752	0.0304104	0.214328	0.0297833	0.159245	4.49035
Gene	CLEC7A	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.66382
Gene	OR6V1	DOWN	V	In Vivo-sp.	0.01	0.01	0.0563402	0.01	0.325473	3.62145

Gene	CACNA2D3	DOWN	V	In Vivo-sp.	0.0863776	0.467627	0.538906	0.295752	1.63425	30.8696
Gene	ABCG2	DOWN	V	In Vivo-sp.	0.0401681	0.01	0.0126349	0.01	0.652243	14.3361
Gene	GPRASP1	DOWN	V	In Vivo-sp.	0.0771258	0.636684	1.344	0.85595	1.71936	27.4938
Gene	KCTD4	DOWN	V	In Vivo-sp.	0.0226022	0.0900832	0.695674	0.331394	0.955042	8.05282
Gene	ZNF676	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.0553399	3.54214
Gene	KLK6	DOWN	V	In Vivo-sp.	0.0503496	0.01	0.01	0.01	0.677026	17.7409
Gene	SLA	DOWN	V	In Vivo-sp.	0.0163554	0.01	0.136977	0.0192034	0.621201	5.72447
Gene	ATP2B3	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.0396074	3.32756
Gene	P2RY13	DOWN	V	In Vivo-sp.	0.038128	0.145242	0.44512	0.0918992	0.42347	12.6524
Gene	GALNT14	DOWN	V	In Vivo-sp.	0.01	0.01	0.0700708	0.01	0.453079	3.30938
Gene	RAPGEF3	DOWN	V	In Vivo-sp.	0.0305585	0.0968968	0.192362	0.492381	0.803506	10.11
Gene	TPPP	DOWN	V	In Vivo-sp.	0.0684813	0.0362108	0.0652011	0.0180636	0.242138	22.4499
Gene	IP6K3	DOWN	V	In Vivo-sp.	0.01	0.261917	0.0867483	0.026594	0.249808	3.26259
Gene	ANKRD24	DOWN	V	In Vivo-sp.	0.01	0.01	0.0138455	0.309046	0.122177	3.25505
Gene	ACVR1C	DOWN	V	In Vivo-sp.	0.0344614	0.467631	0.223963	0.162047	2.15404	11.2062
Gene	UBE2QL1	DOWN	V	In Vivo-sp.	0.01	0.132072	0.213537	0.0498924	0.529606	3.24348
Gene	LRRC3B	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.24037
Gene	MNDA	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.20708
Gene	CAPN3	DOWN	V	In Vivo-sp.	0.101073	0.535429	1.92822	4.97356	3.80975	32.2922
Gene	PCDHB6	DOWN	V	In Vivo-sp.	0.01	0.0482197	0.123107	0.0140628	0.237435	3.16448
Gene	CXorf36	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.15016
Gene	SLC12A5	DOWN	V	In Vivo-sp.	0.0255038	0.0965773	0.163666	0.00798854	0.0186771	8.03313

Gene	PCDHA5	DOWN	V	In Vivo-sp.	0.01	0.01	0.157693	0.36221	0.151617	3.14689
Gene	WASF3	DOWN	V	In Vivo-sp.	0.203088	0.847371	0.761118	1.86633	9.20359	63.5532
Gene	CD84	DOWN	V	In Vivo-sp.	0.01	0.01	0.0188337	0.01	0.01	3.11426
Gene	CXorf1	DOWN	V	In Vivo-sp.	0.01	0.0731555	0.022493	0.0674286	0.133879	3.11293
Gene	LRTM2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.11114
Gene	B3GALT1	DOWN	V	In Vivo-sp.	0.0198507	0.01	0.0886737	0.0717375	1.15189	6.16778
Gene	CLIC5	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.10635
Gene	ALDH1L1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	3.08173
Gene	PDLIM3	DOWN	V	In Vivo-sp.	0.0189057	0.0971114	0.01	0.01	0.794823	5.80805
Gene	ANGPTL1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.284298	3.05271
Gene	PTPRN2	DOWN	V	In Vivo-sp.	0.0176212	0.01	0.01	0.0826927	1.23598	5.37641
Gene	KCTD16	DOWN	V	In Vivo-sp.	0.0638864	0.316005	0.462921	0.17757	1.06046	19.4391
Gene	ATRNL1	DOWN	V	In Vivo-sp.	0.599676	18.0435	14.875	8.14858	8.70149	181.968
Gene	B3GAT1	DOWN	V	In Vivo-sp.	0.0605645	0.141785	0.0978116	0.190057	1.22921	18.3648
Gene	KIAA1324	DOWN	V	In Vivo-sp.	0.01	0.0131203	0.0135732	0.260396	0.237029	2.99157
Gene	SLC5A11	DOWN	V	In Vivo-sp.	0.01	0.01	0.111378	0.01	0.01	2.98669
Gene	ADCY5	DOWN	V	In Vivo-sp.	0.0111865	0.0289336	0.585111	0.163261	0.160656	3.29269
Gene	MYCT1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.93553
Gene	SEC14L5	DOWN	V	In Vivo-sp.	0.00924814	0.104158	0.119075	0.01	0.0326102	2.6944
Gene	FRMPD4	DOWN	V	In Vivo-sp.	0.01	0.01	0.12185	0.004182	0.01	2.90624
Gene	DNAH6	DOWN	V	In Vivo-sp.	0.130946	0.683286	0.327667	0.154559	3.99512	37.8567
Gene	OR9A2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.89097

Gene	CD163	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.88836
Gene	NINJ2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.88694
Gene	PRR18	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.86523
Gene	GPR17	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.86075
Gene	SNPH	DOWN	V	In Vivo-sp.	0.01	0.0553088	0.103045	0.381122	0.1857	2.82003
Gene	GRIN2A	DOWN	V	In Vivo-sp.	0.0359463	0.100577	0.160775	0.0827114	0.514776	10.1188
Gene	GAS7	DOWN	V	In Vivo-sp.	0.236805	1.52832	6.41918	7.82336	11.0712	66.5478
Gene	GDA	DOWN	V	In Vivo-sp.	0.0369803	0.265167	0.649348	0.105981	1.12359	10.3703
Gene	KCNJ9	DOWN	V	In Vivo-sp.	0.0457113	0.144398	0.154452	0.489605	0.549145	12.7619
Gene	SELL	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.01	2.74791
Gene	C1orf95	DOWN	V	In Vivo-sp.	0.01	0.0223245	0.0377307	0.124248	0.0786573	2.73349
Gene	C3AR1	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.171575	2.73261
Gene	PRRT2	DOWN	V	In Vivo-sp.	0.0533829	0.563381	0.355999	1.65548	2.63276	14.4294
Gene	RNF180	DOWN	V	In Vivo-sp.	0.0552357	0.348413	0.52704	0.388321	0.976063	14.9261
Gene	FOXF2	DOWN	V	In Vivo-sp.	0.01	0.01	0.01	0.01	0.225132	2.69355
Gene	GRAMD1B	DOWN	V	In Vivo-sp.	0.0488844	0.0188683	0.0161054	0.234968	2.67271	12.9333
Gene	B3GALT2	DOWN	V	In Vivo-sp.	0.0767534	0.807158	2.15973	1.16114	3.02543	20.2959
Gene	EDIL3	DOWN	V	In Vivo-sp.	0.603275	22.3934	25.1537	4.72532	3.94108	159.102
Gene	DOCK9	DOWN	V	In Vivo-sp.	0.266994	0.566732	2.01127	3.97511	8.29002	70.1839
Gene	GPAT2	DOWN	V	In Vivo-sp.	0.01	0.0901647	0.0739306	0.2425	0.184839	2.61534
Gene	KLHL32	DOWN	V	In Vivo-sp.	0.0625357	0.0493532	0.0438259	0.00773735	0.01	16.3193
Gene	CABP1	DOWN	V	In Vivo-sp.	0.0426521	0.01	0.0605164	0.01	1.54533	10.7522

Gene	PPM1H	DOWN	V	In Vivo-sp.	0.0461769	0.271123	0.152902	0.214324	1.80122	11.6088
Gene	BSN	DOWN	V	In Vivo-sp.	0.0769442	0.135713	0.179619	0.105264	0.168714	18.7355
Gene	TLR4	DOWN	V	In Vivo-sp.	0.0519914	0.509475	0.0475527	0.0284489	0.0431388	12.6368
Gene	SLAIN1	DOWN	V	In Vivo-sp.	1.74327	15.8035	8.71454	5.13383	25.6122	416.096
Gene	CHGB	DOWN	V	In Vivo-sp.	0.118564	0.119141	0.445621	0.0956563	5.63235	28.0386
Gene	SYN1	DOWN	V	In Vivo-sp.	0.0914935	0.0424903	0.240224	0.268008	0.310414	21.4445
Gene	EDNRB	DOWN	V	In Vivo-sp.	0.198864	0.331711	3.14197	1.91286	4.52261	46.1949
Gene	KIAA1377	DOWN	V	In Vivo-sp.	0.0998798	0.191095	1.57943	0.668772	2.57097	23.0414
Gene	GJB6	DOWN	V	In Vivo-sp.	0.129661	0.01	0.01	0.01	0.01	29.6472
Gene	SH3GL2	DOWN	V	In Vivo-sp.	0.0748345	0.403168	0.176895	0.579406	0.132031	17.0522
Gene	PCDHGA3	DOWN	V	In Vivo-sp.	0.0214447	0.104516	0.129063	0.482139	0.164665	4.87779
Gene	GNAQ	DOWN	V	In Vivo-sp.	0.236108	0.433559	4.86233	1.29929	10.2852	53.5576
Gene	AGT	DOWN	V	In Vivo-sp.	0.138708	0.289152	0.335812	0.160979	0.407543	31.2444
Gene	GLDN	DOWN	V	In Vivo-sp.	0.138954	0.01	0.033764	0.01	0.589122	30.9937
Gene	HTR1F	DOWN	V	In Vivo-sp.	0.0235823	0.221205	0.13376	0.01	0.53184	5.21074
Gene	RANBP3L	DOWN	V	In Vivo-sp.	0.750315	1.08727	1.59222	0.358536	2.21635	163.534
Gene	PRSS35	DOWN	V	In Vivo-sp.	0.0177967	0.043767	0.270115	0.0767016	0.133936	3.86177
Gene	NACAD	DOWN	V	In Vivo-sp.	0.0682674	0.72768	0.812066	1.95587	1.06207	14.7503
Gene	KCNN2	DOWN	V	In Vivo-sp.	0.0410008	1.01774	0.411696	0.516132	0.813543	8.8458
Gene	MRVI1	DOWN	V	In Vivo-sp.	0.0381376	0.129796	0.272929	0.106746	0.164203	8.19149
Gene	PBOV1	DOWN	V	In Vivo-sp.	0.0562247	0.115731	0.768194	0.141699	0.501875	11.887
Gene	RASGRP3	DOWN	V	In Vivo-sp.	0.16166	0.332671	0.874366	1.19141	4.68166	33.8973

Gene	BAI3	DOWN	V	In Vivo-sp.	0.287085	3.98769	4.76843	3.29885	0.771365	58.924
Gene	CAMK4	DOWN	V	In Vivo-sp.	0.0713674	0.781633	1.6348	0.185744	2.03862	14.5885
Gene	ELOVL2	DOWN	V	In Vivo-sp.	0.0541245	0.193966	0.201712	0.0843304	0.910827	11.0478
Gene	ADARB2	DOWN	V	In Vivo-sp.	0.0437557	0.465977	0.42079	0.827469	0.893219	8.91376
Gene	NNAT	DOWN	V	In Vivo-sp.	0.109204	0.422439	0.558874	1.76518	0.38375	21.9397
Gene	CFI	DOWN	V	In Vivo-sp.	0.0238629	0.651249	0.0797507	0.165227	0.595652	4.71124
Gene	KCNC1	DOWN	V	In Vivo-sp.	0.0240069	0.0292935	0.00792324	0.0952427	0.167678	4.73579
Gene	GPR27	DOWN	V	In Vivo-sp.	0.060389	0.571503	1.14375	0.223553	0.557111	11.8582
Gene	PAIP2B	DOWN	V	In Vivo-sp.	0.390804	0.731606	1.13568	1.0544	2.86544	76.6535
Gene	FAM107B	DOWN	V	In Vivo-sp.	0.340672	1.91419	4.24313	0.996163	7.25847	65.8498
Gene	ARHGAP20	DOWN	V	In Vivo-sp.	0.0226811	0.249003	0.192592	0.576751	0.688466	4.33916
Gene	KIAA2022	DOWN	V	In Vivo-sp.	0.0343005	0.00777069	0.0889726	0.01	0.468088	6.5442
Gene	SEMA4D	DOWN	V	In Vivo-sp.	0.133043	0.710087	1.72821	1.61084	3.77609	25.1448
Gene	SYT7	DOWN	V	In Vivo-sp.	0.0543148	0.01	0.0888274	0.55934	1.89301	10.241
Gene	CLCN4	DOWN	V	In Vivo-sp.	0.0476835	0.369186	0.0430125	0.141468	1.42778	8.98107
Gene	C11orf87	DOWN	V	In Vivo-sp.	0.040544	0.23075	0.134063	0.141489	0.401807	7.60338
Gene	APLP1	DOWN	V	In Vivo-sp.	0.192712	0.350548	0.442089	0.171191	3.33376	35.9402
Gene	KCNJ16	DOWN	V	In Vivo-sp.	0.109564	0.137112	0.0421144	0.01	0.0821708	20.2811
Gene	WDR96	DOWN	V	In Vivo-sp.	0.0798108	0.693758	0.242064	0.188922	0.538271	14.6978
Gene	IGSF11	DOWN	V	In Vivo-sp.	0.124907	0.591773	1.39266	0.514022	4.895	22.7068
Gene	SEPP1	DOWN	V	In Vivo-sp.	1.37397	15.1755	21.1213	12.6791	22.7366	248.173
Gene	MAGI2	DOWN	V	In Vivo-sp.	0.413002	3.53246	3.48427	3.92339	13.3861	74.286

Gene	RS1	DOWN	V	In Vivo-sp.	0.0183924	0.138405	0.01	0.0267456	0.0750173	3.29367
Gene	ITGA2	DOWN	V	In Vivo-sp.	0.0488674	0.240948	0.474846	0.40721	1.19192	8.69165
Gene	KCNH8	DOWN	V	In Vivo-sp.	0.0690516	1.37202	1.28486	0.932895	0.632227	11.8253
Gene	ADRB1	DOWN	V	In Vivo-sp.	0.0198949	0.01	0.01	0.01	0.01	3.40428
Gene	SSPN	DOWN	V	In Vivo-sp.	0.0685739	0.51088	0.545288	0.548911	0.139042	11.6641
Gene	RGS4	DOWN	V	In Vivo-sp.	0.13676	0.446875	0.493006	0.01	0.416214	22.9963
Gene	PABPC1L2B	DOWN	V	In Vivo-sp.	0.0631428	0.01	0.01	0.01	1.29797	10.5043
Gene	FGF2	DOWN	V	In Vivo-sp.	0.0703929	0.663327	1.4707	0.384535	2.09282	11.6528
Gene	CABLES1	DOWN	V	In Vivo-sp.	0.058597	0.242861	0.187864	0.400709	1.2903	9.58574
Gene	P2RY14	DOWN	V	In Vivo-sp.	0.0623263	0.162578	0.124018	0.0142002	0.903707	10.104
Gene	ADRB2	DOWN	V	In Vivo-sp.	0.0246466	0.0996398	0.0909412	0.105337	0.483941	3.9742
Gene	GNG3	DOWN	V	In Vivo-sp.	0.364267	0.417895	0.0827995	0.277171	11.3891	58.3613
Gene	NFASC	DOWN	V	In Vivo-sp.	0.489643	0.399757	0.207378	0.95148	3.32306	78.3142
Gene	ZDHHC22	DOWN	V	In Vivo-sp.	0.0297403	0.01	0.01	0.01	0.478319	4.70511
Gene	SERPINI1	DOWN	V	In Vivo-sp.	0.380868	2.24704	6.26103	3.82262	6.18676	59.7422
Gene	GABBR1	DOWN	V	In Vivo-sp.	4.06354	47.7655	84.9509	77.4635	100.947	634.15
Gene	SNTB1	DOWN	V	In Vivo-sp.	0.0406009	0.0305698	0.215434	0.0621195	0.0494249	6.3016
Gene	IL17D	DOWN	V	In Vivo-sp.	0.351519	2.42952	10.5647	5.8408	4.46454	54.2797
Gene	CTTNBP2	DOWN	V	In Vivo-sp.	0.20792	1.44609	0.13249	0.654351	5.95956	31.6799
Gene	PLEKHH1	DOWN	V	In Vivo-sp.	0.206795	0.10492	0.511129	0.548688	0.770785	31.0461
Gene	ZEB2	DOWN	V	In Vivo-sp.	1.73844	58.4442	61.9791	43.269	39.5704	260.866
Gene	LYNX1	DOWN	V	In Vivo-sp.	0.0644318	0.121665	0.485547	1.11781	0.420869	9.48427

Gene	ATP2B2	DOWN	V	In Vivo-sp.	0.182601	0.01	0.01	0.01	0.0395382	25.7223
Gene	S100A1	DOWN	V	In Vivo-sp.	0.151685	1.38577	0.01	1.46542	1.56166	21.3227
Gene	MPP2	DOWN	V	In Vivo-sp.	0.173749	0.0451797	0.0912877	0.0707248	2.33965	24.3503
Gene	GOLGA7B	DOWN	V	In Vivo-sp.	0.0238634	0.01	0.01	0.0819678	0.0292729	3.28852
Gene	ST3GAL6	DOWN	V	In Vivo-sp.	0.142461	0.589441	1.3818	0.817523	4.03082	19.368
Gene	HHATL	DOWN	V	In Vivo-sp.	0.19513	0.01	0.01	0.01	0.01	26.3299
Gene	SLC14A1	DOWN	V	In Vivo-sp.	0.151432	0.50466	0.128085	0.0554075	0.18931	20.1963
Gene	C10orf90	DOWN	V	In Vivo-sp.	0.13788	0.01	0.01	0.0866243	0.01	18.3351
Gene	GAD2	DOWN	V	In Vivo-sp.	0.0292408	0.63368	0.094415	0.214272	0.167158	3.87321
Gene	WBP2NL	DOWN	V	In Vivo-sp.	0.0401365	0.124701	0.343076	0.203281	0.491563	5.3085
Gene	IDS	DOWN	V	In Vivo-sp.	6.98894	24.273	60.9898	20.9283	33.3896	917.755
Gene	AMY2B	DOWN	V	In Vivo-sp.	0.148476	0.733841	1.64764	0.896457	3.55417	19.2493
Gene	FAM171B	DOWN	V	In Vivo-sp.	1.31244	7.7556	6.92798	2.52449	5.81889	167.011
Gene	DLGAP1	DOWN	V	In Vivo-sp.	1.45245	8.04552	13.0062	15.2914	17.5947	184.445
Gene	BEX5	DOWN	V	In Vivo-sp.	0.266183	0.01	0.566676	0.057891	0.614975	33.7045
Gene	KIAA1462	DOWN	V	In Vivo-sp.	0.114264	0.0274419	0.0376707	0.01	0.630674	14.4245
Gene	SPATA6	DOWN	V	In Vivo-sp.	0.157064	0.545902	0.469172	1.15532	3.70854	19.6473
Gene	NME5	DOWN	V	In Vivo-sp.	0.28333	1.66422	2.99204	2.30945	8.7062	35.3495
Gene	BCAN	DOWN	V	In Vivo-sp.	0.0362826	0.01	0.0726994	0.01	0.126943	4.47791
Gene	SYBU	DOWN	V	In Vivo-sp.	0.230793	1.19904	1.13489	0.852498	3.19071	28.3284
Gene	CYP4F11	DOWN	V	In Vivo-sp.	0.0945526	0.0209855	0.0293721	0.175317	1.15905	11.5791
Gene	GLT25D2	DOWN	V	In Vivo-sp.	0.129696	0.696933	0.360558	1.45566	2.79942	15.8788

Gene	GNG7	DOWN	V	In Vivo-sp.	0.157242	0.388542	0.269976	0.468942	1.2537	19.1428
Gene	C12orf39	DOWN	V	In Vivo-sp.	0.239534	0.01	0.557343	0.0538197	0.588361	28.6024
Gene	SDPR	DOWN	V	In Vivo-sp.	0.0291014	0.01	0.0209332	0.01	0.01	3.43206
Gene	FSTL4	DOWN	V	In Vivo-sp.	0.0306271	0.01	0.229285	0.01	0.415601	3.6081
Gene	ATP1B2	DOWN	V	In Vivo-sp.	1.60929	15.2464	8.65848	12.4228	19.2518	184.411
Gene	BEND6	DOWN	V	In Vivo-sp.	0.154704	0.163353	0.112408	0.170268	0.758719	17.7018
Gene	ENDOD1	DOWN	V	In Vivo-sp.	0.159159	0.497737	2.13468	1.17217	2.424	17.7406
Gene	C10orf68	DOWN	V	In Vivo-sp.	0.0967804	0.585066	0.844915	0.32128	0.170614	10.59
Gene	PRKACB	DOWN	V	In Vivo-sp.	1.55466	9.6993	15.3702	5.58213	13.0988	169.233
Gene	GATM	DOWN	V	In Vivo-sp.	0.687367	0.385397	0.185067	0.0717918	2.70446	74.2134
Gene	SH3TC2	DOWN	V	In Vivo-sp.	0.181566	0.922178	0.481856	0.718222	0.0645878	19.5848
Gene	SLC9A9	DOWN	V	In Vivo-sp.	0.169768	0.0966616	0.171976	0.733388	1.61053	18.2985
Gene	PREX2	DOWN	V	In Vivo-sp.	0.718273	1.00409	0.482672	0.143513	6.58458	77.3963
Gene	CCDC30	DOWN	V	In Vivo-sp.	0.458726	1.56464	1.94902	4.99119	5.20957	49.3695
Gene	AMPD3	DOWN	V	In Vivo-sp.	0.0704253	0.47356	0.205053	0.199346	0.495976	7.5726
Gene	CBX7	DOWN	V	In Vivo-sp.	0.119732	0.0268346	0.167492	0.627036	0.433542	12.7906
Gene	CCNI2	DOWN	V	In Vivo-sp.	0.895563	3.35902	6.53785	14.0201	9.78754	95.5509
Gene	MFAP3L	DOWN	V	In Vivo-sp.	0.369612	0.503883	1.10529	1.017	2.27124	39.2162
Gene	TCEAL6	DOWN	V	In Vivo-sp.	0.176613	0.125511	1.30831	0.346958	0.287444	18.6974
Gene	CD53	DOWN	V	In Vivo-sp.	0.0914293	0.01	0.01	0.01	0.01	9.65121
Gene	CA10	DOWN	V	In Vivo-sp.	0.135623	0.27663	0.110493	0.0646024	0.503108	14.3093
Gene	CADPS2	DOWN	V	In Vivo-sp.	0.129994	0.0791094	0.274655	0.38444	0.880614	13.5767

Gene	FAM81A	DOWN	V	In Vivo-sp.	0.0418774	0.01	0.0156565	0.01	0.0465943	4.343
Gene	CGNL1	DOWN	V	In Vivo-sp.	0.0782837	0.066988	0.0955009	0.743433	1.00395	8.11724
Gene	FGFR3	DOWN	V	In Vivo-sp.	0.0854133	0.01	0.143971	0.0501856	1.05551	8.85062
Gene	ICA1L	DOWN	V	In Vivo-sp.	0.257401	0.813874	1.10048	0.61234	1.63641	26.2865
Gene	DYSF	DOWN	V	In Vivo-sp.	0.0454668	0.176722	0.01	0.01	0.583086	4.64251
Gene	MTSS1	DOWN	V	In Vivo-sp.	0.482364	0.473689	2.19631	6.94706	4.94396	48.6363
Gene	DNM3	DOWN	V	In Vivo-sp.	1.2596	7.06855	12.5161	14.1922	26.2207	125.943
Gene	ILDR2	DOWN	V	In Vivo-sp.	0.0319289	0.01	0.270069	0.0483294	0.379925	3.17865
Gene	NOL4	DOWN	V	In Vivo-sp.	0.0951732	0.8871	1.03333	0.981701	0.317241	9.45471
Gene	TMCC2	DOWN	V	In Vivo-sp.	0.138447	0.631278	0.278626	0.415451	1.13855	13.7041
Gene	SLC17A7	DOWN	V	In Vivo-sp.	0.565071	0.249298	0.779131	0.175202	1.69321	55.9014
Gene	C3	DOWN	V	In Vivo-sp.	0.474006	0.34185	0.707437	5.37191	2.15659	46.2263
Gene	CCDC152	DOWN	V	In Vivo-sp.	0.206289	0.378449	0.187038	0.246425	0.50619	19.5238
Gene	MAP1A	DOWN	V	In Vivo-sp.	4.81027	14.7734	16.0502	12.0078	20.5876	454.914
Gene	OSBPL1A	DOWN	V	In Vivo-sp.	0.658459	0.335625	2.48802	0.40081	9.49716	61.6758
Gene	FRMD5	DOWN	V	In Vivo-sp.	0.204253	0.480169	0.413319	0.308034	0.730152	19.0034
Gene	KLKB1	DOWN	V	In Vivo-sp.	0.07972	0.600778	0.0849665	0.543233	0.299035	7.41607
Gene	EML5	DOWN	V	In Vivo-sp.	0.0442381	0.118458	0.161556	0.0261625	0.13097	4.08787
Gene	RHBDL2	DOWN	V	In Vivo-sp.	0.124782	0.390245	0.510131	0.689026	2.42082	11.5235
Gene	TIMP3	DOWN	V	In Vivo-sp.	0.269539	1.23631	5.23371	1.86877	4.74375	24.6872
Gene	FAM13C	DOWN	V	In Vivo-sp.	0.541194	0.403987	0.01	0.0409629	1.16327	49.4719
Gene	LDB3	DOWN	V	In Vivo-sp.	0.076409	0.252494	0.364059	0.232674	0.346357	6.87171

Gene	PLSCR4	DOWN	V	In Vivo-sp.	0.199689	0.8925	3.25379	1.81062	2.65438	17.8675
Gene	SLC25A18	DOWN	V	In Vivo-sp.	0.121701	0.340996	0.01	0.201532	0.202129	10.764
Gene	OMG	DOWN	V	In Vivo-sp.	0.884025	1.49213	6.47674	2.57951	7.98601	77.4131
Gene	GLIPR1L2	DOWN	V	In Vivo-sp.	0.109051	0.235474	0.800532	0.898044	0.621905	9.52618
Gene	IQUB	DOWN	V	In Vivo-sp.	0.034489	0.0981654	0.192822	0.01	0.214493	2.99057
Gene	ABCA6	DOWN	V	In Vivo-sp.	0.0598262	0.294866	0.68606	0.152751	0.462685	5.17695
Gene	OTUD7A	DOWN	V	In Vivo-sp.	0.0551009	0.589125	0.460319	0.382576	0.271128	4.6964
Gene	PURG	DOWN	V	In Vivo-sp.	0.302628	2.66999	3.26457	0.57223	3.22629	25.5841
Gene	NPAS3	DOWN	V	In Vivo-sp.	0.55509	0.989692	0.337537	0.622893	6.24298	45.8797
Gene	ENKUR	DOWN	V	In Vivo-sp.	0.113297	0.101794	0.156313	0.110711	0.622243	9.28719
Gene	GNAL	DOWN	V	In Vivo-sp.	0.135559	0.142655	0.269701	0.193173	0.640773	11.0666
Gene	TGFB3	DOWN	V	In Vivo-sp.	0.496673	1.69846	3.30761	3.56136	3.28162	40.499
Gene	C8orf46	DOWN	V	In Vivo-sp.	0.262169	1.41917	0.761656	0.927014	0.249339	21.2576
Gene	GPR155	DOWN	V	In Vivo-sp.	0.108055	0.234473	0.929547	1.22399	1.65107	8.75388
Gene	GLRB	DOWN	V	In Vivo-sp.	0.0576183	0.417029	0.841811	0.286296	0.896866	4.66027
Gene	YPEL1	DOWN	V	In Vivo-sp.	0.146985	0.347287	0.713137	0.522036	1.98584	11.647
Gene	C13orf15	DOWN	V	In Vivo-sp.	0.248162	0.882765	1.98357	1.61035	1.09585	19.632
Gene	XKR9	DOWN	V	In Vivo-sp.	0.0671834	0.139602	0.562722	0.0742935	0.542755	5.26807
Gene	AK5	DOWN	V	In Vivo-sp.	1.78051	2.21879	4.41841	3.26121	4.66117	139.208
Gene	JAKMIP3	DOWN	V	In Vivo-sp.	0.0486843	0.0265443	0.0540751	0.01	0.270646	3.80313
Gene	CSPG5	DOWN	V	In Vivo-sp.	0.214577	0.844306	1.54502	0.84778	1.90594	16.5711
Gene	C9orf125	DOWN	V	In Vivo-sp.	0.110319	0.0279923	0.112096	0.0574526	1.19913	8.46104

Gene	B4GALNT1	DOWN	V	In Vivo-sp.	0.106271	0.032598	0.091906	0.0642083	0.0287704	8.13404
Gene	ADAM28	DOWN	V	In Vivo-sp.	0.315545	0.560934	0.822549	0.701084	0.379377	24.0001
Gene	FBXL16	DOWN	V	In Vivo-sp.	0.0951293	0.01	0.01	0.01	0.0640613	7.20908
Gene	CLIP4	DOWN	V	In Vivo-sp.	0.911455	3.16767	13.4322	5.98265	17.1906	68.9431
Gene	TBC1D30	DOWN	V	In Vivo-sp.	0.0570563	0.259264	0.0763567	0.227416	0.339066	4.25046
Gene	OXTR	DOWN	V	In Vivo-sp.	0.0859828	1.18951	1.50852	0.564664	1.13566	6.38722
Gene	RGN	DOWN	V	In Vivo-sp.	0.40537	0.01	0.01	2.18406	0.512365	30.0724
Gene	PPP2R2C	DOWN	V	In Vivo-sp.	0.209199	0.01	0.01	0.01	0.10084	15.4749
Gene	WDR49	DOWN	V	In Vivo-sp.	0.093005	0.0526291	0.312841	0.01	0.905634	6.74664
Gene	PLD1	DOWN	V	In Vivo-sp.	0.566395	1.65968	5.80078	5.62827	9.5451	40.6766
Gene	APOLD1	DOWN	V	In Vivo-sp.	0.135345	0.424548	0.660729	0.218586	0.112251	9.69825
Gene	YJEFN3	DOWN	V	In Vivo-sp.	4.14491	11.4421	29.2708	9.9517	17.7109	293.504
Gene	CRB1	DOWN	V	In Vivo-sp.	0.386518	0.828966	0.966533	0.761117	0.854542	27.311
Gene	KLHL3	DOWN	V	In Vivo-sp.	0.279769	0.272497	0.430358	0.0864709	3.75234	19.6161
Gene	EVI2A	DOWN	V	In Vivo-sp.	0.615413	1.03725	3.08027	0.332334	1.53919	43.0239
Gene	CYBB	DOWN	V	In Vivo-sp.	0.1345	0.238729	0.0720756	0.0167669	0.315451	8.82432
Gene	LPAR1	DOWN	V	In Vivo-sp.	6.33193	4.47492	13.4472	28.9564	70.9735	407.279
Gene	EPB41L4B	DOWN	V	In Vivo-sp.	0.359133	0.284018	0.479706	0.214467	2.87869	22.7397
Gene	ZCWPW2	DOWN	V	In Vivo-sp.	0.174728	1.18446	2.53303	1.04087	2.33125	10.9941
Gene	ATL1	DOWN	V	In Vivo-sp.	0.355035	0.28221	0.362505	0.358038	0.584624	22.2654
Gene	C9orf174	DOWN	V	In Vivo-sp.	0.19745	0.210118	1.10945	2.59044	2.8175	12.1213
Gene	EFCAB6	DOWN	V	In Vivo-sp.	0.304161	0.751699	1.78614	1.39516	2.95266	18.5556

Gene	MAL	DOWN	V	In Vivo-sp.	1.19537	6.64119	12.7234	8.75398	5.2022	72.8005
Gene	RIMS3	DOWN	V	In Vivo-sp.	0.107008	0.515208	0.316734	0.604945	1.09628	6.50421
Gene	ZNF208	DOWN	V	In Vivo-sp.	0.0880563	0.208427	0.253312	0.142538	0.237818	5.25455
Gene	OPCML	DOWN	V	In Vivo-sp.	0.442667	1.26824	3.75774	2.47784	2.5413	26.2504
Gene	GRIA3	DOWN	V	In Vivo-sp.	2.38947	6.84554	4.5951	17.5738	27.3791	140.801
Gene	IQCK	DOWN	V	In Vivo-sp.	0.390253	1.53944	3.17905	2.41414	3.69483	22.4632
Gene	ANGPT2	DOWN	V	In Vivo-sp.	0.216237	0.366111	1.14439	0.838796	2.98304	12.2489
Gene	KCNIP4	DOWN	V	In Vivo-sp.	0.631426	2.50576	3.18054	2.91785	0.252161	35.7311
Gene	CAMK2N2	DOWN	V	In Vivo-sp.	0.101875	0.01	0.01	0.01	0.32929	5.70629
Gene	SGK3	DOWN	V	In Vivo-sp.	0.553288	0.153598	0.424557	0.496592	1.1666	30.9574
Gene	ACSL5	DOWN	V	In Vivo-sp.	0.109329	0.703354	0.688464	1.21801	1.27536	6.03103
Gene	BCL2	DOWN	V	In Vivo-sp.	0.153692	0.413421	0.121002	0.254887	0.646578	8.45608
Gene	SUSD4	DOWN	V	In Vivo-sp.	0.497449	1.59463	3.45016	3.1882	5.53053	27.3316
Gene	SLC2A13	DOWN	V	In Vivo-sp.	0.288376	0.460957	1.29805	0.54666	0.995557	15.7875
Gene	NRSN1	DOWN	V	In Vivo-sp.	0.615756	0.909903	0.353995	1.44351	3.10026	33.5546
Gene	CKMT2	DOWN	V	In Vivo-sp.	0.193286	1.88128	1.63759	2.44547	1.07202	10.4022
Gene	RGS5	DOWN	V	In Vivo-sp.	1.30207	0.417214	1.66236	0.324865	1.87078	69.5865
Gene	DBNDD2	DOWN	V	In Vivo-sp.	1.69962	2.2373	2.24936	3.46069	4.61502	90.2456
Gene	SLC22A17	DOWN	V	In Vivo-sp.	0.229634	0.786522	0.840249	0.658789	1.89371	12.1608
Gene	CAPS2	DOWN	V	In Vivo-sp.	0.381781	4.80076	1.55196	1.46912	1.31302	20.1361
Gene	BBOX1	DOWN	V	In Vivo-sp.	0.188273	0.01	0.379854	0.214595	0.496562	9.91167
Gene	SRCIN1	DOWN	V	In Vivo-sp.	0.174677	0.260683	0.414013	0.42642	0.614858	8.98791

Gene	ALDH1A1	DOWN	V	In Vivo-sp.	0.673115	1.58465	0.357656	0.13986	0.234057	34.3207
Gene	BTBD8	DOWN	V	In Vivo-sp.	0.0933595	0.163576	0.429997	0.01	0.384774	4.73127
Gene	NDRG4	DOWN	V	In Vivo-sp.	4.10142	4.13923	2.71312	2.27586	12.9715	207.412
Gene	CCDC7	DOWN	V	In Vivo-sp.	1.51828	5.17325	5.74116	3.08182	2.55793	76.6821
Gene	IGSF6	DOWN	V	In Vivo-sp.	0.123624	0.245477	0.0968268	0.796101	0.290735	6.15207
Gene	NEBL	DOWN	V	In Vivo-sp.	1.60332	0.074673	0.0957373	0.0742738	4.48299	79.6491
Gene	CCDC148	DOWN	V	In Vivo-sp.	0.108206	0.346498	0.941131	0.2175	0.870158	5.16471
Gene	AATK	DOWN	V	In Vivo-sp.	0.721933	1.52763	1.5547	1.89937	0.636621	34.4275
Gene	RAPGEF4	DOWN	V	In Vivo-sp.	4.36615	3.96562	2.74684	6.36164	7.6656	207.858
Gene	DOCK4	DOWN	V	In Vivo-sp.	5.83652	9.93173	28.0443	27.5787	49.7144	277.673
Gene	TRPC1	DOWN	V	In Vivo-sp.	0.617765	0.791178	0.787238	0.333102	6.45657	29.3446
Gene	CMPK2	DOWN	V	In Vivo-sp.	0.0676304	0.639715	0.563447	0.465318	0.0908824	3.15035
Gene	CCDC11	DOWN	V	In Vivo-sp.	0.434977	0.217811	1.23868	0.858433	3.52594	20.125
Gene	MED12L	DOWN	V	In Vivo-sp.	0.586528	0.569456	0.724989	0.541761	4.22604	27.1007
Gene	ACSBG1	DOWN	V	In Vivo-sp.	0.138345	0.114895	0.440484	0.059516	0.032	6.38279
Gene	ARMC2	DOWN	V	In Vivo-sp.	0.57574	1.64854	3.27136	1.7603	2.5722	26.5518
Gene	TMEM56	DOWN	V	In Vivo-sp.	0.494086	0.837372	1.01003	0.321387	0.333204	22.6606
Gene	C6orf225	DOWN	V	In Vivo-sp.	0.281043	0.835906	1.15134	0.596895	1.08769	12.8503
Gene	SLC8A3	DOWN	V	In Vivo-sp.	0.130456	0.252885	0.162282	0.149193	0.375003	5.95363
Gene	ARHGAP30	DOWN	V	In Vivo-sp.	0.0973115	0.0746565	0.20534	0.234814	0.294784	4.40506
Gene	DNAH7	DOWN	V	In Vivo-sp.	0.225348	0.531812	1.22922	1.26446	2.22837	10.1336
Gene	SLC30A3	DOWN	V	In Vivo-sp.	0.623848	0.395986	1.04716	2.30908	1.97007	28.0488

Gene	GPR22	DOWN	V	In Vivo-sp.	0.105899	0.488156	0.450283	0.0575122	0.280623	4.72629
Gene	RAB6B	DOWN	V	In Vivo-sp.	0.264206	0.203069	0.6411	1.08285	2.55851	11.5669
Gene	ARHGAP23	DOWN	V	In Vivo-sp.	0.453166	2.81364	1.78342	3.85438	2.53768	19.8372
Gene	ATP8A1	DOWN	V	In Vivo-sp.	1.97404	4.34034	7.28399	2.89096	7.11894	86.3932
Gene	PLCXD3	DOWN	V	In Vivo-sp.	0.0775689	0.430043	0.201284	0.0623028	0.151672	3.39167
Gene	ELN	DOWN	V	In Vivo-sp.	0.113589	0.01	0.0846455	0.209375	0.06023	4.94742
Gene	HRH1	DOWN	V	In Vivo-sp.	0.0954682	0.01	0.301062	0.338662	0.0622224	4.12975
Gene	EAF2	DOWN	V	In Vivo-sp.	0.250498	2.5775	2.42245	1.7909	2.40354	10.8356
Gene	NPY1R	DOWN	V	In Vivo-sp.	0.304819	1.40652	1.07178	0.186522	0.530228	13.1113
Gene	KLF15	DOWN	V	In Vivo-sp.	0.067594	0.0979198	0.242005	0.0907349	0.215938	2.79648
Gene	ADAMTS6	DOWN	V	In Vivo-sp.	0.0848767	0.0944862	0.103672	0.138682	0.436523	3.49742
Gene	SLC31A2	DOWN	V	In Vivo-sp.	1.20674	1.02258	0.759223	0.75346	0.705396	48.9668
Gene	ZNF540	DOWN	V	In Vivo-sp.	0.121782	0.243136	0.312003	0.167127	0.497767	4.88728
Gene	PDE1A	DOWN	V	In Vivo-sp.	0.831401	1.95651	3.91548	3.75603	5.70792	33.3204
Gene	LMOD3	DOWN	V	In Vivo-sp.	0.0910943	0.0831576	0.705637	0.228605	0.652121	3.65028
Gene	RALGPS1	DOWN	V	In Vivo-sp.	0.547463	2.1591	2.67585	3.16207	3.06909	21.9352
Gene	MAGEE1	DOWN	V	In Vivo-sp.	0.102862	0.192553	0.662154	0.593163	0.145164	4.11161
Gene	CACNG8	DOWN	V	In Vivo-sp.	0.867909	0.632535	0.069338	0.0917709	2.33899	34.6778
Gene	GMFG	DOWN	V	In Vivo-sp.	0.218727	0.436814	1.07587	1.81818	0.611104	8.70364
Gene	LRP4	DOWN	V	In Vivo-sp.	0.58516	0.120761	0.0691496	0.560689	3.58022	23.0204
Gene	ANKH	DOWN	V	In Vivo-sp.	0.585453	0.290457	0.514348	0.383553	0.654133	23.0118
Gene	RERGL	DOWN	V	In Vivo-sp.	0.152961	0.01	0.319487	0.01	0.01	6.0094

Gene	KCNMB4	DOWN	V	In Vivo-sp.	0.367519	0.217348	0.427382	0.49312	1.13883	14.1036
Gene	ARMS2	DOWN	V	In Vivo-sp.	0.102996	0.01	0.0725699	0.01	0.01	3.89418
Gene	FBXO2	DOWN	V	In Vivo-sp.	0.194522	0.01	0.161984	0.01	0.381265	7.31161
Gene	DAAM2	DOWN	V	In Vivo-sp.	1.31263	2.31276	2.52989	1.90761	1.24035	48.8718
Gene	CMYA5	DOWN	V	In Vivo-sp.	0.187654	0.232355	0.154353	0.139522	0.224129	6.97393
Gene	ZNF488	DOWN	V	In Vivo-sp.	0.103714	0.392586	0.0578161	0.158196	0.0478686	3.83661
Gene	GUCY1A2	DOWN	V	In Vivo-sp.	0.276857	0.81593	1.11654	0.889347	1.03019	10.2405
Gene	DUSP26	DOWN	V	In Vivo-sp.	0.0969528	0.190141	0.693494	0.413905	0.257288	3.57609
Gene	DSCAM	DOWN	V	In Vivo-sp.	0.172795	1.405	0.81631	0.542587	0.242642	6.3667
Gene	USP54	DOWN	V	In Vivo-sp.	3.45732	5.22109	6.10716	4.97877	12.6544	126.354
Gene	ALDH2	DOWN	V	In Vivo-sp.	4.42794	6.92524	5.14284	8.03667	5.74171	161.537
Gene	REEP1	DOWN	V	In Vivo-sp.	0.473698	1.05185	1.15733	0.91828	3.55853	17.2348
Gene	KIAA1244	DOWN	V	In Vivo-sp.	0.43293	0.94157	1.58078	0.651254	1.52251	15.5872
Gene	RAB11FIP4	DOWN	V	In Vivo-sp.	0.248739	0.228849	0.221369	0.243058	0.608308	8.84117
Gene	STX1A	DOWN	V	In Vivo-sp.	0.474663	0.884837	0.950605	0.667807	0.152504	16.8556
Gene	RUNDC3B	DOWN	V	In Vivo-sp.	0.295555	0.569562	0.194401	0.155071	0.41604	10.4827
Gene	RGAG4	DOWN	V	In Vivo-sp.	0.106551	0.222824	0.289505	0.176083	0.722748	3.76818
Gene	CTNNA3	DOWN	V	In Vivo-sp.	1.90166	4.93903	3.63902	3.60054	3.04414	67.2136
Gene	CPNE4	DOWN	V	In Vivo-sp.	0.202029	0.264179	0.127653	0.370731	0.993765	7.13259
Gene	KBTBD10	DOWN	V	In Vivo-sp.	0.14087	0.307589	1.03873	0.432348	0.894699	4.95836
Gene	C1orf162	DOWN	V	In Vivo-sp.	0.189388	0.375598	0.61841	0.337904	1.17845	6.60229
Gene	MFSD4	DOWN	V	In Vivo-sp.	0.206291	0.306652	0.232915	0.188684	0.957863	7.12828

Gene	ACSL6	DOWN	V	In Vivo-sp.	0.896233	0.0256198	0.0833672	0.0187017	0.552409	30.8628
Gene	ZC3H6	DOWN	V	In Vivo-sp.	6.68949	22.739	50.5006	10.6229	30.9177	228.339
Gene	TMC7	DOWN	V	In Vivo-sp.	0.252313	0.242087	0.30355	0.01	1.61272	8.5364
Gene	NDRG1	DOWN	V	In Vivo-sp.	3.53955	5.33943	13.2431	18.4872	29.7262	119.015
Gene	SLC1A4	DOWN	V	In Vivo-sp.	0.551418	0.796113	1.4321	1.90168	2.44145	18.4171
Gene	HEY2	DOWN	V	In Vivo-sp.	0.203389	0.589418	0.310954	0.0492675	0.383167	6.75037
Gene	CATSPER2	DOWN	V	In Vivo-sp.	1.49822	2.01834	3.46767	6.265	4.22279	49.6212
Gene	PTPRE	DOWN	V	In Vivo-sp.	0.218484	0.078068	0.01	0.0802688	0.701365	7.05234
Gene	SYT3	DOWN	V	In Vivo-sp.	0.104652	0.170909	0.01	0.01	0.288573	3.36806
Gene	KCNIP3	DOWN	V	In Vivo-sp.	0.31246	1.3321	0.705749	1.0513	0.967544	10.0118
Gene	DDN	DOWN	V	In Vivo-sp.	0.163782	0.0305465	0.0436193	0.205659	0.0935126	5.2455
Gene	AGXT2L1	DOWN	V	In Vivo-sp.	3.56045	0.510429	0.0890317	0.116317	0.278599	112.38
Gene	KIAA0408	DOWN	V	In Vivo-sp.	1.61333	3.79292	3.19386	0.929309	3.35126	50.4509
Gene	N4BP2L1	DOWN	V	In Vivo-sp.	0.388098	0.920753	0.902248	0.563189	1.53099	12.1014
Gene	NPM2	DOWN	V	In Vivo-sp.	0.667828	0.01	0.350715	0.505377	1.15766	20.5628
Gene	MAN1A1	DOWN	V	In Vivo-sp.	0.11341	0.0974158	0.182983	0.0304218	0.15984	3.46287
Gene	CASC1	DOWN	V	In Vivo-sp.	0.112856	0.209176	0.461248	0.151466	0.597583	3.38383
Gene	TACC1	DOWN	V	In Vivo-sp.	5.26575	6.39084	15.6871	12.5138	14.7192	156.058
Gene	SLC6A17	DOWN	V	In Vivo-sp.	0.133368	0.361184	0.493933	0.616899	0.471913	3.90837
Gene	C4orf32	DOWN	V	In Vivo-sp.	0.12682	0.195066	0.310995	0.138691	0.239954	3.64295
Gene	PDE2A	DOWN	V	In Vivo-sp.	3.47487	12.3768	10.6256	4.59775	2.69766	99.6423
Gene	RASSF4	DOWN	V	In Vivo-sp.	0.335834	0.837766	0.393963	1.02989	0.798104	9.60685

Gene	STOX1	DOWN	V	In Vivo-sp.	0.466349	0.730313	1.03177	0.158463	1.52035	13.2893
Gene	GLUL	DOWN	V	In Vivo-sp.	22.9836	46.753	44.2077	35.0794	104.423	652.332
Gene	PTK2B	DOWN	V	In Vivo-sp.	0.388934	0.460552	1.7398	0.864759	0.916755	11.0335
Gene	ASRGL1	DOWN	V	In Vivo-sp.	0.708005	1.54475	2.27209	0.211323	4.61186	19.8998
Gene	RGS20	DOWN	V	In Vivo-sp.	0.212157	0.349481	0.396816	0.118192	0.453488	5.94579
Gene	KAT2B	DOWN	V	In Vivo-sp.	2.80295	4.6803	8.6705	3.66819	10.1112	78.1986
Gene	MERTK	DOWN	V	In Vivo-sp.	1.20241	3.92274	5.42867	4.97577	5.60696	33.5309
Gene	TP53INP2	DOWN	V	In Vivo-sp.	3.7593	12.8166	17.8042	14.3083	24.4073	104.144
Gene	WDR17	DOWN	V	In Vivo-sp.	1.00322	2.83183	0.798156	0.34187	1.14687	27.6761
Gene	SLC6A1	DOWN	V	In Vivo-sp.	0.843938	0.750204	0.0411464	0.01	0.01	23.1534
Gene	RAPGEF5	DOWN	V	In Vivo-sp.	2.16272	2.07885	1.57038	1.65466	4.0014	59.1111
Gene	ALDH6A1	DOWN	V	In Vivo-sp.	0.923614	1.97228	3.05859	3.18886	5.2224	25.1606
Gene	CDK18	DOWN	V	In Vivo-sp.	0.510327	1.60256	0.64187	2.61063	0.490285	13.5775
Gene	CCDC62	DOWN	V	In Vivo-sp.	0.132181	0.0912502	0.124996	0.297407	0.485524	3.50176
Gene	LRRC39	DOWN	V	In Vivo-sp.	0.325347	1.48451	1.40466	0.266147	0.320126	8.58073
Gene	ACYP2	DOWN	V	In Vivo-sp.	2.00285	3.76622	12.5973	4.05549	7.4875	52.1724
Gene	ALS2CR12	DOWN	V	In Vivo-sp.	0.561002	1.70551	0.533474	0.743093	1.18847	14.3526
Gene	C14orf37	DOWN	V	In Vivo-sp.	0.208503	0.164634	0.455918	0.726541	0.771999	5.33327
Gene	CTSH	DOWN	V	In Vivo-sp.	0.423449	0.31841	0.155623	0.459091	0.583348	10.8007
Gene	MTMR7	DOWN	V	In Vivo-sp.	1.24734	7.35595	6.0394	2.10054	4.91084	31.4737
Gene	PCLO	DOWN	V	In Vivo-sp.	8.80296	18.6253	37.0723	29.6463	22.5345	220.142
Gene	FAM19A2	DOWN	V	In Vivo-sp.	0.321108	0.171343	1.32805	0.466109	0.463372	8.01038

Gene	QDPR	DOWN	V	In Vivo-sp.	11.3922	9.5871	12.9993	9.9238	13.1582	283.942
Gene	ASPHD1	DOWN	V	In Vivo-sp.	0.492449	1.42055	2.15595	1.81898	0.505613	12.2653
Gene	MAN1A2	DOWN	V	In Vivo-sp.	17.8702	39.2639	59.5702	48.7298	70.1072	442.448
Gene	FA2H	DOWN	V	In Vivo-sp.	0.233276	0.0734679	0.01	0.01	0.0672255	5.66005
Gene	GPR137B	DOWN	V	In Vivo-sp.	0.929268	0.903935	4.63168	3.61879	4.87853	22.4725
Gene	KALRN	DOWN	V	In Vivo-sp.	2.26604	2.6795	6.71058	8.74689	11.7562	54.5338
Gene	CLVS2	DOWN	V	In Vivo-sp.	0.179074	0.01	0.01	0.01	0.521638	4.2968
Gene	PACSIN1	DOWN	V	In Vivo-sp.	0.676912	0.13588	0.0746915	0.26836	0.464768	16.016
Gene	GNAO1	DOWN	V	In Vivo-sp.	6.83392	0.799906	0.192582	1.76528	18.209	159.66
Gene	PIP5K1B	DOWN	V	In Vivo-sp.	0.436383	2.45619	0.788233	0.0728892	1.70272	10.1079
Gene	F3	DOWN	V	In Vivo-sp.	2.58293	3.32135	10.2379	0.813313	5.55023	59.1665
Gene	WDR78	DOWN	V	In Vivo-sp.	0.857188	1.85966	1.44252	0.781458	3.87775	19.6027
Gene	PAPLN	DOWN	V	In Vivo-sp.	0.162802	0.311974	0.636592	0.388592	0.649166	3.71822
Gene	GPR137C	DOWN	V	In Vivo-sp.	0.119656	0.329726	0.123807	0.0689679	0.35781	2.71766
Gene	RAB3IP	DOWN	V	In Vivo-sp.	1.37586	2.77601	1.46519	0.526663	6.77924	31.2061
Gene	FMO5	DOWN	V	In Vivo-sp.	0.210336	0.516436	0.727503	0.904508	0.523777	4.75989
Gene	TRIM9	DOWN	V	In Vivo-sp.	1.60168	4.71741	5.31172	3.62581	4.7456	35.8855
Gene	CORO2B	DOWN	V	In Vivo-sp.	0.307132	0.297556	0.451364	0.269035	0.401608	6.81521
Gene	CDK5R1	DOWN	V	In Vivo-sp.	0.694734	0.779131	0.905974	0.642219	2.10851	15.299
Gene	C11orf41	DOWN	V	In Vivo-sp.	1.0734	0.0114431	0.0368251	0.117575	0.177719	23.5145
Gene	RBM11	DOWN	V	In Vivo-sp.	0.193524	0.114099	0.01	0.0595707	0.271921	4.2305
Gene	ABCA2	DOWN	V	In Vivo-sp.	1.32285	0.415081	0.456923	3.54759	2.28971	28.5902

Gene	SLC16A10	DOWN	V	In Vivo-sp.	0.386615	0.75788	0.423892	0.203917	1.25471	8.32896
Gene	NPL	DOWN	V	In Vivo-sp.	0.498313	0.281076	0.573083	0.44476	0.815326	10.7271
Gene	CAB39L	DOWN	V	In Vivo-sp.	0.676853	2.06484	1.78255	1.16553	2.02191	14.4377
Gene	MYH11	DOWN	V	In Vivo-sp.	0.393772	0.208198	0.555914	0.78287	0.6499	8.1661
Gene	ZC3H12B	DOWN	V	In Vivo-sp.	0.173769	0.0947951	0.214508	0.14851	0.376289	3.53148
Gene	RASSF2	DOWN	V	In Vivo-sp.	1.5049	2.39649	3.39956	1.96725	2.37911	29.9727
Gene	CDKL3	DOWN	V	In Vivo-sp.	0.763204	1.14646	2.15826	2.84927	0.908529	15.0609
Gene	CES4A	DOWN	V	In Vivo-sp.	0.458126	0.769918	0.768628	1.75389	0.930195	8.96799
Gene	RXFP1	DOWN	V	In Vivo-sp.	0.443093	0.453268	0.01	0.01	0.01	8.67274
Gene	C2orf72	DOWN	V	In Vivo-sp.	0.575862	0.01	0.0173338	0.01	0.627647	11.2048
Gene	MAP7	DOWN	V	In Vivo-sp.	3.81737	2.12153	2.61984	1.55292	17.4128	74.1968
Gene	GUCY1B3	DOWN	V	In Vivo-sp.	0.964524	0.214216	0.248953	0.473501	0.962022	18.5573
Gene	LINGO2	DOWN	V	In Vivo-sp.	0.434493	1.92187	1.04424	0.521739	0.451806	8.34494
Gene	RAB3C	DOWN	V	In Vivo-sp.	1.18379	5.06616	0.532251	1.29652	4.55251	22.6685
Gene	MAPT	DOWN	V	In Vivo-sp.	1.48401	0.189706	0.286287	0.328451	2.09106	28.3439
Gene	ARHGAP26	DOWN	V	In Vivo-sp.	4.96676	5.54088	13.4736	14.5532	14.9025	93.6386
Gene	FIBIN	DOWN	V	In Vivo-sp.	0.307439	0.111686	0.910908	0.27128	0.668432	5.70927
Gene	TMEM63A	DOWN	V	In Vivo-sp.	1.97281	1.67539	2.18233	7.60265	4.7915	36.4013
Gene	MYO1D	DOWN	V	In Vivo-sp.	0.486173	0.246627	0.116491	0.282123	0.405059	8.95197
Gene	SPTBN2	DOWN	V	In Vivo-sp.	0.920172	0.39457	1.05795	1.3872	1.18292	16.7527
Gene	PDE8B	DOWN	V	In Vivo-sp.	0.791635	1.35516	1.60972	0.70486	1.47356	14.366
Gene	CRYL1	DOWN	V	In Vivo-sp.	0.309544	0.301146	0.532435	1.05055	0.894254	5.58821

Gene	SLC8A1	DOWN	V	In Vivo-sp.	5.90821	1.09597	13.9295	15.1123	23.012	105.84
Gene	MAST3	DOWN	V	In Vivo-sp.	0.42833	0.366394	0.750316	1.42709	1.23295	7.60174
Gene	PXK	DOWN	V	In Vivo-sp.	10.0394	4.84335	7.67175	5.96888	11.87	178.14
Gene	CNTN1	DOWN	V	In Vivo-sp.	9.11383	3.25024	9.59258	25.0471	26.3568	161.379
Gene	SLC45A4	DOWN	V	In Vivo-sp.	0.568556	0.715679	1.13262	0.721303	1.16774	9.88836
Gene	FGL2	DOWN	V	In Vivo-sp.	0.175821	0.2278	0.337652	0.427005	0.200499	3.04833
Gene	BDNF	DOWN	V	In Vivo-sp.	0.176013	0.0579483	0.138284	0.0253231	0.441119	2.97954
Gene	XKR6	DOWN	V	In Vivo-sp.	0.761535	1.16719	2.12379	0.988028	1.4249	12.7359
Gene	EMCN	DOWN	V	In Vivo-sp.	0.432955	0.406907	0.0792454	0.01	0.01	7.18314
Gene	LRRTM3	DOWN	V	In Vivo-sp.	1.57166	1.31766	2.33932	0.928073	0.749228	26.0737
Gene	TSPAN13	DOWN	V	In Vivo-sp.	0.870354	3.03378	2.3655	0.382646	0.663625	14.4314
Gene	ANKRD12	DOWN	V	In Vivo-sp.	42.2712	78.627	167.373	29.9984	73.2667	679.283
Gene	ANO3	DOWN	V	In Vivo-sp.	0.443678	0.886709	0.0268234	0.914108	0.251881	7.05829
Gene	SORT1	DOWN	V	In Vivo-sp.	5.00161	9.63694	9.84314	6.4201	14.2773	79.3545
Gene	GNG11	DOWN	V	In Vivo-sp.	0.288219	0.287684	0.01	0.01	0.454166	4.51683
Gene	KCNAB1	DOWN	V	In Vivo-sp.	0.605628	1.12631	1.52461	0.529031	0.280349	9.46226
Gene	PTPRC	DOWN	V	In Vivo-sp.	0.934839	2.33561	0.969803	0.450103	0.338868	14.4112
Gene	STAMBPL1	DOWN	V	In Vivo-sp.	0.873945	0.0353421	0.392413	0.465716	0.566784	13.4674
Gene	TLR2	DOWN	V	In Vivo-sp.	0.610468	0.251043	0.272868	0.379356	1.07652	9.38355
Gene	C1orf115	DOWN	V	In Vivo-sp.	0.316772	0.0517635	0.01	0.210805	0.430593	4.85628
Gene	HSPA2	DOWN	V	In Vivo-sp.	4.44038	2.96673	5.31541	4.20937	2.55911	67.2891
Gene	PPFIA4	DOWN	V	In Vivo-sp.	0.242354	0.384292	0.128564	0.259371	0.73461	3.63163

Gene	TTLL11	DOWN	V	In Vivo-sp.	0.91885	1.10046	1.50843	1.38128	1.33394	13.6888
Gene	CLDND1	DOWN	V	In Vivo-sp.	123.583	195.491	246.452	400.744	374.977	1833.06
Gene	KIAA0930	DOWN	V	In Vivo-sp.	2.56505	1.89061	3.16787	5.48345	4.35351	36.8935
Gene	MAP7D2	DOWN	V	In Vivo-sp.	3.35075	2.05916	4.71931	2.29628	2.36502	47.3652
Gene	NKAPL	DOWN	V	In Vivo-sp.	0.350957	0.111008	0.307864	0.217539	0.101576	4.80671
Gene	PKP4	DOWN	V	In Vivo-sp.	13.8108	26.3285	37.7241	17.9539	32.5777	187.449
Gene	MCF2L2	DOWN	V	In Vivo-sp.	3.21193	0.715019	2.63707	2.22876	5.7482	43.4351
Gene	KIF6	DOWN	V	In Vivo-sp.	1.07437	1.59661	0.861352	0.747012	2.87277	14.4701
Gene	KBTBD3	DOWN	V	In Vivo-sp.	1.76091	2.89239	4.48023	1.35783	2.78976	23.6309
Gene	ANK3	DOWN	V	In Vivo-sp.	21.0079	10.1715	6.76175	2.17196	26.9748	270.992
Gene	PEA15	DOWN	V	In Vivo-sp.	29.1218	28.3203	46.8712	38.1925	83.236	371.073
Gene	ZNF662	DOWN	V	In Vivo-sp.	0.492781	1.5466	1.3694	0.407278	0.849833	6.27122
Gene	TMEM151B	DOWN	V	In Vivo-sp.	0.411287	0.446	0.212455	0.501177	1.11004	5.20439
Gene	IPCEF1	DOWN	V	In Vivo-sp.	1.75574	5.02538	4.12835	1.69584	2.07642	21.9631
Gene	TYRO3	DOWN	V	In Vivo-sp.	0.65101	0.354729	0.598904	1.7491	1.2371	7.89749
Gene	RASA4	DOWN	V	In Vivo-sp.	0.384822	0.504822	0.723789	0.679975	0.847701	4.64659
Gene	ANKRD20A3	DOWN	V	In Vivo-sp.	1.84598	1.03755	1.05245	0.0995936	0.540245	21.2922
Gene	C1QL3	DOWN	V	In Vivo-sp.	0.901436	0.791156	0.904226	0.442344	0.92271	10.3242
Gene	UPP1	DOWN	V	In Vivo-sp.	0.390011	0.177746	0.53973	0.313746	0.81916	4.4442
Gene	CPEB3	DOWN	V	In Vivo-sp.	1.40121	1.14572	1.34961	0.314051	0.931511	15.8698
Gene	CNP	DOWN	V	In Vivo-sp.	2.74092	3.11675	4.14124	7.24201	7.28529	30.9084
Gene	TTC7B	DOWN	V	In Vivo-sp.	1.13696	0.998038	3.13223	2.11331	2.73962	12.7803

Gene	ANKRD20A2	DOWN	V	In Vivo-sp.	0.845656	0.5669	0.457618	0.0502532	0.1438	9.46434
Gene	RAP1GAP	DOWN	V	In Vivo-sp.	1.25373	0.752048	0.716712	1.9355	2.93822	14.03
Gene	S1PR1	DOWN	V	In Vivo-sp.	6.11856	1.07998	2.37882	2.81156	2.87502	68.3264
Gene	CCDC39	DOWN	V	In Vivo-sp.	0.413526	0.71102	0.972201	0.121668	0.151093	4.59304
Gene	RASD1	DOWN	V	In Vivo-sp.	8.17233	1.40425	1.72451	1.16434	11.2288	90.3203
Gene	ZNF536	DOWN	V	In Vivo-sp.	0.575729	0.575633	0.80537	0.500996	0.557867	6.36222
Gene	EXOC6	DOWN	V	In Vivo-sp.	1.98955	4.93297	5.38988	1.43024	3.83053	21.9613
Gene	NCOA7	DOWN	V	In Vivo-sp.	17.1584	18.6254	28.9388	7.09081	14.8834	183.745
Gene	KHDRBS3	DOWN	V	In Vivo-sp.	4.18556	3.13243	3.45661	3.22602	7.93984	44.6253
Gene	UGT8	DOWN	V	In Vivo-sp.	7.65652	5.5722	3.65139	0.632405	3.57013	81.2765
Gene	ANKRD20A4	DOWN	V	In Vivo-sp.	0.566766	0.522019	0.260511	0.0875753	0.194869	6.00379
Gene	HTRA1	DOWN	V	In Vivo-sp.	7.49953	0.284961	1.55017	5.60085	9.60834	78.5745
Gene	ZNF774	DOWN	V	In Vivo-sp.	0.973352	1.28188	1.5975	1.32993	1.19598	10.0324
Gene	TBC1D12	DOWN	V	In Vivo-sp.	2.21312	2.48449	5.52747	3.11008	4.96203	22.5085
Gene	ANKRD20A1	DOWN	V	In Vivo-sp.	1.02064	0.866552	0.652547	0.184165	0.214893	10.2607
Gene	NRCAM	DOWN	V	In Vivo-sp.	25.9963	14.8683	18.3554	23.2883	42.9453	260.24
Gene	PURA	DOWN	V	In Vivo-sp.	4.12524	6.04864	10.2086	4.82701	5.51557	41.0242
Gene	MRO	DOWN	V	In Vivo-sp.	5.78628	0.706679	1.3898	1.06167	2.90299	57.475
Gene	TMEM65	DOWN	V	In Vivo-sp.	1.25061	1.13425	1.87417	0.436636	0.270741	12.2258
Gene	PPP1R1B	DOWN	V	In Vivo-sp.	1.06578	0.18956	0.21576	0.542503	0.130983	10.2257
Gene	B3GAT2	DOWN	V	In Vivo-sp.	0.739393	0.460474	0.52967	0.108891	0.622073	6.96892
Gene	C14orf45	DOWN	V	In Vivo-sp.	2.25764	1.7722	3.49687	1.80464	2.57104	20.9253

Gene	ANKAR	DOWN	V	In Vivo-sp.	1.01509	0.832644	1.2266	0.557228	0.59583	8.97273
Gene	PIP4K2A	DOWN	V	In Vivo-sp.	43.8313	27.9848	34.5945	27.9947	71.1716	382.942
Gene	PTPRT	DOWN	V	In Vivo-sp.	0.35897	0.0400824	0.162775	0.01	0.516605	3.13368
Gene	CACNB1	DOWN	V	In Vivo-sp.	0.82896	0.613126	0.954472	0.785177	0.96134	7.21144
Gene	CLMN	DOWN	V	In Vivo-sp.	1.4672	1.426	1.40517	1.37897	2.40158	12.6915
Gene	C17orf51	DOWN	V	In Vivo-sp.	0.890321	1.31193	0.875087	0.667142	1.24873	7.69378
Gene	PDE3B	DOWN	V	In Vivo-sp.	1.44635	2.87172	2.24686	1.3002	3.04197	12.3879
Gene	TARSL2	DOWN	V	In Vivo-sp.	2.1203	3.43313	3.35002	1.54475	3.88143	18.1039
Gene	LHX2	DOWN	V	In Vivo-sp.	2.11168	0.679892	0.694691	0.826316	0.01	17.9556
Gene	MAGEH1	DOWN	V	In Vivo-sp.	4.29576	6.10909	8.05766	1.23386	2.0274	36.0406
Gene	ERBB3	DOWN	V	In Vivo-sp.	3.5317	0.479971	0.726054	0.0744408	1.32141	29.5936
Gene	PIK3R1	DOWN	V	In Vivo-sp.	28.0495	33.5614	43.9049	33.0084	53.999	234.685
Gene	SERINC5	DOWN	V	In Vivo-sp.	0.763879	1.24265	1.23917	1.35955	1.29543	6.36471
Gene	PHLPP1	DOWN	V	In Vivo-sp.	17.0139	6.32358	8.15513	16.6226	27.6453	138.605
Gene	ELAVL4	DOWN	V	In Vivo-sp.	2.87451	0.174112	0.677295	0.0065934	5.57014	23.2176
Gene	ACBD7	DOWN	V	In Vivo-sp.	6.09504	0.573842	2.2629	4.16379	10.0646	49.0876
Gene	METTL7A	DOWN	V	In Vivo-sp.	5.32913	5.00682	6.59828	0.819082	1.76278	42.5632
Gene	PLXND1	DOWN	V	In Vivo-sp.	2.51798	2.80459	3.86523	1.08024	3.12102	19.869
Gene	ANKRD18A	DOWN	V	In Vivo-sp.	8.29459	2.785	4.03322	1.93175	3.91603	63.0166
Gene	OGFRL1	DOWN	V	In Vivo-sp.	5.12798	3.31641	3.51928	5.08108	7.44949	38.7907
Gene	AIF1	DOWN	V	In Vivo-sp.	2.70656	1.30117	1.92619	0.680347	3.88711	20.1001
Gene	MAP6D1	DOWN	V	In Vivo-sp.	0.865437	0.213267	1.12554	1.24606	1.26314	6.35034

Gene	RNF141	DOWN	V	In Vivo-sp.	6.73434	7.44956	11.6536	5.10451	10.9759	49.1216
Gene	PHACTR3	DOWN	V	In Vivo-sp.	14.2342	1.00337	1.09629	1.73119	5.30122	101.87
Gene	STEAP2	DOWN	V	In Vivo-sp.	1.14995	0.913814	0.328461	0.776411	1.51568	8.15532
Gene	CHN1	DOWN	V	In Vivo-sp.	57.9905	9.53056	1.96392	5.63815	92.5357	400.052
Gene	REPS2	DOWN	V	In Vivo-sp.	6.14295	3.699	4.89459	2.08297	4.61563	41.2213
Gene	USP35	DOWN	V	In Vivo-sp.	0.618509	0.4181	0.529646	0.730619	0.435606	4.14977
Gene	KITLG	DOWN	V	In Vivo-sp.	1.00475	0.570243	0.67369	0.572813	1.04938	6.57891
Gene	C4orf39	DOWN	V	In Vivo-sp.	0.435763	0.325249	0.468046	0.100034	0.145585	2.8119
Gene	LMTK2	DOWN	V	In Vivo-sp.	2.28502	2.44135	2.76849	2.53253	3.06211	14.7401
Gene	UNC13A	DOWN	V	In Vivo-sp.	3.32026	0.116863	0.0509453	0.449577	4.0884	21.3227
Gene	GJA1	DOWN	V	In Vivo-sp.	112.746	29.3944	10.9123	8.48956	117.75	698.412
Gene	CCDC64	DOWN	V	In Vivo-sp.	2.18841	0.577244	1.51035	0.779131	2.09829	13.522
Gene	GRIA4	DOWN	V	In Vivo-sp.	26.9179	11.3747	6.72606	2.51485	33.4327	164.106
Gene	ARHGAP44	DOWN	V	In Vivo-sp.	0.886841	0.424614	0.815746	0.956298	0.781303	5.40245
Gene	GFOD1	DOWN	V	In Vivo-sp.	2.20518	1.97936	2.0145	1.00121	2.35739	13.1098
Gene	SFXN5	DOWN	V	In Vivo-sp.	3.50586	3.14256	3.72255	4.13524	2.1593	20.7884
Gene	SYNGR1	DOWN	V	In Vivo-sp.	1.33432	0.875003	0.85867	1.70122	1.41379	7.68302
Gene	PCGF5	DOWN	V	In Vivo-sp.	8.40873	5.01077	7.25711	3.87328	9.18481	48.3155
Gene	UNC5C	DOWN	V	In Vivo-sp.	2.11237	0.448392	0.595553	0.837921	0.983011	11.965
Gene	PSD3	DOWN	V	In Vivo-sp.	11.1348	12.074	11.7313	5.34986	12.5814	62.1186
Gene	ALDOC	DOWN	V	In Vivo-sp.	10.5006	4.07725	3.11287	7.98092	6.94481	57.5117
Gene	CHN2	DOWN	V	In Vivo-sp.	14.4899	12.9059	4.22506	6.33803	11.1595	77.2972

Gene	TMCC3	DOWN	V	In Vivo-sp.	1.53854	1.28016	1.55752	1.47681	1.49118	8.11035
Gene	MAP3K5	DOWN	V	In Vivo-sp.	3.89084	0.219557	0.212401	0.227436	0.162311	20.2013
Gene	ADCYAP1R1	DOWN	V	In Vivo-sp.	6.04397	5.12489	5.58898	6.41523	3.10729	31.3736
Gene	CDKN2D	DOWN	V	In Vivo-sp.	5.30705	1.54782	4.19783	2.29607	2.01637	27.4761
Gene	DPYD	DOWN	V	In Vivo-sp.	3.76837	3.17396	3.58494	2.90155	1.99035	18.7109
Gene	RNLS	DOWN	V	In Vivo-sp.	0.923623	0.818551	0.699438	0.323952	0.37111	4.55333
Gene	ACCN1	DOWN	V	In Vivo-sp.	1.36544	0.01	0.0335276	1.04901	0.723979	6.67797
Gene	SPATA13	DOWN	V	In Vivo-sp.	3.09363	0.626246	1.35409	0.880371	1.35636	15.0897
Gene	NALCN	DOWN	V	In Vivo-sp.	8.34409	5.36301	6.52574	7.93464	6.78642	40.3365
Gene	PDK4	DOWN	V	In Vivo-sp.	12.0273	2.47423	1.59389	0.213751	0.475916	58.0943
Gene	PRKCA	DOWN	V	In Vivo-sp.	6.17121	1.04522	2.13221	0.768032	4.02281	29.6912
Gene	TM6SF1	DOWN	V	In Vivo-sp.	1.10214	0.812067	0.90765	0.353574	0.482453	5.14807
Gene	LONRF2	DOWN	V	In Vivo-sp.	7.48761	1.70512	2.62684	2.3489	3.91776	33.5598
Gene	KIAA1644	DOWN	V	In Vivo-sp.	1.07231	1.07108	0.438315	0.527279	0.590802	4.73271
Gene	FAM184A	DOWN	V	In Vivo-sp.	10.2064	3.88777	3.95786	1.01256	3.23638	44.5697
Gene	PEX5L	DOWN	V	In Vivo-sp.	34.0418	22.2685	19.2068	8.05563	4.98932	147.99
Gene	HSPA1A	DOWN	V	In Vivo-sp.	56.9662	28.4849	43.5707	45.6103	33.0897	246.349
Gene	KIAA1598	DOWN	V	In Vivo-sp.	118.804	63.0727	69.1508	24.3213	27.8973	498.737
Gene	ACTN2	DOWN	V	In Vivo-sp.	2.23525	0.70563	0.954011	0.594992	1.26995	9.362
Gene	SLC7A14	DOWN	V	In Vivo-sp.	1.89763	0.111327	0.198839	0.0752341	0.282515	7.62881
lincRNA	linc-OPCML	UP	I	early	116.145	0.01	0.01	0.01	9.89971	0.01
lincRNA	linc-KLHL29-9	UP	I	early	82.4978	0.01	0.01	0.01	0.01	0.01

lincRNA	linc-C10orf119-1	UP	I	early	75.0602	4.18187	1.39603	0.01	11.4666	0.01
lincRNA	linc-CHMP7	UP	I	early	70.8149	4.76307	21.0118	17.1471	9.04622	0.01
lincRNA	linc-DGCR6-1	UP	I	early	68.8051	33.0682	7.62485	8.32175	7.15619	0.01
lincRNA	linc-HNRNPA3-4	UP	I	early	44.2978	15.565	13.1263	13.9824	2.03585	0.01
lincRNA	linc-LRRC32-2	UP	I	early	42.4707	7.91042	6.85625	11.94	15.0071	0.01
lincRNA	linc-CCND1-4	UP	I	early	39.7513	0.01	0.01	0.01	4.10552	0.01
lincRNA	linc-ZNF236-4	UP	I	early	39.4523	6.07915	16.7932	0.01	1.59173	0.01
lincRNA	linc-PIK3C3-2	UP	I	early	30.5923	15.3722	30.0155	27.2763	5.57638	0.01
lincRNA	linc-GGTLC1-2	UP	I	early	86.127	0.01	0.01	1.80775	6.21863	0.448121
lincRNA	linc-TMEM90B-2	UP	I	early	2945.04	6.68591	3.4051	8.72741	42.8962	15.4258
lincRNA	linc-EVX2-8	UP	I	early	545.353	51.2354	105.596	38.6965	46.731	4.44876
lincRNA	linc-OR52K2-1	UP	I	early	412.342	22.7722	1.56491	2.62622	3.21341	3.70815
lincRNA	linc-GPNMB	UP	I	early	163.954	22.1803	4.4463	5.47478	8.77121	2.93188
lincRNA	linc-ITPRIP-1	UP	I	early	257.758	26.8832	14.835	19.8478	47.8261	7.66117
lincRNA	linc-RASD2	UP	I	early	32.806	16.6334	8.83569	0.556303	22.5219	1.68836
lincRNA	linc-TMEM90B-1	UP	I	early	323.372	0.01	1.49914	3.7814	7.32405	17.12
lincRNA	linc-CSMD1-1	UP	I	early	58.9229	18.2754	17.2208	16.2696	8.17262	3.61411
lincRNA	linc-ZIC5	UP	I	early	151.187	15.5709	29.1747	38.0007	62.0329	9.42939
lincRNA	linc-BTF3-2	UP	I	early	324.63	83.0632	114.916	73.0675	14.359	20.7033
lincRNA	linc-IGFBP2-3	UP	I	early	597.293	22.9162	41.5887	33.7007	154.383	46.8526
lincRNA	linc-C1orf227-1	UP	I	early	121.811	11.9966	13.1397	25.0393	29.3329	10.9906
lincRNA	linc-CHST7	UP	I	early	112.049	39.7752	66.7911	46.2963	58.6916	10.5494

lincRNA	linc-AGAP5-1	UP	I	early	111.13	24.7731	65.9444	41.905	40.1363	12.1858
lincRNA	linc-GALNTL5-1	UP	I	early	209.962	59.8341	54.7369	62.8236	39.3234	24.0793
lincRNA	linc-PEX14	UP	I	early	2144.32	522.497	706.792	668.1	422.277	255.026
lincRNA	linc-CREBBP	UP	I	early	44.2818	7.33568	5.78383	7.67122	6.13731	5.45104
lincRNA	linc-HIATL1-1	UP	I	early	6144.43	2635.96	2988.6	2227.44	2055.78	769.231
lincRNA	linc-PCF11-2	UP	I	early	3149.5	1323.51	1473.76	1003.8	660.76	409.194
lincRNA	linc-DHX37-22	UP	I	early	176.292	28.8005	27.2292	29.042	13.5595	24.7751
lincRNA	linc-AP3B1	UP	I	early	92.6525	33.0785	45.6332	52.8486	50.0022	13.1452
lincRNA	linc-NDRG1	UP	I	early	2295.1	666.178	1017.96	675.421	1196.51	328.539
lincRNA	linc-TLN2-1	UP	I	early	211.38	112.349	183.305	102.159	88.5	33.0647
lincRNA	linc-MRPL22	UP	I	early	63.8797	14.1577	34.5652	16.2695	19.5514	10.0689
lincRNA	linc-STXBP5-2	UP	I	early	261.558	7.5542	0.01	0.01	0.01	42.6329
lincRNA	linc-BCL2A1-1	UP	I	early	372.454	110.43	14.4872	24.1485	51.8089	62.6713
lincRNA	linc-BRAP-2	UP	I	early	812.763	296.604	341.678	244.176	353.434	142.644
lincRNA	linc-MTHFD2	UP	I	early	917.321	320.104	503.791	380.973	370.211	165.291
lincRNA	linc-CCT5-8	UP	I	early	313.132	109.098	183.549	175.501	124.357	56.6703
lincRNA	linc-NUSAP1	UP	I	early	6661.63	1600.2	2242.89	2504.92	2397.39	1249.59
lincRNA	linc-ITGB2-1	UP	I	early	318.012	35.9815	59.0392	128.906	107.379	61.2884
lincRNA	linc-STIM2-1	UP	I	early	649.741	280.519	408.769	222.319	215.188	126.564
lincRNA	linc-RPS7-1	UP	I	early	464.073	174.636	229.869	130.255	109.352	93.9005
lincRNA	linc-RGS18-3	UP	I	early	759.355	324.853	198.644	141.715	40.3595	156.752
lincRNA	linc-NADSYN1-1	UP	I	early	213.412	36.7299	75.9076	63.7466	84.3037	47.9917
lincRNA	linc-XRCC6	UP	I	early	338.889	116.244	128.241	220.06	146.979	79.7876
lincRNA	linc-CTDSP2-1	UP	I	early	928.833	282.866	225.765	382.591	406.586	231.472

lincRNA	linc-EXD1	UP	II	early-mid	485.013	201.562	92.2694	15.4474	11.405	46.1597
lincRNA	linc-JPH1-6	UP	III	early-late	111.167	97.3599	103.135	51.1833	41.1561	3.69133
lincRNA	linc-CDH6-5	UP	V	InVivo-sp.	1483.21	405.002	587.423	845.931	2524.98	1.96336
lincRNA	linc-CXXC4-1	UP	V	InVivo-sp.	5922.94	2029.97	1639.19	500.709	1276.2	68.3217
lincRNA	linc-PXN	UP	V	InVivo-sp.	1315.89	240.431	482.779	613.214	385.961	28.4573
lincRNA	linc-ITGB8-4	UP	V	InVivo-sp.	243.365	335.292	221.559	99.1429	157.387	5.35704
lincRNA	linc-IRX3-5	UP	V	InVivo-sp.	649.863	936.28	1539.42	919.042	306.923	19.1878
lincRNA	linc-DLGAP5-1	UP	V	InVivo-sp.	2259.58	547.438	736.532	635.719	778.314	133.823
lincRNA	linc-TMEM132C-2	UP	V	InVivo-sp.	584.773	327.795	385.987	349.045	248.826	47.6478
lincRNA	linc-ARHGAP28-2	UP	V	InVivo-sp.	498.807	270.892	406.353	351.207	419.68	54.062
lincRNA	linc-OPRK1-4	UP	V	InVivo-sp.	80.6886	48.8705	121.704	119.945	140.971	9.98352
lincRNA	linc-C1orf201-2	UP	V	InVivo-sp.	419.69	846.102	1430.84	494.366	750.287	69.5695
lincRNA	linc-DDX51	DOWN	I	early	0.01	19.8808	347.883	108.893	173.8	277.937
lincRNA	linc-NCKAP1-1	DOWN	I	early	0.01	66.8243	255.054	238.307	408.948	214.518
lincRNA	linc-LSAMP-2	DOWN	I	early	0.01	15.4043	20.5022	17.3327	10.2675	94.8731
lincRNA	linc-TET2-4	DOWN	I	early	0.01	13.8285	37.3407	11.0536	8.06111	73.9332
lincRNA	linc-TRIM29-3	DOWN	I	early	0.01	23.2257	14.2843	11.5659	14.469	57.6074
lincRNA	linc-CRYL1	DOWN	I	early	0.01	20.746	4.37584	22.6837	6.86677	42.6146
lincRNA	linc-TEKT1-3	DOWN	I	early	0.01	3.44952	10.0474	20.1519	13.8111	31.667
lincRNA	linc-SPNS3	DOWN	I	early	4.0811	77.9455	34.8028	118.869	27.6573	185.51
lincRNA	linc-HIST1H2AG-4	DOWN	I	early	8.59544	67.4487	318.566	121.587	88.769	244.681
lincRNA	linc-COL28A1	DOWN	I	early	17.3267	145.699	467.236	192.353	896.638	417.24
lincRNA	linc-CBLB-6	DOWN	I	early	6.61285	63.9232	22.6903	24.8402	26.2061	127.526

lincRNA	linc-FAM103A1	DOWN	I	early	5.15828	20.3876	56.0902	57.2142	30.3673	51.4267
lincRNA	linc-FAM116B-1	DOWN	I	early	67.765	175.793	316.953	590.492	382.934	561.526
lincRNA	linc-CXADR-2	DOWN	I	early	78.7996	875.985	1343.47	673.02	314.59	610.616
lincRNA	linc-ZNF227	DOWN	I	early	17.5864	75.5178	62.4812	34.0479	30.9803	127.351
lincRNA	linc-CCDC54	DOWN	I	early	47.7848	106.422	260.851	109.27	86.8815	345.14
lincRNA	linc-LRCH2-1	DOWN	I	early	22.5481	53.0649	207.333	61.7038	111.306	158.297
lincRNA	linc-ATP6V1G3-2	DOWN	I	early	44.23	134.482	231.968	272.933	124.75	219.159
lincRNA	linc-GABRA5-5	DOWN	I	early	260.182	366.049	605.978	333.416	392.982	1247.93
lincRNA	linc-DR1	DOWN	I	early	25.5408	70.3441	130.219	47.8667	83.1226	107.544
lincRNA	linc-METAP1-2	DOWN	II	early-mid	0.01	1.91409	46.3349	71.039	82.6442	150.429
lincRNA	linc-C3orf30-7	DOWN	II	early-mid	0.01	7.49809	41.6235	22.9576	55.0042	102.508
lincRNA	linc-ADAR	DOWN	II	early-mid	0.01	11.0962	65.4625	21.2219	33.9282	93.4977
lincRNA	linc-GLA-1	DOWN	II	early-mid	2.66992	83.7508	203.948	105.987	229.239	400.242
lincRNA	linc-CBLB-4	DOWN	II	early-mid	10.8099	48.5368	327.209	169.662	339.979	637.365
lincRNA	linc-ID2-1	DOWN	II	early-mid	2.98224	16.7024	46.3857	24.7196	45.249	110.48
lincRNA	linc-GLRX3-2	DOWN	II	early-mid	1.88284	6.73503	46.4919	14.7538	23.5979	43.3583
lincRNA	linc-MKLN1-1	DOWN	II	early-mid	21.1187	31.8101	242.581	63.4316	66.3829	246.316
lincRNA	linc-C17orf87	DOWN	II	early-mid	13.0793	22.6122	205.503	59.1895	182.632	137.86
lincRNA	linc-ZNF674	DOWN	II	early-mid	10.2803	4.50661	21.8032	24.4728	21.6396	106.377
lincRNA	linc-PSMD11	DOWN	II	early-mid	4.48268	6.46583	28.8026	9.9306	12.3887	35.0797
lincRNA	linc-ZNF467-1	DOWN	II	early-mid	25.6669	26.4061	144.441	30.4965	25.9347	110.786
lincRNA	linc-GALNT10	DOWN	III	early-late	0.01	0.01	0.01	11.1392	10.4945	166.097
lincRNA	linc-S100B-2	DOWN	III	early-late	18650.5	12826.7	10703.6	47364.8	25523.3	90666.1

lincRNA	linc-PDE10A-1	DOWN	IV	late	0.01	0.01	20.3077	0.01	138.52	562.565
lincRNA	linc-SLC6A19-1	DOWN	IV	late	0.01	0.01	96.9263	0.01	93.0232	539.509
lincRNA	linc-P2RY1-2	DOWN	IV	late	0.01	0.01	1.88549	0.01	10.7693	259.635
lincRNA	linc-CLDN10-2	DOWN	IV	late	0.01	0.01	0.01	0.01	84.9703	110.013
lincRNA	linc-C15orf2-1	DOWN	IV	late	0.01	0.01	3.37162	0.01	15.6568	63.0937
lincRNA	linc-TGDS-1	DOWN	IV	late	0.01	0.01	0.01	0.01	103.75	37.7873
lincRNA	linc-PPDPF-3	DOWN	IV	late	0.01	0.01	0.01	0.01	8.33852	36.2504
lincRNA	linc-MRPS33-3	DOWN	IV	late	0.01	0.01	0.01	0.01	28.4757	35.7679
lincRNA	linc-YIPF5-3	DOWN	IV	late	0.01	0.01	0.405252	0.611163	17.6673	34.3327
lincRNA	linc-PPP1R3B-3	DOWN	IV	late	3.14017	52.5047	1.49652	2.42855	919.956	592.966
lincRNA	linc-RPL19-3	DOWN	IV	late	1.09166	3.00521	2.22939	1.57587	21.2074	66.0037
lincRNA	linc-FAM136B	DOWN	IV	late	6.49027	4.94097	7.84233	11.2622	25.868	136.099
lincRNA	linc-BRD9-1	DOWN	V	InVivo-sp.	0.01	0.01	44.6191	0.01	392.605	2534.31
lincRNA	linc-RECK-3	DOWN	V	InVivo-sp.	0.01	113.535	99.5564	107.902	113.559	1133.08
lincRNA	linc-TMPRSS15-5	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	844.018
lincRNA	linc-PHYHIPL	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	571.452
lincRNA	linc-RAB23-1	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	473.072
lincRNA	linc-NEUROG3	DOWN	V	InVivo-sp.	0.01	0.01	6.42298	11.0523	19.5966	411.785
lincRNA	linc-NAV3-1	DOWN	V	InVivo-sp.	0.01	0.01	5.51615	0.01	71.4462	348.146
lincRNA	linc-RSAD2-2	DOWN	V	InVivo-sp.	0.01	0.278525	1.68504	0.152923	8.62943	261.819
lincRNA	linc-KCNV1-1	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	244.522
lincRNA	linc-CEP110-14	DOWN	V	InVivo-sp.	0.01	0.01	17.1866	0.01	23.8044	194.968

lincRNA	linc-PARK2-4	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	12.2983	192.318
lincRNA	linc-SPACA3	DOWN	V	InVivo-sp.	0.01	0.01	0.01	1.62419	3.48003	184.172
lincRNA	linc-ZC3H12B-2	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	2.84278	156.774
lincRNA	linc-TSPO2-2	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	150.053
lincRNA	linc-BCL2L10	DOWN	V	InVivo-sp.	0.01	27.4187	5.36229	8.71505	3.0106	145.873
lincRNA	linc-EMX2	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	9.85212	142.172
lincRNA	linc-ZC3H12B-3	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	139.657
lincRNA	linc-GPC5-8	DOWN	V	InVivo-sp.	0.01	7.29959	9.60873	7.98632	1.76188	137.725
lincRNA	linc-DTHD1-3	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	137.367
lincRNA	linc-P2RX4	DOWN	V	InVivo-sp.	0.01	0.01	0.77723	3.81076	2.77833	132.047
lincRNA	linc-EIF2AK3-7	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	108.788
lincRNA	linc-ERICH1-8	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	94.893
lincRNA	linc-CMPK2-2	DOWN	V	InVivo-sp.	0.01	0.01	1.54194	2.54255	2.77675	93.8576
lincRNA	linc-ABHD13-1	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	89.2861
lincRNA	linc-CTTNBP2-1	DOWN	V	InVivo-sp.	0.01	14.6551	11.3238	11.7786	6.98669	86.7669
lincRNA	linc-PAX9-5	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	79.756
lincRNA	linc-PARK2-6	DOWN	V	InVivo-sp.	0.01	6.6748	0.01	4.36368	0.01	75.3761
lincRNA	linc-ADAM12	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	70.0191
lincRNA	linc-CBR3-1	DOWN	V	InVivo-sp.	0.01	1.05335	0.830449	0.01	1.06494	66.4071
lincRNA	linc-PRDM9-8	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	61.3342
lincRNA	linc-FMR1	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	59.809
lincRNA	linc-PITRM1-4	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	57.1138

lincRNA	linc-KCNN4	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	57.1106
lincRNA	linc-IGFL4	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.761637	54.1921
lincRNA	linc-CYP7B1-2	DOWN	V	InVivo-sp.	0.01	2.57199	3.29368	0.73573	0.01	53.2174
lincRNA	linc-COG6-2	DOWN	V	InVivo-sp.	0.01	0.792304	0.01	0.01	0.01	47.8983
lincRNA	linc-FAM120B-2	DOWN	V	InVivo-sp.	0.01	0.01	8.2241	0.01	0.01	37.8895
lincRNA	linc-CLLU1-4	DOWN	V	InVivo-sp.	0.01	0.01	0.798681	0.01	1.06068	37.4126
lincRNA	linc-EDNRB-1	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	30.3656
lincRNA	linc-MMEL1-3	DOWN	V	InVivo-sp.	0.01	0.01	0.01	0.01	0.01	30.1776
lincRNA	linc-CBWD3-2	DOWN	V	InVivo-sp.	0.788404	0.01	3.5469	2.07191	0.706287	154.037
lincRNA	linc-SEPT7-1	DOWN	V	InVivo-sp.	3.71828	14.1418	17.2596	9.72931	43.1974	247.327
lincRNA	linc-ERICH1-7	DOWN	V	InVivo-sp.	18.409	0.01	18.8901	0.01	88.1585	1032.64
lincRNA	linc-RALGAPA1-4	DOWN	V	InVivo-sp.	20.8549	68.1513	86.0433	41.4483	7.07914	1098.65
lincRNA	linc-PDE6B	DOWN	V	InVivo-sp.	2.33586	0.01	0.01	0.01	7.73738	89.6723
lincRNA	linc-PICK1	DOWN	V	InVivo-sp.	2.4484	1.91901	15.3221	2.42278	3.38302	91.248
lincRNA	linc-SPANXB1-2	DOWN	V	InVivo-sp.	7.27923	40.2681	57.8303	27.6662	51.6022	262.167
lincRNA	linc-CLRN2-1	DOWN	V	InVivo-sp.	67.5701	21.6818	34.8474	50.5977	62.4374	908.396
lincRNA	linc-SOD3-2	DOWN	V	InVivo-sp.	78.2569	124.45	148.108	110.758	35.6499	1020.17

APPENDIX C

SIGNIFICANT GO PROCESSES FOR ALL MODELS (I-V)

MODEL I – UP

#	GO Processes	pValue	Ratio	
1	cellular macromolecular complex assembly	6.597E-10	30	484
2	organelle organization	2.784E-09	70	2040
3	cellular macromolecular complex subunit organization	3.875E-09	33	618
4	cellular component organization or biogenesis	5.637E-09	117	4304
5	cellular component organization or biogenesis at cellular level	5.848E-09	98	3367
6	small molecule metabolic process	1.229E-08	77	2428
7	macromolecular complex subunit organization	1.768E-08	46	1132
8	cellular component organization	3.167E-08	112	4177
9	mitotic cell cycle	4.057E-08	34	716
10	macromolecular complex assembly	5.809E-08	41	984
11	cell cycle phase	9.448E-08	37	851
12	cellular component biogenesis	9.549E-08	56	1611
13	cellular component organization at cellular level	1.680E-07	91	3253
14	protein-DNA complex assembly	7.858E-07	13	143
15	cell cycle	1.039E-06	45	1262
16	protein-DNA complex subunit organization	1.460E-06	13	151
17	translation	2.037E-06	22	417
18	M phase	2.263E-06	25	521
19	primary metabolic process	3.460E-06	184	8592
20	cell cycle process	4.595E-06	37	1001
21	mitosis	4.686E-06	19	341
22	nuclear division	4.686E-06	19	341
23	nucleosome assembly	5.569E-06	11	121
24	M phase of mitotic cell cycle	6.535E-06	19	349
25	organelle fission	8.329E-06	19	355
26	mitochondrial membrane organization	8.542E-06	7	45
27	chromatin assembly	8.883E-06	11	127
28	cellular component assembly	9.006E-06	47	1458
29	metabolic process	1.315E-05	200	9707
30	M/G1 transition of mitotic cell cycle	1.401E-05	9	87
31	small molecule biosynthetic process	1.612E-05	26	621
32	cellular component assembly at cellular level	1.629E-05	36	1018
33	glycerolipid catabolic process	1.805E-05	6	34
34	nucleosome organization	1.825E-05	11	137
35	catabolic process	2.207E-05	55	1875
36	cellular metabolic process	2.209E-05	180	8579
37	monosaccharide metabolic process	2.312E-05	16	284
38	alcohol metabolic process	2.344E-05	25	597
39	glucose metabolic process	2.521E-05	13	196
40	chromatin assembly or disassembly	2.726E-05	11	143
41	cellular process	2.777E-05	276	14653
42	branching involved in mammary gland duct morphogenesis	2.992E-05	6	37
43	organic ether metabolic process	3.102E-05	11	145
44	DNA packaging	3.322E-05	12	173
45	biosynthetic process	3.455E-05	106	4475
46	nucleotide biosynthetic process	3.542E-05	14	232
47	mitochondrial transport	3.665E-05	10	122
48	cellular nitrogen compound biosynthetic process	4.093E-05	21	469
49	heterocycle biosynthetic process	4.850E-05	16	302
50	cellular biosynthetic process	5.397E-05	103	4362
51	neutral lipid catabolic process	6.004E-05	5	26
52	glycerol ether catabolic process	6.004E-05	5	26

53	acylglycerol catabolic process	6.004E-05	5	26
54	DNA damage response, signal transduction by p53 class mediator	6.325E-05	9	105
55	nucleoside metabolic process	6.813E-05	9	106
56	signal transduction by p53 class mediator	7.332E-05	9	107
57	nucleobase, nucleoside and nucleotide biosynthetic process	7.617E-05	14	249
58	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	7.617E-05	14	249
59	cell division	8.827E-05	19	422
60	ribonucleoprotein complex biogenesis	1.023E-04	14	256
61	neurological system process involved in regulation of systemic arterial blood pressure	1.041E-04	5	29
62	nuclear-transcribed mRNA catabolic process, exonucleolytic	1.041E-04	5	29
63	glucose catabolic process	1.089E-04	7	66
64	ribonucleotide biosynthetic process	1.106E-04	10	139
65	ribosome biogenesis	1.381E-04	11	171
66	DNA conformation change	1.474E-04	12	202
67	regulation of icosanoid secretion	1.488E-04	4	17
68	protein import into mitochondrial outer membrane	1.504E-04	3	7
69	meiotic spindle organization	1.504E-04	3	7
70	mammary gland duct morphogenesis	1.523E-04	6	49
71	cellular component biogenesis at cellular level	1.653E-04	14	268
72	response to heat	1.663E-04	9	119
73	cytokine production	1.825E-04	8	95
74	protein secretion	1.907E-04	6	51
75	mitotic prometaphase	1.963E-04	8	96
76	ribonucleoside monophosphate biosynthetic process	1.970E-04	5	33
77	monosaccharide biosynthetic process	2.063E-04	7	73
78	cellular protein metabolic process	2.156E-04	73	2939
79	triglyceride metabolic process	2.264E-04	8	98
80	generation of precursor metabolites and energy	2.313E-04	21	531
81	hexose metabolic process	2.321E-04	13	244
82	icosanoid secretion	2.361E-04	4	19
83	response to water	2.361E-04	4	19
84	arachidonic acid secretion	2.361E-04	4	19
85	outer mitochondrial membrane organization	2.377E-04	3	8
86	ribose phosphate metabolic process	2.377E-04	3	8
87	monocarboxylic acid transport	2.428E-04	8	99
88	coenzyme biosynthetic process	2.428E-04	8	99
89	cellular catabolic process	2.459E-04	45	1576
90	one-carbon metabolic process	2.494E-04	15	313
91	maintenance of blood-brain barrier	2.740E-04	2	2
92	Golgi to plasma membrane CFTR protein transport	2.740E-04	2	2
93	response to inorganic substance	2.741E-04	22	577
94	cellular carbohydrate metabolic process	3.194E-04	21	544
95	response to DNA damage stimulus	3.232E-04	23	624
96	response to metal ion	3.380E-04	17	394
97	cofactor metabolic process	3.452E-04	14	288
98	positive regulation of endopeptidase activity	3.521E-04	3	9
99	hexose biosynthetic process	3.536E-04	6	57
100	multi-organism process	3.775E-04	41	1420
101	glycerol ether metabolic process	3.823E-04	9	133
102	hexose catabolic process	4.239E-04	7	82
103	regulation of interleukin-1 beta secretion	4.285E-04	4	22
104	alcohol biosynthetic process	4.390E-04	8	108
105	alcohol catabolic process	4.390E-04	8	108
106	signal transduction in response to DNA damage	4.504E-04	9	136
107	D-ribose metabolic process	4.969E-04	3	10

108	brain renin-angiotensin system	4.969E-04	3	10
109	icosanoid transport	5.120E-04	4	23
110	regulation of interleukin-1 secretion	5.120E-04	4	23
111	acylglycerol metabolic process	5.275E-04	8	111
112	ribonucleoside monophosphate metabolic process	5.581E-04	5	41
113	monosaccharide catabolic process	5.664E-04	7	86
114	regulation of cell cycle process	5.751E-04	18	451
115	neutral lipid metabolic process	5.942E-04	8	113
116	triglyceride catabolic process	6.064E-04	4	24
117	regulation of cellular carbohydrate catabolic process	6.250E-04	5	42
118	regulation of carbohydrate catabolic process	6.250E-04	5	42
119	regulation of interleukin-1 beta production	6.250E-04	5	42
120	pyrimidine-containing compound biosynthetic process	6.250E-04	5	42
121	chromosome segregation	6.484E-04	9	143
122	cofactor biosynthetic process	6.484E-04	9	143
123	cellular protein complex assembly	6.545E-04	12	238
124	cholesterol homeostasis	6.631E-04	6	64
125	sterol homeostasis	6.631E-04	6	64
126	protein metabolic process	6.914E-04	82	3529
127	hydrogen peroxide metabolic process	6.977E-04	5	43
128	DNA integrity checkpoint	7.165E-04	9	145
129	fatty acid transport	7.816E-04	6	66
130	ncRNA metabolic process	7.854E-04	14	313
131	nucleotide metabolic process	7.985E-04	27	837
132	nucleoside phosphate metabolic process	7.985E-04	27	837
133	dichotomous subdivision of terminal units involved in mammary gland duct morphogenesis	8.129E-04	2	3
134	T-helper 17 cell chemotaxis	8.129E-04	2	3
135	negative regulation of eosinophil degranulation	8.129E-04	2	3
136	regulation of T cell extravasation	8.129E-04	2	3
137	gamma-delta T cell activation	8.129E-04	2	3
138	regulation of eosinophil degranulation	8.129E-04	2	3
139	regulation of arachidonic acid secretion	8.129E-04	2	3
140	T cell chemotaxis	8.129E-04	2	3
141	positive regulation of arachidonic acid secretion	8.129E-04	2	3
142	helper T cell chemotaxis	8.129E-04	2	3
143	monocyte extravasation	8.129E-04	2	3
144	urate biosynthetic process	8.129E-04	2	3
145	positive regulation of T cell extravasation	8.129E-04	2	3
146	regulation of Fc receptor mediated stimulatory signaling pathway	8.129E-04	2	3
147	negative regulation of icosanoid secretion	8.129E-04	2	3
148	regulation of fatty acid transport	8.312E-04	4	26
149	cellular carbohydrate catabolic process	8.832E-04	8	120
150	nucleoside diphosphate biosynthetic process	8.888E-04	3	12
151	mammary gland morphogenesis	9.159E-04	6	68
152	gluconeogenesis	9.541E-04	5	46
153	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	9.631E-04	4	27
154	parturition	9.631E-04	4	27
155	tumor necrosis factor-mediated signaling pathway	9.631E-04	4	27
156	motor axon guidance	9.631E-04	4	27
157	regulation of interleukin-1 production	1.053E-03	5	47
158	long-chain fatty acid transport	1.053E-03	5	47
159	mitochondrion organization	1.081E-03	11	218
160	heterocycle metabolic process	1.119E-03	31	1035
161	response to hydroperoxide	1.141E-03	3	13

162	positive regulation of circadian sleep/wake cycle, sleep	1.141E-03	3	13
163	small molecule catabolic process	1.149E-03	27	858
164	chromosome organization	1.156E-03	24	728
165	carbohydrate metabolic process	1.178E-03	24	729
166	acid secretion	1.270E-03	4	29
167	branching morphogenesis of a tube	1.315E-03	10	190
168	positive regulation of ligase activity	1.386E-03	7	100
169	regulation of glycogen catabolic process	1.435E-03	3	14
170	nitric oxide mediated signal transduction	1.446E-03	4	30
171	coenzyme metabolic process	1.495E-03	11	227
172	organic substance transport	1.584E-03	19	534
173	interspecies interaction between organisms	1.584E-03	19	534
174	regulation of cellular ketone metabolic process	1.597E-03	10	195
175	lysophospholipid transport	1.608E-03	2	4
176	cell proliferation in hindbrain	1.608E-03	2	4
177	regulation of metanephros size	1.608E-03	2	4
178	regulation of immune complex clearance by monocytes and macrophages	1.608E-03	2	4
179	response to lipid hydroperoxide	1.608E-03	2	4
180	vasodilation by angiotensin involved in regulation of systemic arterial blood pressure	1.608E-03	2	4
181	positive regulation of immune complex clearance by monocytes and macrophages	1.608E-03	2	4
182	respiratory electron transport chain	1.632E-03	8	132
183	nucleobase metabolic process	1.638E-03	6	76
184	mammary gland epithelium development	1.638E-03	6	76
185	pyrimidine nucleoside biosynthetic process	1.772E-03	3	15
186	histamine secretion	1.772E-03	3	15
187	low-density lipoprotein particle remodeling	1.772E-03	3	15
188	glycolysis	1.818E-03	5	53
189	interphase of mitotic cell cycle	1.846E-03	16	420
190	protein-lipid complex subunit organization	1.849E-03	4	32
191	plasma lipoprotein particle organization	1.849E-03	4	32
192	mRNA metabolic process	1.850E-03	20	583
193	response to abiotic stimulus	1.930E-03	26	845
194	regulation of interphase of mitotic cell cycle	2.008E-03	9	168
195	DNA damage checkpoint	2.063E-03	8	137
196	pyrimidine nucleotide biosynthetic process	2.077E-03	4	33
197	regulation of lipoprotein lipase activity	2.077E-03	4	33
198	chromatin organization	2.077E-03	19	547
199	carboxylic acid transport	2.099E-03	11	237
200	mitotic cell cycle G1/S transition DNA damage checkpoint	2.131E-03	6	80
201	cytokine secretion	2.154E-03	3	16
202	lipid digestion	2.154E-03	3	16
203	negative regulation of cAMP biosynthetic process	2.154E-03	3	16
204	RNA catabolic process	2.160E-03	8	138
205	interphase	2.178E-03	16	427
206	nucleobase, nucleoside and nucleotide metabolic process	2.231E-03	27	899
207	organic acid transport	2.241E-03	11	239
208	cellular macromolecule catabolic process	2.253E-03	20	593
209	negative regulation of catalytic activity	2.255E-03	23	722
210	regulation of cell cycle arrest	2.311E-03	12	276
211	glycerolipid metabolic process	2.452E-03	12	278
212	regulation of mitotic cell cycle	2.490E-03	14	354
213	mRNA catabolic process	2.521E-03	7	111
214	negative regulation of nucleotide biosynthetic process	2.583E-03	3	17
215	pentose metabolic process	2.583E-03	3	17
216	histamine transport	2.583E-03	3	17

217	negative regulation of cyclic nucleotide biosynthetic process	2.583E-03	3	17
218	negative regulation of cAMP metabolic process	2.583E-03	3	17
219	positive regulation of metanephric glomerulus development	2.651E-03	2	5
220	bombesin receptor signaling pathway	2.651E-03	2	5
221	cellular chaperone-mediated protein complex assembly	2.651E-03	2	5
222	positive regulation of metanephros development	2.651E-03	2	5
223	sensory perception of sweet taste	2.651E-03	2	5
224	positive regulation of cellular extravasation	2.651E-03	2	5
225	T cell migration	2.651E-03	2	5
226	positive regulation of somatostatin secretion	2.651E-03	2	5
227	keratinocyte development	2.651E-03	2	5
228	sebaceous gland development	2.651E-03	2	5
229	multicellular organismal lipid catabolic process	2.651E-03	2	5
230	stem cell differentiation	2.651E-03	7	112
231	S phase of mitotic cell cycle	2.694E-03	8	143
232	response to stress	2.727E-03	73	3216
233	methylation	2.800E-03	11	246
234	response to nicotine	2.925E-03	5	59
235	negative regulation of cyclic nucleotide metabolic process	3.062E-03	3	18
236	acute inflammatory response to antigenic stimulus	3.062E-03	3	18
237	nucleoside monophosphate biosynthetic process	3.070E-03	6	86
238	regulation of cellular amino acid metabolic process	3.148E-03	5	60
239	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	3.148E-03	5	60
240	negative regulation of lipid transport	3.183E-03	4	37
241	electron transport chain	3.193E-03	9	180
242	cellular aromatic compound metabolic process	3.266E-03	12	288
243	cellular respiration	3.313E-03	9	181
244	purine nucleotide biosynthetic process	3.313E-03	9	181
245	negative regulation of kinase activity	3.313E-03	9	181
246	carbohydrate catabolic process	3.327E-03	8	148
247	S phase	3.327E-03	8	148
248	protein polymerization	3.384E-03	5	61
249	cellular carbohydrate biosynthetic process	3.385E-03	7	117
250	regulation of cellular amine metabolic process	3.443E-03	6	88
251	protein complex subunit organization	3.452E-03	25	837
252	positive regulation of circadian rhythm	3.592E-03	3	19
253	negative regulation of blood vessel endothelial cell migration	3.592E-03	3	19
254	fructose metabolic process	3.592E-03	3	19
255	peptidyl-lysine methylation	3.592E-03	3	19
256	mitochondrial ATP synthesis coupled proton transport	3.592E-03	3	19
257	epithelial cell development	3.642E-03	6	89
258	regulation of ligase activity	3.718E-03	7	119
259	positive regulation of cell cycle process	3.759E-03	8	151
260	regulation of generation of precursor metabolites and energy	3.892E-03	5	63
261	positive regulation of glomerulus development	3.932E-03	2	6
262	activation of phospholipase A2 activity	3.932E-03	2	6
263	germ-line stem cell maintenance	3.932E-03	2	6
264	complement receptor mediated signaling pathway	3.932E-03	2	6
265	renin-angiotensin regulation of aldosterone production	3.932E-03	2	6
266	renal control of peripheral vascular resistance involved in regulation of systemic arterial blood pressure	3.932E-03	2	6
267	positive regulation of circadian sleep/wake cycle, non-REM sleep	3.932E-03	2	6
268	fructose 1,6-bisphosphate metabolic process	3.932E-03	2	6
269	generation of ovulation cycle rhythm	3.932E-03	2	6
270	regulation of blood vessel size by renin-angiotensin	3.932E-03	2	6

MODEL I – DOWN

#	GO Processes	pValue	Ratio	
1	nervous system development	5.463E-17	144	2143
2	regulation of primary metabolic process	4.505E-15	255	4978
3	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	6.988E-15	215	3968
4	regulation of cellular metabolic process	9.976E-15	255	5010
5	regulation of metabolic process	2.635E-14	279	5690
6	regulation of macromolecule metabolic process	3.352E-14	240	4667
7	regulation of nitrogen compound metabolic process	8.374E-14	215	4061
8	regulation of transcription, DNA-dependent	1.147E-13	184	3300
9	regulation of RNA metabolic process	3.659E-13	185	3366
10	regulation of cellular biosynthetic process	1.055E-12	204	3881
11	regulation of cellular macromolecule biosynthetic process	2.899E-12	190	3568
12	enzyme linked receptor protein signaling pathway	3.111E-12	68	819
13	regulation of biosynthetic process	3.156E-12	204	3925
14	neurogenesis	1.900E-11	96	1425
15	transcription, DNA-dependent	2.196E-11	148	2614
16	regulation of macromolecule biosynthetic process	2.667E-11	190	3657
17	regulation of gene expression	3.942E-11	194	3775
18	regulation of cellular process	4.798E-11	400	9537
19	cell projection morphogenesis	5.536E-11	60	720
20	intracellular signal transduction	5.686E-11	106	1673
21	generation of neurons	1.123E-10	90	1342
22	cell part morphogenesis	1.133E-10	60	733
23	neuron differentiation	1.193E-10	76	1050
24	neuron development	1.312E-10	68	891
25	cell projection organization	2.223E-10	69	922
26	behavior	2.230E-10	52	596
27	system development	2.356E-10	197	3930
28	RNA biosynthetic process	2.595E-10	148	2704
29	neuron projection development	3.879E-10	59	737
30	regulation of biological process	4.252E-10	415	10123
31	negative regulation of cellular process	9.646E-10	158	3002
32	cell morphogenesis	1.249E-09	65	879
33	biological regulation	1.460E-09	429	10630
34	neuron projection morphogenesis	1.499E-09	53	648
35	locomotory behavior	1.651E-09	26	195
36	multicellular organismal development	1.825E-09	219	4605
37	cell morphogenesis involved in neuron differentiation	1.853E-09	52	633
38	regulation of signaling	2.489E-09	121	2139
39	nerve growth factor receptor signaling pathway	3.012E-09	31	275
40	transmembrane receptor protein tyrosine kinase signaling pathway	3.346E-09	51	625
41	developmental process	3.599E-09	233	5016
42	intracellular protein kinase cascade	3.804E-09	48	571
43	anatomical structure development	4.201E-09	207	4329
44	cell morphogenesis involved in differentiation	4.242E-09	56	726
45	MAPKKK cascade	6.775E-09	34	333
46	cellular component morphogenesis	7.352E-09	66	940
47	adult locomotory behavior	8.041E-09	17	92
48	regulation of molecular function	8.820E-09	127	2330
49	cellular macromolecule metabolic process	1.060E-08	276	6261
50	response to inorganic substance	1.489E-08	47	577
51	cell development	1.543E-08	90	1482
52	positive regulation of cell death	1.599E-08	57	774

53	negative regulation of signaling	1.615E-08	50	636
54	central nervous system development	1.850E-08	63	900
55	negative regulation of cell communication	1.879E-08	50	639
56	regulation of signal transduction	1.920E-08	103	1788
57	anatomical structure morphogenesis	3.383E-08	117	2141
58	negative regulation of biological process	4.132E-08	163	3296
59	positive regulation of programmed cell death	4.165E-08	55	755
60	regulation of cell death	5.018E-08	91	1543
61	regulation of programmed cell death	5.806E-08	89	1502
62	axonogenesis	6.004E-08	47	604
63	cognition	6.025E-08	28	263
64	macromolecule metabolic process	6.649E-08	294	6885
65	death	7.043E-08	74	1171
66	learning or memory	7.709E-08	27	250
67	positive regulation of apoptosis	7.809E-08	54	749
68	regulation of catalytic activity	8.998E-08	107	1939
69	cellular macromolecule biosynthetic process	1.043E-07	169	3497
70	macromolecule biosynthetic process	1.128E-07	170	3527
71	cell death	1.174E-07	73	1164
72	positive regulation of molecular function	1.291E-07	85	1437
73	neuron recognition	1.302E-07	10	35
74	regulation of apoptosis	1.545E-07	87	1489
75	negative regulation of heart contraction	1.802E-07	9	28
76	negative regulation of signal transduction	1.858E-07	45	588
77	adult walking behavior	2.274E-07	11	46
78	response to morphine	2.274E-07	11	46
79	adult behavior	2.670E-07	20	157
80	response to isoquinoline alkaloid	2.880E-07	11	47
81	regulation of heart contraction	3.044E-07	19	144
82	response to metal ion	4.051E-07	34	394
83	regulation of transferase activity	4.468E-07	50	708
84	regulation of protein phosphorylation	5.745E-07	59	904
85	response to estradiol stimulus	5.810E-07	22	195
86	regulation of phosphorylation	5.956E-07	62	970
87	regulation of lipase activity	5.976E-07	23	211
88	regulation of phosphorus metabolic process	7.608E-07	63	999
89	regulation of phosphate metabolic process	7.608E-07	63	999
90	cellular developmental process	7.933E-07	145	2981
91	response to alkaloid	8.020E-07	20	168
92	regulation of cell communication	1.027E-06	87	1557
93	regulation of kinase activity	1.035E-06	48	687
94	signaling	1.124E-06	233	5359
95	positive regulation of myeloid cell differentiation	1.131E-06	14	88
96	regulation of synaptic transmission, GABAergic	1.145E-06	9	34
97	regulation of response to stimulus	1.168E-06	123	2441
98	positive regulation of transferase activity	1.452E-06	37	474
99	forebrain development	1.455E-06	31	361
100	SMAD protein import into nucleus	1.519E-06	7	19
101	protein import into nucleus	1.605E-06	17	131
102	regulation of system process	1.687E-06	45	637
103	regulation of multicellular organismal process	1.712E-06	106	2036
104	lymphocyte proliferation	1.838E-06	13	79
105	positive regulation of myeloid leukocyte differentiation	1.877E-06	11	56
106	negative regulation of DNA binding	1.936E-06	9	36
107	regulation of protein kinase activity	1.941E-06	46	661

108	regulation of hydrolase activity	2.008E-06	61	984
109	positive regulation of kinase activity	2.095E-06	36	462
110	cell differentiation	2.176E-06	140	2905
111	nuclear import	2.206E-06	17	134
112	negative regulation of systemic arterial blood pressure	2.270E-06	7	20
113	protein phosphorylation	2.299E-06	57	900
114	regulation of synaptic transmission	2.366E-06	27	297
115	ephrin receptor signaling pathway	2.418E-06	8	28
116	regulation of multicellular organismal development	2.445E-06	73	1262
117	regulation of phospholipase activity	2.600E-06	20	181
118	positive regulation of protein kinase activity	2.602E-06	35	447
119	positive regulation of catalytic activity	2.744E-06	72	1243
120	mononuclear cell proliferation	2.836E-06	13	82
121	positive regulation of hydrolase activity	2.903E-06	46	671
122	negative regulation of biosynthetic process	3.104E-06	66	1110
123	regulation of cell differentiation	3.198E-06	66	1111
124	leukocyte proliferation	3.262E-06	13	83
125	primary metabolic process	3.270E-06	343	8592
126	macromolecule modification	3.365E-06	116	2316
127	circulatory system development	3.450E-06	52	803
128	cardiovascular system development	3.450E-06	52	803
129	protein modification process	3.602E-06	111	2194
130	biosynthetic process	3.615E-06	198	4475
131	regulation of transmission of nerve impulse	3.667E-06	28	322
132	response to organic cyclic compound	3.759E-06	36	474
133	inhibition of adenylate cyclase activity by G-protein signaling pathway	3.979E-06	12	72
134	cellular metabolic process	4.011E-06	342	8579
135	negative regulation of nitrogen compound metabolic process	4.460E-06	61	1009
136	negative regulation of cellular biosynthetic process	4.501E-06	64	1077
137	regulation of dephosphorylation	4.535E-06	11	61
138	negative regulation of cellular macromolecule biosynthetic process	4.745E-06	61	1011
139	anatomical structure formation involved in morphogenesis	4.850E-06	51	791
140	regulation of transcription from RNA polymerase II promoter	4.937E-06	75	1334
141	negative regulation of molecular function	4.975E-06	55	879
142	regulation of neurological system process	5.088E-06	29	346
143	cellular biosynthetic process	5.130E-06	193	4362
144	vasculature development	5.477E-06	38	522
145	positive regulation of phospholipase activity	5.962E-06	19	175
146	signal transduction	6.048E-06	213	4921
147	smooth muscle contraction	6.289E-06	11	63
148	neural precursor cell proliferation	6.289E-06	11	63
149	regulation of cardiac muscle contraction	6.581E-06	7	23
150	brain development	6.824E-06	45	672
151	positive regulation of biological process	7.140E-06	169	3736
152	blood vessel development	7.538E-06	36	489
153	regulation of myeloid cell differentiation	7.546E-06	18	162
154	metabolic process	7.703E-06	378	9707
155	positive regulation by host of viral transcription	7.827E-06	6	16
156	negative regulation of response to stimulus	8.600E-06	49	764
157	protein import	8.763E-06	20	196
158	activation of phospholipase C activity	8.960E-06	18	164
159	regulation of developmental process	9.052E-06	83	1548
160	negative regulation of osteoblast differentiation	9.327E-06	8	33
161	negative regulation of binding	9.383E-06	12	78
162	negative regulation of macromolecule biosynthetic process	9.575E-06	62	1057

163	limbic system development	9.608E-06	14	105
164	positive regulation of phospholipase C activity	9.752E-06	18	165
165	programmed cell death	9.910E-06	59	990
166	cellular component organization at cellular level	1.018E-05	150	3253
167	negative regulation of RNA metabolic process	1.140E-05	56	927
168	negative regulation of transmission of nerve impulse	1.140E-05	10	55
169	RNA metabolic process	1.145E-05	156	3419
170	two-component signal transduction system (phosphorelay)	1.176E-05	6	17
171	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.186E-05	59	996
172	cAMP-mediated signaling	1.233E-05	19	184
173	negative regulation of transcription, DNA-dependent	1.348E-05	55	910
174	cyclic nucleotide metabolic process	1.396E-05	12	81
175	gene expression	1.434E-05	162	3593
176	positive regulation of lipase activity	1.553E-05	19	187
177	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.574E-05	203	4713
178	regulation of binding	1.587E-05	20	204
179	regulation of membrane potential	1.588E-05	24	274
180	modulation by host of symbiont transcription	1.619E-05	7	26
181	modulation by host of viral transcription	1.619E-05	7	26
182	telencephalon cell migration	1.685E-05	9	46
183	positive regulation of action potential	1.703E-05	4	6
184	negative regulation of adenylate cyclase activity	1.799E-05	12	83
185	negative regulation of lyase activity	1.799E-05	12	83
186	negative regulation of cyclase activity	1.799E-05	12	83
187	regulation of DNA binding	1.799E-05	12	83
188	cellular nitrogen compound metabolic process	1.845E-05	220	5196
189	cellular component organization	1.862E-05	183	4177
190	nucleic acid metabolic process	1.954E-05	172	3882
191	modulation of transcription in other organism involved in symbiotic interaction	2.124E-05	7	27
192	apoptosis	2.169E-05	57	971
193	response to tropane	2.174E-05	10	59
194	response to cocaine	2.174E-05	10	59
195	positive regulation of cellular process	2.372E-05	153	3385
196	negative regulation of synaptic transmission	2.417E-05	9	48
197	transmembrane receptor protein serine/threonine kinase signaling pathway	2.552E-05	18	177
198	regulation of osteoblast differentiation	2.618E-05	13	100
199	phosphate metabolic process	2.793E-05	77	1451
200	phosphorus metabolic process	2.859E-05	77	1452
201	forebrain cell migration	2.875E-05	9	49
202	cell proliferation	2.982E-05	47	757
203	phosphorylation	3.316E-05	67	1219
204	negative regulation of programmed cell death	3.400E-05	45	717
205	negative regulation of neurological system process	3.403E-05	10	62
206	organic alcohol transport	3.467E-05	8	39
207	regulation of epithelial cell migration	3.523E-05	7	29
208	vocalization behavior	3.628E-05	3	3
209	positive regulation of developmental process	3.839E-05	48	787
210	leading edge cell differentiation	3.869E-05	4	7
211	activation of phospholipase C activity by muscarinic acetylcholine receptor signaling pathway	3.869E-05	4	7
212	protein localization to nucleus	3.886E-05	17	166
213	regulation of vasoconstriction	3.960E-05	11	76
214	regulation of nucleotide metabolic process	4.044E-05	38	571
215	negative regulation of heart rate	4.070E-05	5	13
216	cellular component organization or biogenesis at cellular level	4.091E-05	151	3367

217	membrane depolarization	4.120E-05	12	90
218	regulation of growth	4.174E-05	41	636
219	positive regulation of amine transport	4.209E-05	8	40
220	negative regulation of cell death	4.279E-05	46	746
221	negative regulation of developmental process	4.359E-05	38	573
222	positive regulation of protein serine/threonine kinase activity	4.371E-05	23	273
223	response to estrogen stimulus	4.467E-05	24	292
224	regulation of locomotion	4.611E-05	33	470
225	response to external stimulus	4.644E-05	79	1522
226	nitrogen compound metabolic process	4.792E-05	222	5326
227	gliogenesis	4.882E-05	17	169
228	negative regulation of Wnt receptor signaling pathway	4.885E-05	13	106
229	regulation of protein modification process	4.906E-05	61	1093
230	angiogenesis	4.996E-05	25	313
231	cAMP metabolic process	5.079E-05	8	41
232	outflow tract morphogenesis	5.079E-05	8	41
233	regulation of small GTPase mediated signal transduction	5.238E-05	30	412
234	positive regulation of growth	5.303E-05	18	187
235	memory	5.395E-05	13	107
236	negative regulation of apoptosis	5.401E-05	44	709
237	regulation of cell development	5.852E-05	38	581
238	telencephalon development	6.072E-05	20	224
239	positive regulation of epithelial cell migration	6.151E-05	6	22
240	synaptic transmission	6.362E-05	42	670
241	regulation of cell migration	6.813E-05	30	418
242	axon guidance	6.845E-05	32	459
243	multicellular organismal signaling	7.097E-05	46	762
244	transmission of nerve impulse	7.097E-05	46	762
245	protein targeting	7.147E-05	25	320
246	cellular component organization or biogenesis	7.395E-05	184	4304
247	positive regulation of phosphoprotein phosphatase activity	7.535E-05	4	8
248	regulation of vascular smooth muscle contraction	7.535E-05	4	8
249	axial mesoderm morphogenesis	7.535E-05	4	8
250	positive regulation of MAP kinase activity	7.770E-05	20	228
251	regulation of Ras protein signal transduction	7.897E-05	25	322
252	negative regulation of catalytic activity	8.204E-05	44	722
253	regulation of MAP kinase activity	8.423E-05	24	304
254	response to lithium ion	8.623E-05	9	56
255	interaction with symbiont	8.631E-05	8	44
256	positive regulation of synaptic transmission, GABAergic	8.987E-05	5	15
257	regulation of smooth muscle cell proliferation	9.050E-05	14	128
258	negative regulation of transcription from RNA polymerase II promoter	9.156E-05	37	572
259	response to hydrogen peroxide	9.738E-05	15	145
260	positive regulation of epithelial cell proliferation	1.004E-04	16	162
261	negative regulation of cell differentiation	1.023E-04	32	469
262	modification by host of symbiont morphology or physiology	1.051E-04	7	34
263	membrane hyperpolarization	1.051E-04	7	34
264	regulation of the force of heart contraction	1.051E-04	7	34
265	positive regulation of response to stimulus	1.058E-04	63	1171
266	cell recognition	1.060E-04	12	99
267	regulation of ossification	1.073E-04	17	180
268	regulation of muscle system process	1.080E-04	16	163
269	behavioral interaction between organisms	1.118E-04	10	71
270	response to oxidative stress	1.126E-04	26	349
271	cell communication	1.133E-04	73	1416

272	embryonic appendage morphogenesis	1.137E-04	15	147
273	embryonic limb morphogenesis	1.137E-04	15	147
274	regulation of blood vessel endothelial cell migration	1.199E-04	8	46
275	regulation of cell motility	1.226E-04	30	432
276	negative regulation of cell proliferation	1.229E-04	40	646
277	glial cell migration	1.272E-04	5	16
278	negative regulation of synaptic transmission, GABAergic	1.272E-04	5	16
279	fat cell differentiation	1.363E-04	13	117
280	blood vessel morphogenesis	1.365E-04	29	414
281	regulation of phosphatidylinositol dephosphorylation	1.415E-04	3	4
282	territorial aggressive behavior	1.415E-04	3	4
283	Notch signaling pathway	1.418E-04	10	73
284	regulation of cell proliferation	1.434E-04	73	1427
285	tissue remodeling	1.486E-04	13	118
286	regulation of anatomical structure morphogenesis	1.497E-04	38	608
287	positive regulation of ion transmembrane transporter activity	1.540E-04	7	36
288	positive regulation of transcription, DNA-dependent	1.618E-04	61	1141
289	activation of protein kinase activity	1.621E-04	18	204
290	regulation of synaptic transmission, glutamatergic	1.635E-04	8	48
291	induction of programmed cell death	1.687E-04	32	482
292	heart development	1.687E-04	32	482
293	neural tube development	1.779E-04	15	153
294	patterning of blood vessels	1.898E-04	8	49
295	regulation of adenylate cyclase activity	1.912E-04	15	154
296	positive regulation of GTPase activity	1.996E-04	23	302
297	negative regulation of neuron apoptosis	2.079E-04	13	122
298	cellular chemical homeostasis	2.104E-04	45	776
299	regulation of phosphoprotein phosphatase activity	2.119E-04	6	27
300	cellular ion homeostasis	2.138E-04	43	731
301	aggressive behavior	2.144E-04	4	10
302	axial mesoderm development	2.144E-04	4	10
303	cellular response to potassium ion starvation	2.144E-04	4	10
304	positive regulation of monocyte differentiation	2.144E-04	4	10
305	regulation of angiogenesis	2.159E-04	16	173
306	T cell proliferation	2.195E-04	8	50
307	positive regulation of transcription from RNA polymerase II promoter	2.227E-04	45	778
308	ion homeostasis	2.227E-04	45	778
309	cyclic-nucleotide-mediated signaling	2.266E-04	19	228
310	negative regulation of gene expression	2.270E-04	55	1012
311	locomotion	2.299E-04	60	1132
312	skeletal system development	2.304E-04	29	427
313	protein localization to organelle	2.324E-04	24	325
314	regulation of cAMP biosynthetic process	2.462E-04	16	175
315	organ development	2.500E-04	128	2875
316	vasodilation	2.529E-04	8	51
317	regulation of cyclase activity	2.534E-04	15	158
318	positive regulation of transporter activity	2.603E-04	7	39
319	positive regulation of nitrogen compound metabolic process	2.722E-04	69	1359
320	positive regulation of RNA metabolic process	2.798E-04	62	1189
321	appendage development	2.801E-04	16	177
322	limb development	2.801E-04	16	177
323	muscle system process	2.877E-04	22	290
324	regulation of lyase activity	2.905E-04	15	160
325	regulation of muscle contraction	2.936E-04	14	143
326	taxis	2.949E-04	40	674

327	regulation of cAMP metabolic process	2.985E-04	16	178
328	regulation of protein serine/threonine kinase activity	3.019E-04	29	434
329	osteoblast differentiation	3.059E-04	11	95
330	social behavior	3.066E-04	7	40
331	inositol phosphate metabolic process	3.117E-04	5	19
332	negative regulation by host of viral transcription	3.117E-04	5	19
333	induction of apoptosis	3.184E-04	31	478
334	neurological system process involved in regulation of systemic arterial blood pressure	3.213E-04	6	29
335	forebrain neuroblast division	3.280E-04	4	11
336	neuroblast division	3.280E-04	4	11
337	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	3.302E-04	67	1319
338	regulation of blood vessel size	3.353E-04	11	96
339	positive regulation of angiogenesis	3.353E-04	11	96
340	cardiolipin biosynthetic process	3.451E-04	3	5
341	regulation of mismatch repair	3.451E-04	3	5
342	termination of signal transduction	3.451E-04	3	5
343	brainstem development	3.451E-04	3	5
344	male courtship behavior	3.451E-04	3	5
345	inhibition of adenylate cyclase activity by muscarinic acetylcholine receptor signaling pathway	3.451E-04	3	5
346	phosphatidylglycerol biosynthetic process	3.451E-04	3	5
347	norepinephrine-epinephrine vasoconstriction involved in regulation of systemic arterial blood pressure	3.451E-04	3	5
348	regulation of anatomical structure size	3.469E-04	37	612
349	regulation of neuron apoptosis	3.506E-04	19	236
350	reproductive behavior	3.593E-04	7	41
351	regulation of ion transmembrane transporter activity	3.671E-04	11	97
352	regulation of Ras GTPase activity	3.783E-04	17	200
353	positive regulation of neuron apoptosis	3.787E-04	8	54
354	negative regulation of phosphorus metabolic process	3.891E-04	13	130
355	negative regulation of phosphate metabolic process	3.891E-04	13	130
356	multicellular organismal process	3.896E-04	265	6739
357	regulation of synapse structure and activity	3.941E-04	9	68
358	regulation of tube size	4.014E-04	11	98
359	cAMP biosynthetic process	4.043E-04	5	20
360	regulation of cellular component movement	4.160E-04	30	464
361	positive regulation of muscle contraction	4.190E-04	7	42
362	cellular protein metabolic process	4.243E-04	129	2939
363	regulation of cellular protein metabolic process	4.261E-04	69	1381
364	regulation of GTP catabolic process	4.303E-04	24	339
365	mating	4.304E-04	8	55
366	negative regulation of blood pressure	4.304E-04	8	55
367	positive regulation of cell differentiation	4.492E-04	36	598
368	chemical homeostasis	4.521E-04	53	993
369	associative learning	4.548E-04	10	84
370	stress-activated protein kinase signaling cascade	4.598E-04	15	167
371	mating behavior	4.708E-04	6	31
372	cellular response to calcium ion	4.708E-04	6	31
373	pallium development	4.788E-04	14	150
374	regulation of calcium ion transport via store-operated calcium channel activity	4.792E-04	4	12
375	positive regulation of granulocyte differentiation	4.792E-04	4	12
376	positive regulation of blood pressure by epinephrine-norepinephrine	4.792E-04	4	12
377	response to calcium ion	4.852E-04	13	133
378	regulation of receptor activity	4.904E-04	9	70
379	negative regulation of cellular metabolic process	4.982E-04	68	1364

380	regulation of intracellular protein kinase cascade	5.153E-04	37	625
381	negative regulation of viral transcription	5.162E-04	5	21
382	microglial cell activation	5.162E-04	5	21
383	response to organic substance	5.199E-04	107	2368
384	circadian rhythm	5.214E-04	13	134
385	positive regulation of cell proliferation	5.370E-04	46	834
386	cellular response to peptide hormone stimulus	5.394E-04	26	386
387	cellular process	5.412E-04	524	14653
388	stem cell development	5.454E-04	9	71
389	positive regulation of Ras GTPase activity	5.471E-04	14	152
390	appendage morphogenesis	5.548E-04	15	170
391	limb morphogenesis	5.548E-04	15	170
392	regulation of sensory perception of pain	5.620E-04	7	44
393	regulation of sensory perception	5.620E-04	7	44
394	synaptic transmission, cholinergic	5.633E-04	6	32
395	regulation of transmembrane transporter activity	5.665E-04	11	102
396	regulation of cellular component organization	5.694E-04	66	1321
397	second-messenger-mediated signaling	5.726E-04	28	430
398	response to cytokine stimulus	6.065E-04	34	563
399	cellular response to stimulus	6.304E-04	238	6009
400	learning	6.440E-04	13	137
401	muscle contraction	6.462E-04	19	248
402	regulation of striated muscle contraction	6.468E-04	7	45
403	positive regulation of cell migration	6.565E-04	20	268
404	regulation of muscle adaptation	6.694E-04	6	33
405	long-term memory	6.694E-04	6	33
406	regulation of endothelial cell migration	6.705E-04	9	73
407	positive regulation of endothelial cell proliferation	6.705E-04	9	73
408	somatic recombination of T cell receptor gene segments	6.731E-04	3	6
409	T cell receptor V(D)J recombination	6.731E-04	3	6
410	phosphatidylglycerol metabolic process	6.731E-04	3	6
411	cardiolipin metabolic process	6.731E-04	3	6
412	baroreceptor response to increased systemic arterial blood pressure	6.731E-04	3	6
413	branching morphogenesis of a nerve	6.731E-04	3	6
414	somatic diversification of T cell receptor genes	6.731E-04	3	6
415	adrenergic receptor signaling pathway	6.740E-04	4	13
416	regulation of systemic arterial blood pressure by norepinephrine-epinephrine	6.740E-04	4	13
417	positive regulation of protein dephosphorylation	6.740E-04	4	13
418	regulation of catecholamine secretion	6.980E-04	8	59
419	cerebral cortex development	7.225E-04	10	89
420	chondrocyte differentiation	7.413E-04	7	46
421	activation of immune response	7.876E-04	23	333
422	central nervous system neuron differentiation	7.901E-04	13	140
423	release of cytochrome c from mitochondria	7.904E-04	6	34
424	response to iron ion	7.904E-04	6	34
425	macrophage activation	7.904E-04	6	34
426	regulation of dopamine secretion	7.904E-04	6	34
427	positive regulation of smooth muscle contraction	7.904E-04	6	34
428	negative regulation of phosphorylation	8.034E-04	12	123
429	regulation of receptor recycling	8.080E-04	5	23
430	positive regulation of organ growth	8.080E-04	5	23
431	response to peptide hormone stimulus	8.088E-04	35	595
432	immune response-activating signal transduction	8.219E-04	19	253
433	regulation of purine nucleotide catabolic process	8.238E-04	25	376
434	regulation of nucleotide catabolic process	8.238E-04	25	376

435	regeneration	8.609E-04	17	215
436	regulation of cyclic nucleotide biosynthetic process	8.611E-04	16	196
437	regulation of nucleotide biosynthetic process	8.611E-04	16	196
438	positive regulation of gene expression	8.848E-04	61	1219
439	regulation of GTPase activity	8.889E-04	23	336
440	regulation of organ growth	9.012E-04	9	76
441	positive regulation of cell motility	9.041E-04	20	275
442	regulation of protein metabolic process	9.077E-04	74	1547
443	small GTPase mediated signal transduction	9.103E-04	29	465
444	positive regulation of dephosphorylation	9.190E-04	4	14
445	regulation of monocyte differentiation	9.190E-04	4	14
446	negative regulation of protein autophosphorylation	9.190E-04	4	14
447	regulation of epithelial cell proliferation	9.459E-04	19	256
448	regulation of Wnt receptor signaling pathway	9.464E-04	15	179
449	circulatory system process	9.625E-04	23	338
450	regulation of cell growth	9.929E-04	25	381
451	positive regulation of epithelial to mesenchymal transition	9.931E-04	5	24
452	regulation of cardiac muscle hypertrophy	9.931E-04	5	24
453	regulation of dopamine metabolic process	9.931E-04	5	24
454	regulation of inhibitory postsynaptic membrane potential	9.931E-04	5	24
455	regulation of peptide hormone secretion	1.012E-03	16	199
456	chemotaxis	1.022E-03	38	672
457	induction of apoptosis by extracellular signals	1.027E-03	13	144
458	negative regulation of multicellular organismal process	1.051E-03	26	404
459	nucleoside monophosphate metabolic process	1.066E-03	12	127
460	regulation of cell morphogenesis involved in differentiation	1.067E-03	16	200
461	embryonic morphogenesis	1.095E-03	33	560
462	regulation of synaptic activity	1.097E-03	2	2
463	negative regulation of heart rate involved in baroreceptor response to increased systemic arterial blood pressure	1.097E-03	2	2
464	thigmotaxis	1.097E-03	2	2
465	negative regulation of the force of heart contraction involved in baroreceptor response to increased systemic arterial blood pressure	1.097E-03	2	2
466	jump response	1.097E-03	2	2
467	regulation of chondrocyte development	1.097E-03	2	2
468	odontoblast differentiation	1.097E-03	2	2
469	cell-cell signaling	1.098E-03	54	1057
470	regulation of cell size	1.102E-03	27	427
471	positive regulation of adenylate cyclase activity	1.108E-03	10	94
472	biological adhesion	1.118E-03	47	888
473	response to reactive oxygen species	1.120E-03	15	182
474	response to cAMP	1.141E-03	12	128
475	epithelium development	1.145E-03	36	630
476	forebrain ventricular zone progenitor cell division	1.149E-03	3	7
477	regulation of hormone secretion	1.186E-03	18	241
478	regulation of postsynaptic membrane potential	1.206E-03	8	64
479	regulation of cell-cell adhesion	1.206E-03	8	64
480	somatic stem cell division	1.208E-03	5	25
481	paraxial mesoderm development	1.208E-03	5	25
482	positive regulation of catecholamine secretion	1.208E-03	5	25
483	regulation of muscle hypertrophy	1.208E-03	5	25
484	response to lipopolysaccharide	1.214E-03	22	323
485	negative regulation of synaptic transmission, glutamatergic	1.220E-03	4	15
486	estrous cycle phase	1.220E-03	4	15
487	anatomical structure regression	1.220E-03	4	15
488	G-protein signaling, coupled to cAMP nucleotide second messenger	1.226E-03	14	165

489	cyclic nucleotide biosynthetic process	1.234E-03	7	50
490	immune response-regulating signaling pathway	1.243E-03	19	262
491	nucleocytoplasmic transport	1.243E-03	19	262
492	regulation of peptide secretion	1.248E-03	16	203
493	regulation of peptide transport	1.248E-03	16	203
494	negative regulation of macromolecule metabolic process	1.288E-03	67	1389
495	anti-apoptosis	1.305E-03	21	304
496	regulation of myeloid leukocyte differentiation	1.333E-03	11	113
497	regulation of striated muscle tissue development	1.333E-03	11	113
498	fibroblast growth factor receptor signaling pathway	1.336E-03	8	65
499	stem cell maintenance	1.336E-03	8	65
500	regulation of transmembrane transport	1.374E-03	25	390
501	positive regulation of locomotion	1.394E-03	20	285
502	positive regulation of cyclase activity	1.411E-03	10	97
503	regulation of transporter activity	1.432E-03	11	114
504	regulation of phosphatase activity	1.450E-03	6	38
505	positive regulation of blood vessel endothelial cell migration	1.455E-03	5	26
506	B cell proliferation	1.455E-03	5	26
507	muscarinic acetylcholine receptor signaling pathway	1.455E-03	5	26
508	nuclear transport	1.482E-03	19	266
509	tissue development	1.504E-03	65	1347
510	regulation of cyclic nucleotide metabolic process	1.529E-03	16	207
511	regulation of muscle organ development	1.538E-03	11	115
512	calcium ion transport into cytosol	1.561E-03	7	52
513	cellular homeostasis	1.576E-03	46	879
514	reduction of cytosolic calcium ion concentration	1.585E-03	4	16
515	mammary gland development	1.629E-03	14	170
516	regulation of neuron differentiation	1.636E-03	25	395
517	positive regulation of cellular component movement	1.646E-03	20	289
518	regulation of multicellular organism growth	1.648E-03	10	99
519	positive regulation of lyase activity	1.648E-03	10	99
520	vascular process in circulatory system	1.649E-03	11	116
521	release of sequestered calcium ion into cytosol	1.666E-03	6	39
522	negative regulation of sequestering of calcium ion	1.666E-03	6	39
523	cellular component maintenance	1.666E-03	6	39
524	positive regulation of vasoconstriction	1.666E-03	6	39
525	regulation of ion transmembrane transport	1.709E-03	18	249
526	regulation of Rho protein signal transduction	1.722E-03	14	171
527	cell adhesion	1.724E-03	46	883
528	negative regulation of cell-cell adhesion	1.738E-03	5	27
529	regulation of catecholamine metabolic process	1.738E-03	5	27
530	dorsal/ventral neural tube patterning	1.738E-03	5	27
531	motor axon guidance	1.738E-03	5	27
532	sleep	1.738E-03	5	27
533	response to stimulus	1.740E-03	301	7952
534	regulation of excitatory postsynaptic membrane potential	1.748E-03	7	53
535	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway	1.748E-03	7	53
536	regulation of heart rate	1.748E-03	7	53
537	regulation of monocyte chemotaxis	1.793E-03	3	8
538	intramembranous ossification	1.793E-03	3	8
539	positive regulation of chronic inflammatory response	1.793E-03	3	8
540	positive regulation of the force of heart contraction by epinephrine-norepinephrine	1.793E-03	3	8
541	astrocyte cell migration	1.793E-03	3	8
542	positive regulation of monocyte chemotaxis	1.793E-03	3	8

543	male mating behavior	1.793E-03	3	8
544	regulation of amine transport	1.843E-03	9	84
545	activation of MAPK activity	1.921E-03	14	173
546	blood circulation	1.925E-03	22	335
547	regulation of cellular component size	1.928E-03	31	534
548	regulation of nervous system development	1.928E-03	31	534
549	cytosolic calcium ion transport	1.952E-03	7	54
550	regulation of skeletal muscle tissue development	1.971E-03	8	69
551	pattern specification process	1.975E-03	28	467
552	positive regulation of cardiac muscle hypertrophy	2.019E-03	4	17
553	positive regulation of muscle hypertrophy	2.019E-03	4	17
554	positive regulation of phosphatase activity	2.019E-03	4	17
555	dentate gyrus development	2.019E-03	4	17
556	suckling behavior	2.019E-03	4	17
557	catecholamine transport	2.019E-03	4	17
558	response to toxin	2.027E-03	14	174
559	protein metabolic process	2.055E-03	146	3529
560	regulation of epidermal growth factor receptor activity	2.058E-03	5	28
561	central nervous system neuron axonogenesis	2.058E-03	5	28
562	multicellular organismal reproductive behavior	2.058E-03	5	28
563	organ morphogenesis	2.061E-03	50	989
564	negative regulation of metabolic process	2.079E-03	70	1493
565	leukocyte activation	2.100E-03	28	469
566	macromolecule methylation	2.121E-03	13	156
567	regulation of cellular catabolic process	2.164E-03	32	561
568	regulation of sequestering of calcium ion	2.172E-03	6	41
569	negative regulation of protein phosphorylation	2.172E-03	9	86
570	positive regulation of smooth muscle cell proliferation	2.172E-03	9	86
571	embryo development	2.189E-03	54	1091
572	regulation of protein binding	2.219E-03	10	103
573	positive regulation of signaling	2.287E-03	42	799
574	cell activation	2.289E-03	41	775
575	hippocampus development	2.353E-03	9	87
576	positive regulation of Rho GTPase activity	2.367E-03	8	71
577	cell surface receptor linked signaling pathway	2.370E-03	132	3156
578	neuroblast proliferation	2.420E-03	5	29
579	lymphocyte activation	2.444E-03	24	385
580	forebrain generation of neurons	2.464E-03	6	42
581	response to hypoxia	2.484E-03	22	342
582	cyclic nucleotide catabolic process	2.528E-03	4	18
583	chemosensory behavior	2.528E-03	4	18
584	transcription from RNA polymerase II promoter	2.557E-03	27	453
585	neuromuscular process	2.558E-03	10	105
586	maintenance of DNA repeat elements	2.624E-03	3	9
587	positive regulation of heart rate by epinephrine-norepinephrine	2.624E-03	3	9
588	short-term memory	2.624E-03	3	9
589	regulation of phospholipase A2 activity	2.624E-03	3	9
590	positive regulation of the force of heart contraction by chemical signal	2.624E-03	3	9
591	regulation of establishment of protein localization	2.645E-03	20	301
592	synapse assembly	2.676E-03	7	57
593	regulation of neurogenesis	2.750E-03	28	478
594	negative regulation of locomotion	2.758E-03	12	142
595	neural tube patterning	2.784E-03	6	43
596	response to starvation	2.800E-03	11	124
597	divalent metal ion transport	2.850E-03	18	261

598	response to hormone stimulus	2.901E-03	56	1156
599	calcium ion transport	2.964E-03	16	221
600	positive regulation of cell development	2.965E-03	15	201
601	cellular response to hormone stimulus	3.045E-03	33	597
602	negative regulation of canonical Wnt receptor signaling pathway	3.076E-03	8	74
603	positive regulation of synaptic transmission	3.076E-03	8	74
604	cellular response to endogenous stimulus	3.090E-03	39	740
605	response to endogenous stimulus	3.099E-03	64	1363
606	positive regulation of nervous system development	3.119E-03	4	19
607	positive regulation of synaptogenesis	3.119E-03	4	19
608	positive regulation of renal sodium excretion	3.119E-03	4	19
609	positive regulation of synaptic transmission, glutamatergic	3.119E-03	4	19
610	response to amphetamine	3.135E-03	6	44
611	positive regulation of cellular metabolic process	3.215E-03	84	1886
612	thymidine metabolic process	3.220E-03	2	3
613	regulation of cell proliferation in bone marrow	3.220E-03	2	3
614	T-helper 17 cell chemotaxis	3.220E-03	2	3
615	negative regulation of eosinophil degranulation	3.220E-03	2	3
616	muscle cell fate determination	3.220E-03	2	3
617	regulation of apoptosis in bone marrow	3.220E-03	2	3
618	regulation of eosinophil degranulation	3.220E-03	2	3
619	T cell chemotaxis	3.220E-03	2	3
620	helper T cell chemotaxis	3.220E-03	2	3
621	amygdala development	3.220E-03	2	3
622	terminal button organization	3.220E-03	2	3
623	neurohypophysis development	3.220E-03	2	3
624	monocyte extravasation	3.220E-03	2	3
625	positive regulation of T cell extravasation	3.220E-03	2	3
626	negative regulation of icosanoid secretion	3.220E-03	2	3
627	positive regulation of cell proliferation in bone marrow	3.220E-03	2	3
628	regulation of estrogen receptor binding	3.220E-03	2	3
629	neutrophil differentiation	3.220E-03	2	3
630	regulation of T cell extravasation	3.220E-03	2	3
631	negative regulation of apoptosis in bone marrow	3.220E-03	2	3
632	chondrocyte differentiation involved in endochondral bone morphogenesis	3.220E-03	2	3
633	negative regulation of estrogen receptor binding	3.220E-03	2	3
634	synaptic target recognition	3.220E-03	2	3
635	formation of radial glial scaffolds	3.220E-03	2	3
636	activation of MAPKK activity	3.262E-03	7	59
637	positive regulation of macromolecule biosynthetic process	3.269E-03	62	1315
638	cell proliferation in forebrain	3.279E-03	5	31
639	positive regulation of cell morphogenesis involved in differentiation	3.279E-03	5	31
640	cerebral cortex cell migration	3.279E-03	5	31
641	response to molecule of bacterial origin	3.285E-03	22	350
642	cilium morphogenesis	3.346E-03	8	75
643	sensory perception of taste	3.346E-03	8	75
644	divalent inorganic cation transport	3.349E-03	18	265
645	positive regulation of defense response	3.349E-03	18	265
646	feeding behavior	3.370E-03	11	127
647	multi-organism process	3.400E-03	66	1420
648	activation of adenylate cyclase activity	3.446E-03	9	92
649	protein methylation	3.446E-03	9	92
650	protein alkylation	3.446E-03	9	92
651	regulation of homeostatic process	3.474E-03	19	287
652	bone remodeling	3.518E-03	6	45

653	positive regulation of endothelial cell migration	3.518E-03	6	45
654	positive regulation of cellular biosynthetic process	3.524E-03	67	1448
655	cellular response to organic substance	3.557E-03	62	1320
656	tube development	3.566E-03	29	510
657	positive regulation of inflammatory response	3.592E-03	10	110
658	positive regulation of adenylate cyclase activity by G-protein signaling pathway	3.633E-03	8	76
659	regulation of adenylate cyclase activity involved in G-protein signaling pathway	3.633E-03	8	76
660	activation of adenylate cyclase activity by G-protein signaling pathway	3.633E-03	8	76
661	positive regulation of calcium ion transport via store-operated calcium channel activity	3.656E-03	3	10
662	photoperiodism	3.656E-03	3	10
663	regulation of systemic arterial blood pressure by carotid sinus baroreceptor feedback	3.656E-03	3	10
664	positive regulation of macromolecule metabolic process	3.769E-03	81	1818
665	stem cell division	3.782E-03	5	32
666	Notch receptor processing	3.798E-03	4	20
667	positive regulation of cellular component biogenesis	3.798E-03	4	20
668	regulation of protein dephosphorylation	3.798E-03	4	20
669	hypothalamus development	3.798E-03	4	20
670	negative regulation of striated muscle tissue development	3.798E-03	4	20
671	activation of protein kinase A activity	3.798E-03	4	20
672	intracellular protein transport	3.822E-03	31	559
673	regulation of insulin secretion	3.908E-03	14	187
674	regulation of organic acid transport	3.935E-03	6	46
675	negative regulation of hormone secretion	3.940E-03	8	77
676	embryo development ending in birth or egg hatching	3.983E-03	36	679
677	response to oxygen levels	4.004E-03	23	378
678	ossification	4.020E-03	16	228
679	response to mechanical stimulus	4.020E-03	16	228
680	symbiosis, encompassing mutualism through parasitism	4.030E-03	11	130
681	regulation of caspase activity	4.098E-03	14	188
682	regulation of organelle organization	4.212E-03	27	470
683	regulation of cytoskeleton organization	4.238E-03	17	250
684	cellular response to organic cyclic compound	4.265E-03	8	78
685	response to drug	4.266E-03	35	658
686	myeloid cell differentiation	4.274E-03	15	209
687	mesenchyme development	4.308E-03	12	150
688	positive regulation of fibroblast proliferation	4.319E-03	7	62
689	central nervous system neuron development	4.319E-03	7	62
690	histone methylation	4.319E-03	7	62
691	regulation of lipoprotein lipase activity	4.338E-03	5	33
692	positive regulation of vasodilation	4.338E-03	5	33
693	negative regulation of exocytosis	4.570E-03	4	21
694	positive regulation of transmission of nerve impulse	4.612E-03	8	79
695	mesenchymal cell differentiation	4.636E-03	10	114
696	regulation of ion homeostasis	4.789E-03	12	152
697	negative regulation of smooth muscle cell migration	4.904E-03	3	11
698	choline transport	4.904E-03	3	11
699	regulation of the force of heart contraction by chemical signal	4.904E-03	3	11
700	behavioral response to cocaine	4.904E-03	3	11
701	T cell receptor signaling pathway	4.931E-03	10	115
702	positive regulation of multicellular organism growth	4.949E-03	5	34
703	regulation of protein autophosphorylation	4.949E-03	5	34
704	lysosome organization	4.949E-03	5	34
705	leukocyte differentiation	5.016E-03	19	297
706	regulation of endopeptidase activity	5.197E-03	19	298
707	gland development	5.206E-03	22	364

708	positive regulation of multicellular organismal process	5.224E-03	32	595
709	regulation of cellular component biogenesis	5.239E-03	20	320
710	regulation of protein localization	5.239E-03	21	342
711	regulation of endothelial cell proliferation	5.244E-03	9	98
712	segmentation	5.244E-03	9	98
713	positive regulation of biosynthetic process	5.288E-03	67	1474
714	regulation of systemic arterial blood pressure mediated by a chemical signal	5.404E-03	6	49
715	histone lysine methylation	5.404E-03	6	49
716	negative regulation of muscle organ development	5.441E-03	4	22
717	phasic smooth muscle contraction	5.441E-03	4	22
718	morphogenesis of an epithelium	5.469E-03	23	388
719	chordate embryonic development	5.500E-03	35	669
720	positive regulation of cell communication	5.535E-03	40	791
721	divalent inorganic cation homeostasis	5.544E-03	22	366
722	homeostatic process	5.619E-03	63	1374
723	positive regulation of cell-cell adhesion	5.620E-03	5	35
724	astrocyte differentiation	5.620E-03	5	35
725	regulation of synaptogenesis	5.620E-03	5	35
726	receptor internalization	5.620E-03	5	35
727	carbohydrate homeostasis	5.657E-03	11	136
728	glucose homeostasis	5.657E-03	11	136
729	regulation of calcium ion transport	5.673E-03	13	175
730	regulation of MAPKKK cascade	5.720E-03	22	367
731	cellular response to chemical stimulus	5.754E-03	76	1716
732	response to steroid hormone stimulus	5.904E-03	33	624
733	regulation of skeletal muscle fiber development	5.972E-03	6	50
734	transforming growth factor beta receptor signaling pathway	5.982E-03	9	100
735	positive regulation of cell growth	6.261E-03	10	119
736	heart morphogenesis	6.272E-03	15	218
737	regulation of metal ion transport	6.272E-03	15	218
738	respiratory system development	6.289E-03	16	239
739	optic placode formation	6.298E-03	2	4
740	regulation of calcium-dependent cell-cell adhesion	6.298E-03	2	4
741	PML body organization	6.298E-03	2	4
742	negative regulation of interleukin-13 production	6.298E-03	2	4
743	regulation of immune complex clearance by monocytes and macrophages	6.298E-03	2	4
744	stress granule disassembly	6.298E-03	2	4
745	forebrain radial glial cell differentiation	6.298E-03	2	4
746	vasodilation by angiotensin involved in regulation of systemic arterial blood pressure	6.298E-03	2	4
747	establishment of synaptic specificity at neuromuscular junction	6.298E-03	2	4
748	negative regulation of Wnt receptor signaling pathway involved in dorsal/ventral axis specification	6.298E-03	2	4
749	relaxation of cardiac muscle	6.298E-03	2	4
750	cell proliferation in hindbrain	6.298E-03	2	4
751	regulation of cardiac muscle contraction by calcium ion signaling	6.298E-03	2	4
752	regulation of metanephros size	6.298E-03	2	4
753	pyrimidine deoxyribonucleoside metabolic process	6.298E-03	2	4
754	inositol trisphosphate biosynthetic process	6.298E-03	2	4
755	trachea submucosa development	6.298E-03	2	4
756	hypothalamus cell differentiation	6.298E-03	2	4
757	positive regulation of oocyte development	6.298E-03	2	4
758	multicellular organismal iron ion homeostasis	6.298E-03	2	4
759	trachea gland development	6.298E-03	2	4
760	regulation of centromeric sister chromatid cohesion	6.298E-03	2	4
761	positive regulation of immune complex clearance by monocytes and macrophages	6.298E-03	2	4

762	regulation of epithelial to mesenchymal transition	6.352E-03	5	36
763	negative regulation of Ras protein signal transduction	6.352E-03	5	36
764	Toll signaling pathway	6.379E-03	9	101
765	regulation of systemic arterial blood pressure by baroreceptor feedback	6.379E-03	3	12
766	positive regulation of release of cytochrome c from mitochondria	6.379E-03	3	12
767	regulation of nerve growth factor receptor signaling pathway	6.379E-03	3	12
768	histone H3 deacetylation	6.379E-03	3	12
769	dopamine transport	6.379E-03	3	12
770	positive regulation of receptor recycling	6.379E-03	3	12
771	response to vitamin E	6.416E-03	4	23
772	protein secretion	6.583E-03	6	51
773	somitogenesis	6.630E-03	7	67
774	negative regulation of cell migration	6.634E-03	10	120
775	synapse organization	7.023E-03	10	121
776	tissue morphogenesis	7.032E-03	29	536
777	cellular response to insulin stimulus	7.056E-03	18	285
778	negative regulation of small GTPase mediated signal transduction	7.148E-03	5	37
779	phospholipid catabolic process	7.148E-03	5	37
780	startle response	7.148E-03	5	37
781	regulation of stress fiber assembly	7.148E-03	5	37
782	modification of morphology or physiology of other organism involved in symbiotic interaction	7.185E-03	7	68
783	modification of morphology or physiology of other organism	7.185E-03	7	68
784	dorsal/ventral pattern formation	7.235E-03	9	103
785	heart process	7.238E-03	6	52
786	pituitary gland development	7.238E-03	6	52
787	G-protein signaling, coupled to cyclic nucleotide second messenger	7.319E-03	14	201
788	negative regulation of cell motility	7.430E-03	10	122
789	positive regulation of cell-matrix adhesion	7.501E-03	4	24
790	regulation of respiratory gaseous exchange	7.501E-03	4	24
791	positive regulation of heart rate	7.501E-03	4	24
792	immune response-activating cell surface receptor signaling pathway	7.504E-03	12	161
793	regulation of localization	7.550E-03	70	1577
794	regulation of catabolic process	7.761E-03	33	636
795	aging	7.762E-03	20	332
796	glial cell differentiation	7.762E-03	11	142
797	regulation of action potential	7.762E-03	11	142
798	regulation of canonical Wnt receptor signaling pathway	7.855E-03	10	123
799	amine transport	7.956E-03	14	203
800	positive regulation of immune response	7.970E-03	25	447
801	T cell activation	7.980E-03	15	224
802	G-protein coupled purinergic receptor signaling pathway	8.011E-03	5	38
803	regulation of erythrocyte differentiation	8.011E-03	5	38
804	rhythmic process	8.081E-03	19	311
805	positive regulation of circadian sleep/wake cycle, sleep	8.091E-03	3	13
806	regulation of chronic inflammatory response	8.091E-03	3	13
807	growth hormone receptor signaling pathway	8.091E-03	3	13
808	positive regulation of mitochondrion organization	8.091E-03	3	13
809	courtship behavior	8.091E-03	3	13
810	interleukin-6-mediated signaling pathway	8.091E-03	3	13
811	histone H4 deacetylation	8.091E-03	3	13
812	toll-like receptor 3 signaling pathway	8.213E-03	8	87
813	positive regulation of neurological system process	8.213E-03	8	87
814	stress-activated MAPK cascade	8.397E-03	7	70
815	negative regulation of insulin secretion	8.688E-03	6	54

816	regulation of mitochondrion organization	8.700E-03	4	25
817	prepulse inhibition	8.700E-03	4	25
818	regulation of establishment of protein localization in plasma membrane	8.700E-03	4	25
819	cation homeostasis	8.748E-03	29	545
820	mesoderm development	8.761E-03	10	125
821	metal ion homeostasis	8.765E-03	26	474
822	regulation of viral transcription	8.780E-03	8	88
823	myeloid leukocyte differentiation	8.780E-03	8	88
824	positive regulation of cellular component organization	8.924E-03	28	522
825	positive regulation of intracellular protein kinase cascade	8.932E-03	24	428
826	midbrain development	8.944E-03	5	39
827	dendrite development	9.057E-03	7	71
828	cellular component assembly at cellular level	9.126E-03	48	1018
829	chromatin organization	9.172E-03	29	547
830	neuron migration	9.208E-03	9	107
831	mesenchymal cell development	9.208E-03	9	107
832	cellular protein localization	9.338E-03	36	718
833	MyD88-independent toll-like receptor signaling pathway	9.375E-03	8	89
834	response to axon injury	9.375E-03	8	89
835	axon regeneration	9.485E-03	6	55
836	positive regulation of ossification	9.485E-03	6	55
837	regulation of ion transport	9.486E-03	22	384
838	positive regulation of reproductive process	9.745E-03	10	127
839	positive regulation of cell size	9.745E-03	10	127
840	immune response-regulating cell surface receptor signaling pathway	9.902E-03	12	167
841	positive regulation of protein binding	9.950E-03	5	40
842	regulation of nitric-oxide synthase activity	9.950E-03	5	40
843	negative regulation of protein binding	9.950E-03	5	40
844	nucleoside monophosphate catabolic process	1.002E-02	4	26
845	ectodermal placode formation	1.002E-02	4	26
846	ectodermal placode morphogenesis	1.002E-02	4	26
847	regulation of granulocyte differentiation	1.002E-02	4	26
848	ectodermal placode development	1.002E-02	4	26
849	behavioral response to pain	1.002E-02	4	26
850	G-protein coupled receptor internalization	1.005E-02	3	14
851	adenosine receptor signaling pathway	1.005E-02	3	14
852	regulation of focal adhesion assembly	1.005E-02	3	14
853	granulocyte differentiation	1.005E-02	3	14
854	regulation of growth hormone secretion	1.005E-02	3	14
855	serine family amino acid catabolic process	1.005E-02	3	14
856	positive regulation of dopamine secretion	1.005E-02	3	14
857	axonal fasciculation	1.005E-02	3	14
858	regulation of cell-substrate junction assembly	1.005E-02	3	14
859	regulation of cellular localization	1.006E-02	35	697
860	positive regulation of MAPKKK cascade	1.014E-02	14	209
861	intestine smooth muscle contraction	1.027E-02	2	5
862	positive regulation of metanephric glomerulus development	1.027E-02	2	5
863	gastro-intestinal system smooth muscle contraction	1.027E-02	2	5
864	bombesin receptor signaling pathway	1.027E-02	2	5
865	olfactory placode development	1.027E-02	2	5
866	positive regulation of cellular extravasation	1.027E-02	2	5
867	nuclear body organization	1.027E-02	2	5
868	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	1.027E-02	2	5
869	embryonic genitalia morphogenesis	1.027E-02	2	5
870	regulation of oocyte development	1.027E-02	2	5

871	negative regulation of interleukin-5 production	1.027E-02	2	5
872	axial mesoderm formation	1.027E-02	2	5
873	4-hydroxyproline metabolic process	1.027E-02	2	5
874	positive regulation of metanephros development	1.027E-02	2	5
875	positive regulation of cardiac muscle contraction	1.027E-02	2	5
876	radial glial cell differentiation	1.027E-02	2	5
877	positive regulation of transcription of Notch receptor target	1.027E-02	2	5
878	activation of store-operated calcium channel activity	1.027E-02	2	5
879	regulation of Wnt receptor signaling pathway involved in dorsal/ventral axis specification	1.027E-02	2	5
880	olfactory placode morphogenesis	1.027E-02	2	5
881	T cell migration	1.027E-02	2	5
882	positive regulation of somatostatin secretion	1.027E-02	2	5
883	olfactory placode formation	1.027E-02	2	5
884	cellular macromolecule localization	1.033E-02	36	723
885	response to mineralocorticoid stimulus	1.033E-02	6	56
886	JAK-STAT cascade	1.033E-02	6	56
887	cilium assembly	1.033E-02	6	56
888	negative regulation of peptide hormone secretion	1.033E-02	6	56
889	regulation of immune system process	1.034E-02	49	1051

MODEL II – UP

#	GO Processes	pValue	Ratio	
1	nucleosome assembly	2.480E-20	12	121
2	chromatin assembly	4.537E-20	12	127
3	nucleosome organization	1.165E-19	12	137
4	protein-DNA complex assembly	1.981E-19	12	143
5	chromatin assembly or disassembly	1.981E-19	12	143
6	protein-DNA complex subunit organization	3.885E-19	12	151
7	DNA packaging	2.073E-18	12	173
8	DNA conformation change	1.381E-17	12	202
9	chromatin organization	6.712E-14	13	547
10	chromosome organization	9.613E-14	14	728
11	cellular macromolecular complex assembly	4.905E-13	12	484
12	cellular macromolecular complex subunit organization	8.610E-12	12	618
13	cellular component assembly at cellular level	1.663E-10	13	1018
14	macromolecular complex assembly	1.818E-09	12	984
15	organelle organization	7.954E-09	15	2040
16	macromolecular complex subunit organization	8.827E-09	12	1132
17	cellular component assembly	1.330E-08	13	1458
18	cellular component biogenesis	4.383E-08	13	1611
19	cellular component organization at cellular level	5.857E-07	16	3253
20	cellular component organization or biogenesis at cellular level	9.466E-07	16	3367
21	cellular component organization	1.772E-05	16	4177
22	cellular component organization or biogenesis	2.632E-05	16	4304
23	telomere maintenance	1.133E-04	3	70
24	telomere organization	1.182E-04	3	71
25	defense response to bacterium	1.543E-04	4	204
26	regulation of gene silencing	2.082E-04	2	16
27	DNA metabolic process	3.550E-04	6	728
28	DNA fragmentation involved in apoptotic nuclear change	7.967E-04	2	31
29	DNA catabolic process, endonucleolytic	7.967E-04	2	31
30	cytokinesis, initiation of separation	1.349E-03	1	1
31	assembly of actomyosin apparatus involved in cell cycle cytokinesis	1.349E-03	1	1
32	cytokinesis, actomyosin contractile ring assembly	1.349E-03	1	1
33	apoptotic nuclear change	1.393E-03	2	41
34	response to stress	2.008E-03	11	3216
35	multi-organism process	2.288E-03	7	1420
36	glyoxylate cycle	2.697E-03	1	2
37	protein localization to chromosome, centromeric region	2.697E-03	1	2
38	anatomical structure homeostasis	2.739E-03	3	209
39	nucleic acid phosphodiester bond hydrolysis	3.464E-03	2	65

MODEL II – DOWN

#	GO Processes	pValue	Ratio	
1	regulation of lipid metabolic process	2.153E-06	13	254
2	regulation of myotube differentiation	2.370E-06	5	22
3	protein deacetylation	2.537E-06	6	39
4	protein deacylation	2.960E-06	6	40
5	phosphate metabolic process	4.188E-06	34	1451
6	phosphorus metabolic process	4.251E-06	34	1452
7	regulation of endothelial cell migration	9.382E-06	7	73
8	positive regulation of synaptic transmission, GABAergic	1.298E-05	4	15
9	protein modification process	1.808E-05	43	2194
10	histone deacetylation	1.950E-05	5	33
11	peptidyl-lysine deacetylation	2.026E-05	3	6
12	regulation of striated muscle tissue development	2.051E-05	8	113
13	regulation of synaptic transmission, GABAergic	2.268E-05	5	34
14	regulation of muscle organ development	2.330E-05	8	115
15	chromatin silencing	3.958E-05	5	38
16	negative regulation of striated muscle tissue development	4.428E-05	4	20
17	negative regulation of gene expression, epigenetic	6.490E-05	5	42
18	macromolecule modification	6.535E-05	43	2316
19	negative regulation of muscle organ development	6.580E-05	4	22
20	positive regulation of endothelial cell migration	9.093E-05	5	45
21	negative regulation of cell migration involved in sprouting angiogenesis	1.029E-04	2	2
22	canonical Wnt receptor signaling pathway involved in positive regulation of wound healing	1.029E-04	2	2
23	negative regulation of cell volume	1.029E-04	2	2
24	canonical Wnt receptor signaling pathway involved in positive regulation of cell-cell adhesion	1.029E-04	2	2
25	canonical Wnt receptor signaling pathway involved in positive regulation of endothelial cell migration	1.029E-04	2	2
26	dephosphorylation	1.153E-04	10	227
27	central nervous system development	1.332E-04	22	900
28	glutamate signaling pathway	1.373E-04	5	49
29	negative regulation of protein complex assembly	1.437E-04	6	78
30	regulation of skeletal muscle fiber development	1.513E-04	5	50
31	protein localization in endoplasmic reticulum	1.517E-04	4	27
32	sphingolipid metabolic process	1.579E-04	7	113
33	actin cytoskeleton organization	1.629E-04	13	384
34	intracellular signal transduction	1.782E-04	33	1673
35	histone H3 deacetylation	2.130E-04	3	12
36	membrane lipid metabolic process	2.291E-04	7	120
37	nervous system development	2.314E-04	39	2143
38	phospholipid dephosphorylation	2.749E-04	3	13
39	negative regulation of myotube differentiation	2.749E-04	3	13
40	germ cell migration	2.987E-04	4	32
41	regulation of cellular component movement	2.998E-04	14	464
42	cardiac muscle adaptation	3.066E-04	2	3
43	muscle hypertrophy in response to stress	3.066E-04	2	3
44	cardiac muscle hypertrophy in response to stress	3.066E-04	2	3
45	chromatin silencing at telomere	3.066E-04	2	3
46	negative regulation of biological process	3.431E-04	53	3296
47	regulation of lipid biosynthetic process	3.736E-04	7	130
48	negative regulation of synaptic transmission, glutamatergic	4.308E-04	3	15
49	calcium-mediated signaling	4.512E-04	5	63

50	regulation of generation of precursor metabolites and energy	4.512E-04	5	63
51	positive regulation of lipid biosynthetic process	4.512E-04	5	63
52	second-messenger-mediated signaling	4.824E-04	13	430
53	actin filament-based process	4.824E-04	13	430
54	lipid modification	4.904E-04	7	136
55	negative regulation of synaptic transmission, GABAergic	5.262E-04	3	16
56	regulation of cardiac muscle contraction by calcium ion signaling	6.091E-04	2	4
57	regulation of thyroid hormone mediated signaling pathway	6.091E-04	2	4
58	response to muscle inactivity involved in regulation of muscle adaptation	6.091E-04	2	4
59	response to denervation involved in regulation of muscle adaptation	6.091E-04	2	4
60	negative regulation of striated muscle cell differentiation	6.342E-04	3	17
61	regulation of localization	6.579E-04	30	1577
62	regulation of muscle contraction	6.616E-04	7	143
63	phosphorylation	6.661E-04	25	1219
64	regulation of skeletal muscle tissue development	6.867E-04	5	69
65	positive regulation of cellular component movement	7.830E-04	10	289
66	negative regulation of cellular process	8.034E-04	48	3002
67	negative regulation of blood vessel endothelial cell migration	8.903E-04	3	19
68	positive regulation of synaptic transmission, glutamatergic	8.903E-04	3	19
69	protein phosphorylation	8.995E-04	20	900
70	positive regulation of synaptic transmission	9.448E-04	5	74
71	cytoskeleton organization	9.856E-04	17	710
72	regulation of striated muscle cell differentiation	1.004E-03	5	75
73	positive regulation of female receptivity	1.008E-03	2	5
74	regulation of protein complex assembly	1.009E-03	8	199
75	chondroitin sulfate metabolic process	1.040E-03	3	20
76	regulation of blood vessel endothelial cell migration	1.213E-03	4	46
77	regulation of cell migration	1.235E-03	12	418
78	positive regulation of transmission of nerve impulse	1.269E-03	5	79
79	positive regulation of lipid metabolic process	1.318E-03	6	118
80	viral genome replication	1.384E-03	3	22
81	protein kinase B signaling cascade	1.384E-03	3	22
82	regulation of muscle system process	1.422E-03	7	163
83	regulation of synaptic transmission, glutamatergic	1.424E-03	4	48
84	negative regulation of glycolysis	1.502E-03	2	6
85	response to stimulus involved in regulation of muscle adaptation	1.502E-03	2	6
86	negative regulation of RNA polymerase II transcriptional preinitiation complex assembly	1.502E-03	2	6
87	negative regulation of transcription initiation, DNA-dependent	1.502E-03	2	6
88	interleukin-12 production	1.502E-03	2	6
89	regulation of aldosterone metabolic process	1.502E-03	2	6
90	positive regulation of myotube differentiation	1.502E-03	2	6
91	response to muscle inactivity	1.502E-03	2	6
92	regulation of synaptic vesicle fusion to presynaptic membrane	1.502E-03	2	6
93	chondroitin sulfate proteoglycan metabolic process	1.579E-03	3	23
94	regulation of cell motility	1.629E-03	12	432
95	negative regulation of phosphorylation	1.630E-03	6	123
96	regulation of cellular component biogenesis	1.681E-03	10	320
97	gliogenesis	1.748E-03	7	169
98	negative regulation of protein phosphorylation	1.852E-03	5	86

99	regulation of Rho protein signal transduction	1.869E-03	7	171
100	positive regulation of neurological system process	1.949E-03	5	87

MODEL III – UP

#	GO Processes	pValue	Ratio	
1	cell cycle phase	8.787E-16	25	851
2	cell cycle	1.302E-14	28	1262
3	cell cycle process	3.578E-14	25	1001
4	M phase	1.020E-13	19	521
5	mitotic cell cycle	2.872E-13	21	716
6	cell division	6.468E-12	16	422
7	mitosis	5.416E-11	14	341
8	nuclear division	5.416E-11	14	341
9	M phase of mitotic cell cycle	7.359E-11	14	349
10	organelle fission	9.214E-11	14	355
11	organelle organization	1.279E-09	28	2040
12	cellular component organization or biogenesis at cellular level	1.979E-09	36	3367
13	chromosome segregation	4.653E-09	9	143
14	regulation of cell cycle process	1.990E-08	13	451
15	regulation of cell cycle	3.039E-08	17	864
16	cellular component organization at cellular level	5.200E-08	33	3253
17	DNA conformation change	9.346E-08	9	202
18	regulation of mitotic cell cycle	1.272E-07	11	354
19	DNA packaging	3.800E-07	8	173
20	cellular component organization or biogenesis	4.048E-07	37	4304
21	spindle organization	5.568E-07	6	77
22	cell cycle checkpoint	8.388E-07	9	262
23	regulation of cell cycle arrest	1.292E-06	9	276
24	positive regulation of nuclease activity	1.982E-06	3	7
25	mitotic cell cycle G2/M transition DNA damage checkpoint	4.731E-06	3	9
26	cellular component organization	5.971E-06	34	4177
27	mitotic cell cycle G2/M transition checkpoint	1.229E-05	3	12
28	positive regulation of centrosome cycle	1.505E-05	2	2
29	regulation of nuclease activity	1.593E-05	3	13
30	base-excision repair	1.954E-05	4	41
31	cellular process	2.141E-05	73	14653
32	mitotic cell cycle checkpoint	3.222E-05	6	155
33	microtubule cytoskeleton organization	3.433E-05	7	232
34	G2/M transition of mitotic cell cycle	3.588E-05	6	158
35	interphase of mitotic cell cycle	3.765E-05	9	420
36	interphase	4.280E-05	9	427
37	base-excision repair, DNA ligation	4.502E-05	2	3
38	nuclear envelope reassembly	4.502E-05	2	3
39	regulation of cyclin-dependent protein kinase activity	5.433E-05	5	104
40	regulation of nuclear division	5.951E-05	5	106
41	regulation of mitosis	5.951E-05	5	106
42	organ regeneration	6.506E-05	5	108
43	microtubule-based process	7.209E-05	8	354
44	nucleus organization	8.325E-05	4	59
45	regulation of cyclin-dependent protein kinase activity involved in G2/M	8.982E-05	2	4
46	positive regulation of cyclin-dependent protein kinase activity involved in G2/M	8.982E-05	2	4
47	chromosome organization	1.190E-04	11	728
48	regulation of transcription involved in G1/S phase of mitotic cell cycle	1.396E-04	3	26
49	active induction of host immune response by virus	1.493E-04	2	5
50	induction of host immune response by virus	1.493E-04	2	5
51	induction by symbiont of host defense response	1.493E-04	2	5
52	positive regulation of megakaryocyte differentiation	1.493E-04	2	5

53	G2/M transition DNA damage checkpoint	1.566E-04	3	27
54	positive regulation of cell cycle	2.136E-04	5	139
55	induction by organism of defense response of other organism involved in symbiotic interaction	2.234E-04	2	6
56	adenine transport	2.234E-04	2	6
57	DNA ligation involved in DNA repair	3.120E-04	2	7
58	chromosome condensation	3.727E-04	3	36
59	G2/M transition checkpoint	3.727E-04	3	36
60	nucleobase, nucleoside, nucleotide and nucleic acid transport	3.860E-04	5	158
61	spindle assembly checkpoint	4.044E-04	3	37
62	cytoskeleton organization	4.331E-04	10	710
63	organ morphogenesis	4.359E-04	12	989
64	regulation of erythrocyte differentiation	4.379E-04	3	38
65	cellular component disassembly involved in apoptosis	4.448E-04	4	91
66	phosphatidylinositol-mediated signaling	4.636E-04	4	92
67	embryonic skeletal system morphogenesis	4.830E-04	4	93
68	inositol lipid-mediated signaling	4.830E-04	4	93
69	spindle checkpoint	5.100E-04	3	40
70	regulation of interphase of mitotic cell cycle	5.109E-04	5	168
71	mitotic prometaphase	5.447E-04	4	96
72	meiosis	5.837E-04	5	173
73	M phase of meiotic cell cycle	5.837E-04	5	173
74	regulation of G2/M transition of mitotic cell cycle	5.892E-04	3	42
75	meiotic cell cycle	6.474E-04	5	177
76	regulation of megakaryocyte differentiation	6.635E-04	2	10
77	purine base transport	8.089E-04	2	11
78	positive regulation by organism of defense response of other organism involved in symbiotic interaction	1.141E-03	2	13
79	positive regulation by symbiont of host defense response	1.141E-03	2	13
80	modulation by organism of defense response of other organism involved in symbiotic interaction	1.141E-03	2	13
81	DNA topological change	1.141E-03	2	13
82	DNA ligation	1.141E-03	2	13
83	modulation by symbiont of host defense response	1.141E-03	2	13
84	mitotic sister chromatid segregation	1.231E-03	3	54
85	skeletal system morphogenesis	1.276E-03	5	206
86	nucleosome assembly	1.294E-03	4	121
87	nuclear envelope organization	1.328E-03	2	14
88	nucleobase transport	1.328E-03	2	14
89	spermatid nucleus differentiation	1.328E-03	2	14
90	embryonic skeletal system development	1.334E-03	4	122
91	ncRNA metabolic process	1.411E-03	6	313
92	sister chromatid segregation	1.514E-03	3	58
93	regeneration	1.541E-03	5	215
94	chromatin assembly	1.547E-03	4	127
95	G1/S transition of mitotic cell cycle	1.671E-03	5	219
96	ventricular cardiac muscle cell development	1.970E-03	2	17
97	nucleosome organization	2.041E-03	4	137
98	DNA damage checkpoint	2.041E-03	4	137
99	regulation of centrosome cycle	2.211E-03	2	18
100	mitotic chromosome condensation	2.211E-03	2	18
101	purine-containing compound transmembrane transport	2.211E-03	2	18
102	cellular component disassembly at cellular level	2.358E-03	5	237
103	chromatin assembly or disassembly	2.385E-03	4	143
104	protein-DNA complex assembly	2.385E-03	4	143
105	regulation of organelle organization	2.402E-03	7	470

106	immune system development	2.473E-03	8	605
107	cellular component disassembly	2.490E-03	5	240
108	DNA integrity checkpoint	2.508E-03	4	145
109	response to host defenses	2.731E-03	2	20
110	response to host	2.731E-03	2	20
111	response to defenses of other organism involved in symbiotic interaction	2.731E-03	2	20
112	cellular macromolecular complex subunit organization	2.818E-03	8	618
113	cellular macromolecular complex assembly	2.828E-03	7	484
114	protein-DNA complex subunit organization	2.903E-03	4	151
115	response to DNA damage stimulus	2.989E-03	8	624
116	ribonucleoprotein complex biogenesis	3.284E-03	5	256
117	cellular component biogenesis	3.600E-03	14	1611
118	positive chemotaxis	3.609E-03	2	23
119	positive regulation of cyclin-dependent protein kinase activity	3.609E-03	2	23
120	V(D)J recombination	3.609E-03	2	23
121	positive regulation of mitotic centrosome separation	3.903E-03	1	1
122	meiotic sister chromatid cohesion, centromeric	3.903E-03	1	1
123	regulation of mitotic centrosome separation	3.903E-03	1	1
124	endothelial cell fate specification	3.903E-03	1	1
125	centromeric sister chromatid cohesion	3.903E-03	1	1
126	positive regulation of deoxyribonuclease activity	3.903E-03	1	1
127	positive regulation of centriole replication	3.903E-03	1	1
128	DNA geometric change	3.928E-03	2	24
129	cellular component biogenesis at cellular level	3.990E-03	5	268
130	macromolecular complex subunit organization	4.411E-03	11	1132
131	chordate embryonic development	4.548E-03	8	669
132	embryonic organ development	4.586E-03	6	397
133	positive regulation of branching involved in ureteric bud morphogenesis	4.602E-03	2	26

MODEL III – DOWN

#	GO Processes	pValue	Ratio	
1	synaptic transmission	1.287E-11	24	670
2	multicellular organismal signaling	3.008E-11	25	762
3	transmission of nerve impulse	3.008E-11	25	762
4	regulation of neurotransmitter levels	1.045E-10	13	170
5	neurotransmitter secretion	4.350E-10	11	120
6	regulation of exocytosis	4.287E-09	10	114
7	cell-cell adhesion	1.021E-08	16	402
8	synaptic vesicle exocytosis	2.022E-08	7	46
9	neurotransmitter transport	2.097E-08	11	173
10	regulation of secretion	2.324E-08	18	549
11	signal release	2.341E-08	12	218
12	generation of a signal involved in cell-cell signaling	2.341E-08	12	218
13	cell-cell signaling	2.455E-08	25	1057
14	regulation of cellular localization	3.318E-08	20	697
15	regulation of vesicle-mediated transport	5.508E-08	13	285
16	homophilic cell adhesion	7.730E-08	10	154
17	regulation of localization	1.057E-07	30	1577
18	exocytosis	2.727E-07	12	273
19	regulation of transport	4.986E-07	25	1238
20	cell communication	4.988E-07	27	1416
21	synaptic vesicle transport	6.396E-07	7	75
22	phosphatidylinositol-mediated signaling	2.572E-06	7	92
23	neurological system process	2.690E-06	32	2040
24	inositol lipid-mediated signaling	2.766E-06	7	93
25	secretion by cell	3.021E-06	14	472
26	regulation of cell communication	3.081E-06	27	1557
27	learning	3.590E-06	8	137
28	regulation of signaling	7.288E-06	32	2139
29	calcium ion-dependent exocytosis	1.029E-05	5	44
30	glutamate secretion	1.460E-05	4	23
31	synaptic vesicle endocytosis	1.743E-05	4	24
32	system process	2.159E-05	34	2474
33	cGMP catabolic process	2.296E-05	3	9
34	regulation of biological quality	2.717E-05	38	2953
35	second-messenger-mediated signaling	2.894E-05	12	430
36	regulation of cell development	3.124E-05	14	581
37	positive regulation of hydrolase activity	3.815E-05	15	671
38	synaptic vesicle uncoating	4.326E-05	2	2
39	maintenance of presynaptic active zone structure	4.326E-05	2	2
40	vesicle uncoating	4.326E-05	2	2
41	learning or memory	4.343E-05	9	250
42	negative regulation of locomotion	4.440E-05	7	142
43	calcium-dependent cell-cell adhesion	5.662E-05	4	32
44	cognition	6.423E-05	9	263
45	cell adhesion	7.351E-05	17	883
46	biological adhesion	7.876E-05	17	888
47	regulation of system process	8.397E-05	14	637
48	negative regulation of transport	8.477E-05	10	338
49	multicellular organismal process	9.183E-05	66	6739
50	secretion	1.108E-04	14	654
51	radial glia guided migration of Purkinje cell	1.292E-04	2	3
52	regulation of multicellular organismal process	1.354E-04	28	2036

53	negative regulation of cell migration	1.462E-04	6	120
54	cAMP catabolic process	1.480E-04	3	16
55	negative regulation of cell motility	1.601E-04	6	122
56	regulation of synaptic transmission	1.615E-04	9	297
57	behavior	1.638E-04	13	596
58	regulation of muscle cell differentiation	1.750E-04	6	124
59	positive regulation of exocytosis	1.837E-04	4	43
60	neuron-neuron synaptic transmission	1.883E-04	5	80
61	positive regulation of catalytic activity	1.922E-04	20	1243
62	cyclic nucleotide catabolic process	2.136E-04	3	18
63	negative regulation of cellular component movement	2.170E-04	6	129
64	positive regulation of developmental process	2.231E-04	15	787
65	intracellular signal transduction	2.378E-04	24	1673
66	regulation of insulin secretion	2.475E-04	7	187
67	regulation of synapse structural plasticity	2.573E-04	2	4
68	sensory perception of touch	2.573E-04	2	4
69	negative regulation of endothelial cell differentiation	2.573E-04	2	4
70	regulation of hydrolase activity	2.676E-04	17	984
71	carbohydrate homeostasis	2.887E-04	6	136
72	glucose homeostasis	2.887E-04	6	136
73	regulation of locomotion	2.924E-04	11	470
74	cell morphogenesis involved in neuron differentiation	2.936E-04	13	633
75	regulation of transmission of nerve impulse	2.939E-04	9	322
76	visual learning	3.058E-04	4	49
77	response to electrical stimulus	3.058E-04	4	49
78	cell morphogenesis involved in differentiation	3.240E-04	14	726
79	signaling	3.252E-04	54	5359
80	regulation of neurogenesis	3.374E-04	11	478
81	regulation of peptide hormone secretion	3.608E-04	7	199
82	positive regulation of cell development	3.832E-04	7	201
83	regulation of peptide secretion	4.067E-04	7	203
84	regulation of peptide transport	4.067E-04	7	203
85	regulation of cellular component organization	4.239E-04	20	1321
86	histone H3-K27 methylation	4.270E-04	2	5
87	negative regulation of inclusion body assembly	4.270E-04	2	5
88	activation of phospholipase C activity by metabotropic glutamate receptor signaling pathway	4.270E-04	2	5
89	peptidyl-cysteine methylation	4.270E-04	2	5
90	synaptic transmission, GABAergic	4.525E-04	3	23
91	cellular calcium ion homeostasis	4.653E-04	9	343
92	visual behavior	4.775E-04	4	55
93	positive regulation of molecular function	4.800E-04	21	1437
94	regulation of neurological system process	4.954E-04	9	346
95	generation of neurons	5.179E-04	20	1342
96	regulation of myoblast differentiation	5.820E-04	3	25
97	cellular divalent inorganic cation homeostasis	5.836E-04	9	354
98	calcium ion homeostasis	5.836E-04	9	354
99	regulation of cell motility	6.024E-04	10	432
100	positive regulation of cell differentiation	6.190E-04	12	598
101	synaptic vesicle priming	6.378E-04	2	6
102	regulation of synaptic vesicle fusion to presynaptic membrane	6.378E-04	2	6
103	ion homeostasis	6.434E-04	14	778
104	nucleoside monophosphate catabolic process	6.547E-04	3	26
105	neuromuscular process	6.632E-04	5	105

106	axonogenesis	6.755E-04	12	604
107	positive regulation of neurogenesis	6.845E-04	6	160
108	negative regulation of secretion	7.305E-04	6	162
109	nervous system development	7.310E-04	27	2143
110	divalent inorganic cation homeostasis	7.398E-04	9	366
111	regulation of neurotransmitter secretion	7.537E-04	4	62
112	calcium-mediated signaling	8.007E-04	4	63
113	neuron development	8.144E-04	15	891
114	dendrite morphogenesis	8.170E-04	3	28
115	regulation of nervous system development	8.457E-04	11	534
116	chemical homeostasis	8.668E-04	16	993
117	type B pancreatic cell proliferation	8.890E-04	2	7
118	hindbrain radial glia guided cell migration	8.890E-04	2	7
119	smooth muscle contraction involved in micturition	8.890E-04	2	7
120	brain morphogenesis	9.069E-04	3	29
121	regulation of MAP kinase activity	9.451E-04	8	304
122	regulation of transporter activity	9.617E-04	5	114
123	cell projection morphogenesis	9.774E-04	13	720
124	cation homeostasis	9.975E-04	11	545
125	negative regulation of transporter activity	1.003E-03	3	30
126	activation of MAPK activity	1.028E-03	6	173
127	regulation of cellular component movement	1.038E-03	10	464
128	regulation of cell differentiation	1.051E-03	17	1111
129	neurogenesis	1.090E-03	20	1425
130	neuromuscular synaptic transmission	1.105E-03	3	31
131	regulation of hormone secretion	1.118E-03	7	241
132	positive regulation of transport	1.138E-03	11	554
133	cell part morphogenesis	1.149E-03	13	733
134	regulation of response to stimulus	1.150E-03	29	2441
135	regulation of inclusion body assembly	1.180E-03	2	8
136	Rab protein signal transduction	1.180E-03	2	8
137	positive regulation of long-term neuronal synaptic plasticity	1.180E-03	2	8
138	phosphatidylinositol dephosphorylation	1.180E-03	2	8
139	regulation of molecular function	1.195E-03	28	2330
140	negative regulation of cell proliferation	1.206E-03	12	646
141	neuron projection development	1.207E-03	13	737
142	metal ion homeostasis	1.218E-03	10	474
143	neuron projection morphogenesis	1.238E-03	12	648
144	regulation of developmental process	1.245E-03	21	1548
145	regulation of neurotransmitter transport	1.254E-03	4	71
146	dendrite development	1.254E-03	4	71
147	regulation of cellular catabolic process	1.258E-03	11	561
148	optic nerve morphogenesis	1.511E-03	2	9
149	cell migration in hindbrain	1.511E-03	2	9
150	endothelial cell morphogenesis	1.511E-03	2	9
151	synaptic vesicle maturation	1.511E-03	2	9
152	urinary bladder smooth muscle contraction	1.511E-03	2	9
153	cellular response to electrical stimulus	1.511E-03	2	9
154	positive regulation of lipase activity	1.531E-03	6	187
155	regulation of striated muscle cell differentiation	1.537E-03	4	75
156	regulation of vasoconstriction	1.614E-03	4	76
157	regulation of multicellular organismal development	1.645E-03	18	1262
158	negative regulation of response to stimulus	1.663E-03	13	764
159	positive regulation of muscle cell differentiation	1.694E-03	4	77
160	regulation of cell migration	1.859E-03	9	418

161	protein depolymerization	1.880E-03	2	10
162	urinary tract smooth muscle contraction	1.880E-03	2	10
163	locomotory behavior	1.892E-03	6	195
164	cell morphogenesis	2.046E-03	14	879
165	regulation of gliogenesis	2.135E-03	4	82
166	positive regulation of cell communication	2.254E-03	13	791
167	positive regulation of protein serine/threonine kinase activity	2.274E-03	7	273
168	growth hormone secretion	2.288E-03	2	11
169	retinal cone cell development	2.288E-03	2	11
170	negative regulation of smooth muscle cell migration	2.288E-03	2	11
171	retinal cone cell differentiation	2.288E-03	2	11
172	associative learning	2.331E-03	4	84
173	hindbrain development	2.384E-03	5	140
174	regulation of protein serine/threonine kinase activity	2.394E-03	9	434
175	positive regulation of signaling	2.459E-03	13	799
176	cGMP metabolic process	2.497E-03	3	41
177	cAMP metabolic process	2.497E-03	3	41
178	negative regulation of protein phosphorylation	2.540E-03	4	86
179	multicellular organismal development	2.592E-03	45	4605
180	regulation of protein phosphorylation	2.642E-03	14	904
181	regulation of cell proliferation	2.660E-03	19	1427
182	positive regulation of MAPKKK cascade	2.676E-03	6	209
183	regulation of synaptic vesicle exocytosis	2.734E-03	2	12
184	regulation of lipase activity	2.806E-03	6	211
185	regulation of calcium ion-dependent exocytosis	2.864E-03	3	43
186	cellular component assembly at cellular level	2.994E-03	15	1018
187	synaptic transmission, glutamatergic	3.058E-03	3	44
188	cerebellar cortex development	3.058E-03	3	44
189	cell projection organization	3.154E-03	14	922
190	phospholipid dephosphorylation	3.217E-03	2	13
191	regulation of signal transduction	3.227E-03	22	1788
192	protein methylation	3.242E-03	4	92
193	protein alkylation	3.242E-03	4	92
194	regulation of long-term neuronal synaptic plasticity	3.261E-03	3	45
195	regulation of catabolic process	3.336E-03	11	636
196	cellular ion homeostasis	3.349E-03	12	731
197	cellular component assembly	3.372E-03	19	1458
198	cellular metal ion homeostasis	3.520E-03	9	460
199	regulation of nucleotide catabolic process	3.554E-03	8	376
200	regulation of purine nucleotide catabolic process	3.554E-03	8	376
201	camera-type eye morphogenesis	3.638E-03	4	95
202	adherens junction organization	3.691E-03	3	47
203	peptidyl-cysteine modification	3.737E-03	2	14
204	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	3.737E-03	2	14
205	cellular component morphogenesis	3.746E-03	14	940
206	sensory perception of pain	3.777E-03	4	96
207	response to abiotic stimulus	3.959E-03	13	845
208	neuron differentiation	3.994E-03	15	1050
209	cellular component organization	4.017E-03	41	4177
210	regulation of catalytic activity	4.082E-03	23	1939
211	homeostatic process	4.096E-03	18	1374
212	positive regulation of MAP kinase activity	4.102E-03	6	228
213	cell differentiation	4.141E-03	31	2905

214	positive regulation of insulin-like growth factor receptor signaling pathway	4.294E-03	2	15
215	optic nerve development	4.294E-03	2	15
216	respiratory system process	4.294E-03	2	15
217	serotonin metabolic process	4.294E-03	2	15
218	micturition	4.294E-03	2	15
219	regulation of smooth muscle cell apoptosis	4.294E-03	2	15
220	positive regulation of myoblast differentiation	4.294E-03	2	15
221	regulation of vesicle fusion	4.294E-03	2	15
222	regulation of skeletal muscle fiber development	4.398E-03	3	50
223	vesicle-mediated transport	4.507E-03	14	960
224	photoreceptor cell development	4.650E-03	3	51
225	activation of phospholipase C activity	4.689E-03	5	164
226	response to metal ion	4.700E-03	8	394
227	developmental process	4.737E-03	47	5016
228	positive regulation of phospholipase C activity	4.811E-03	5	165
229	positive regulation of leukocyte degranulation	4.886E-03	2	16
230	camera-type eye photoreceptor cell differentiation	4.886E-03	2	16
231	regulation of endothelial cell differentiation	4.886E-03	2	16
232	positive regulation of mast cell degranulation	4.886E-03	2	16
233	positive regulation of mast cell activation involved in immune response	4.886E-03	2	16
234	regulation of phosphorylation	4.932E-03	14	970
235	response to inorganic substance	5.007E-03	10	577
236	brain development	5.029E-03	11	672
237	localization	5.164E-03	41	4235
238	positive regulation of gliogenesis	5.181E-03	3	53
239	cellular chemical homeostasis	5.366E-03	12	776
240	negative regulation of insulin secretion	5.460E-03	3	54
241	negative regulation of signal transduction	5.700E-03	10	588

MODEL IV – UP

#	GO Processes	pValue	Ratio	
1	DNA packaging	9.229E-11	10	173
2	cellular macromolecular complex subunit organization	2.767E-10	15	618
3	DNA conformation change	4.228E-10	10	202
4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.029E-09	36	4713
5	cellular nitrogen compound metabolic process	7.376E-09	37	5196
6	nitrogen compound metabolic process	1.510E-08	37	5326
7	macromolecular complex subunit organization	2.133E-08	17	1132
8	nucleosome assembly	7.251E-08	7	121
9	chromatin assembly	1.012E-07	7	127
10	nucleosome organization	1.702E-07	7	137
11	cellular macromolecular complex assembly	1.723E-07	11	484
12	chromosome organization	1.862E-07	13	728
13	protein-DNA complex assembly	2.280E-07	7	143
14	chromatin assembly or disassembly	2.280E-07	7	143
15	protein-DNA complex subunit organization	3.303E-07	7	151
16	cellular component organization or biogenesis at cellular level	3.362E-07	27	3367
17	nucleic acid metabolic process	4.320E-07	29	3882
18	mitotic sister chromatid segregation	5.705E-07	5	54
19	sister chromatid segregation	8.190E-07	5	58
20	cell cycle phase	1.091E-06	13	851
21	cellular component organization or biogenesis	1.103E-06	30	4304
22	cellular component organization at cellular level	2.638E-06	25	3253
23	M phase	3.040E-06	10	521
24	cell cycle	3.281E-06	15	1262
25	cellular macromolecule metabolic process	4.666E-06	36	6261
26	macromolecular complex assembly	5.401E-06	13	984
27	cell cycle process	6.502E-06	13	1001
28	cellular component organization	7.304E-06	28	4177
29	macromolecule metabolic process	1.643E-05	37	6885
30	mitotic chromosome condensation	2.007E-05	3	18
31	cellular metabolic process	2.358E-05	42	8579
32	primary metabolic process	2.463E-05	42	8592
33	cellular process	4.196E-05	57	14653
34	mitotic cell cycle	4.765E-05	10	716
35	cellular component biogenesis	5.960E-05	15	1611
36	chromosome segregation	6.834E-05	5	143
37	mitosis	6.886E-05	7	341
38	nuclear division	6.886E-05	7	341
39	organelle organization	6.933E-05	17	2040
40	RNA metabolic process	7.307E-05	23	3419
41	M phase of mitotic cell cycle	7.961E-05	7	349
42	organelle fission	8.855E-05	7	355
43	endocrine system development	1.196E-04	6	258
44	viral infectious cycle	1.196E-04	5	161
45	viral transcription	1.522E-04	4	90
46	viral genome expression	1.522E-04	4	90
47	chromosome condensation	1.690E-04	3	36
48	translational termination	1.801E-04	4	94
49	cellular component assembly at cellular level	1.910E-04	11	1018
50	pancreas development	2.120E-04	5	182

51	chromatin organization	2.141E-04	8	547
52	deoxyribonucleoside diphosphate metabolic process	2.431E-04	2	8
53	metabolic process	2.672E-04	43	9707
54	viral reproductive process	2.848E-04	5	194
55	cellular component assembly	3.120E-04	13	1458
56	cellular protein complex disassembly	3.177E-04	4	109
57	protein complex disassembly	3.524E-04	4	112
58	gene expression	4.537E-04	22	3593
59	mitochondrial DNA replication	4.747E-04	2	11
60	mitochondrial DNA metabolic process	5.685E-04	2	12
61	cellular macromolecular complex disassembly	6.014E-04	4	129
62	macromolecular complex disassembly	6.557E-04	4	132
63	deoxyribonucleotide biosynthetic process	6.706E-04	2	13
64	cellular component disassembly at cellular level	7.094E-04	5	237
65	cellular component disassembly	7.507E-04	5	240
66	protein heterotetramerization	7.809E-04	2	14
67	protein complex subunit organization	8.058E-04	9	837
68	cellular macromolecule biosynthetic process	8.453E-04	21	3497
69	endocrine pancreas development	8.616E-04	4	142
70	macromolecule biosynthetic process	9.475E-04	21	3527
71	cellular biosynthetic process	1.102E-03	24	4362
72	translational elongation	1.250E-03	4	157
73	biosynthetic process	1.598E-03	24	4475
74	nucleoside triphosphate metabolic process	1.736E-03	7	584
75	meiosis	1.786E-03	4	173
76	M phase of meiotic cell cycle	1.786E-03	4	173
77	RNA biosynthetic process	1.912E-03	17	2704
78	meiotic cell cycle	1.941E-03	4	177
79	nucleobase, nucleoside and nucleotide interconversion	1.952E-03	2	22
80	mitochondrial genome maintenance	2.134E-03	2	23
81	regulation of cell cycle process	2.241E-03	6	451
82	regulation of transcription involved in G1/S phase of mitotic cell cycle	2.725E-03	2	26
83	S-adenosylhomocysteine catabolic process	2.988E-03	1	1
84	regulation of mRNA stability involved in response to stress	2.988E-03	1	1
85	nucleoside phosphate metabolic process	3.333E-03	8	837
86	nucleotide metabolic process	3.333E-03	8	837
87	positive regulation of DNA repair	3.862E-03	2	31
88	regulation of cell cycle	4.038E-03	8	864
89	microtubule-based process	4.101E-03	5	354
90	energy coupled proton transport, down electrochemical gradient	4.368E-03	2	33
91	ATP synthesis coupled proton transport	4.368E-03	2	33
92	deoxyribonucleotide metabolic process	4.632E-03	2	34
93	pyrimidine base metabolic process	4.904E-03	2	35
94	microtubule cytoskeleton organization	5.114E-03	4	232
95	nucleotide biosynthetic process	5.114E-03	4	232
96	nucleobase, nucleoside and nucleotide metabolic process	5.120E-03	8	899
97	proximal/distal pattern formation	5.761E-03	2	38
98	nucleoside diphosphate metabolic process	5.761E-03	2	38
99	DNA metabolic process	5.857E-03	7	728
100	virion penetration into host cell	5.966E-03	1	2
101	visceral motor neuron differentiation	5.966E-03	1	2
102	viral envelope fusion with host membrane	5.966E-03	1	2

MODEL IV – DOWN

#	GO Processes	pValue	Ratio	
1	nervous system development	6.461E-15	94	2143
2	neurogenesis	6.233E-13	69	1425
3	generation of neurons	9.573E-12	64	1342
4	multicellular organismal signaling	1.888E-11	45	762
5	transmission of nerve impulse	1.888E-11	45	762
6	system development	2.228E-11	130	3930
7	neuron development	9.212E-11	48	891
8	cell differentiation	1.411E-10	103	2905
9	neuron differentiation	2.916E-10	52	1050
10	cellular developmental process	6.149E-10	103	2981
11	synaptic transmission	6.950E-10	39	670
12	anatomical structure development	9.746E-10	134	4329
13	multicellular organismal development	8.204E-09	137	4605
14	cell development	5.806E-08	59	1482
15	developmental process	9.762E-08	142	5016
16	homophilic cell adhesion	2.746E-07	15	154
17	cAMP catabolic process	3.166E-07	6	16
18	cyclic nucleotide catabolic process	7.106E-07	6	18
19	ethanolamine-containing compound metabolic process	7.627E-07	9	54
20	cognition	8.022E-07	19	263
21	calcium-dependent cell-cell adhesion	1.948E-06	7	32
22	neuron projection development	2.128E-06	34	737
23	cell-cell signaling	2.530E-06	43	1057
24	cell projection organization	3.061E-06	39	922
25	cell communication	4.259E-06	52	1416
26	multicellular organismal process	4.395E-06	171	6739
27	cellular biogenic amine metabolic process	5.056E-06	13	147
28	phosphatidylcholine metabolic process	5.488E-06	7	37
29	learning or memory	6.854E-06	17	250
30	nucleoside monophosphate catabolic process	7.744E-06	6	26
31	inner ear receptor cell development	1.122E-05	7	41
32	synapse assembly	1.195E-05	8	57
33	cell morphogenesis involved in neuron differentiation	1.388E-05	29	633
34	cGMP catabolic process	1.525E-05	4	9
35	axonogenesis	1.581E-05	28	604
36	cellular component assembly	2.003E-05	51	1458
37	synapse organization	2.076E-05	11	121
38	regulation of fatty acid biosynthetic process	2.121E-05	7	45
39	neuron projection morphogenesis	2.140E-05	29	648
40	ovulation	2.285E-05	6	31
41	central nervous system development	2.485E-05	36	900
42	detection of calcium ion	2.504E-05	4	10
43	long-chain fatty acid transport	2.845E-05	7	47
44	response to methylmercury	3.019E-05	5	20
45	regulation of lipid metabolic process	3.263E-05	16	254
46	fatty acid transport	3.578E-05	8	66
47	neuron migration	3.875E-05	10	107
48	carnitine shuttle	3.875E-05	4	11
49	cell adhesion	3.890E-05	35	883
50	cell activation	3.893E-05	32	775
51	regulation of localization	4.001E-05	53	1577
52	platelet activation	4.050E-05	18	316

53	biological adhesion	4.361E-05	35	888
54	cell projection morphogenesis	5.787E-05	30	720
55	chemokine metabolic process	6.702E-05	3	5
56	axon guidance	7.963E-05	22	459
57	cell part morphogenesis	7.977E-05	30	733
58	behavior	8.681E-05	26	596
59	signaling	8.896E-05	136	5359
60	synaptic vesicle transport	9.055E-05	8	75
61	monocarboxylic acid transport	1.167E-04	9	99
62	cAMP metabolic process	1.188E-04	6	41
63	platelet activating factor biosynthetic process	1.321E-04	3	6
64	negative regulation of cardiac muscle contraction	1.321E-04	3	6
65	cellular component biogenesis	1.330E-04	52	1611
66	cellular component morphogenesis	1.339E-04	35	940
67	extracellular structure organization	1.494E-04	16	289
68	regulation of microtubule polymerization or depolymerization	1.560E-04	6	43
69	cell morphogenesis involved in differentiation	1.588E-04	29	726
70	inner ear receptor cell differentiation	1.741E-04	7	62
71	protein complex assembly	1.743E-04	29	730
72	intracellular signal transduction	1.820E-04	53	1673
73	protein complex biogenesis	1.867E-04	29	733
74	anatomical structure morphogenesis	1.924E-04	64	2141
75	positive regulation of lipid biosynthetic process	1.927E-04	7	63
76	carnitine transport	1.981E-04	4	16
77	cellular response to antibiotic	1.981E-04	4	16
78	betaine transport	1.981E-04	4	16
79	regulation of lipid biosynthetic process	1.995E-04	10	130
80	associative learning	2.016E-04	8	84
81	cellular component organization	2.177E-04	109	4177
82	positive regulation of response to external stimulus	2.263E-04	12	184
83	platelet activating factor metabolic process	2.280E-04	3	7
84	response to calcium ion	2.402E-04	10	133
85	localization	2.420E-04	110	4235
86	intracellular protein kinase cascade	2.800E-04	24	571
87	learning	3.052E-04	10	137
88	mechanoreceptor differentiation	3.112E-04	7	68
89	detection of temperature stimulus involved in sensory perception of pain	3.596E-04	3	8
90	detection of temperature stimulus involved in sensory perception	3.596E-04	3	8
91	female gonad development	3.631E-04	10	140
92	regulation of iron ion transport	3.632E-04	2	2
93	toluene-containing compound metabolic process	3.632E-04	2	2
94	positive regulation of nucleoside transport	3.632E-04	2	2
95	toluene metabolic process	3.632E-04	2	2
96	cellular response to methylmercury	3.632E-04	2	2
97	platelet-derived growth factor receptor-alpha signaling pathway	3.632E-04	2	2
98	negative regulation of iron ion transport	3.632E-04	2	2
99	regulation of nucleoside transport	3.632E-04	2	2
100	regulation of cell adhesion	3.661E-04	16	313
101	regulation of receptor activity	3.725E-04	7	70
102	response to estradiol stimulus	3.848E-04	12	195
103	cell morphogenesis	3.852E-04	32	879
104	intracellular lipid transport	4.033E-04	4	19
105	Leydig cell differentiation	4.033E-04	4	19

106	ovulation from ovarian follicle	4.033E-04	4	19
107	regulation of vesicle-mediated transport	4.088E-04	15	285
108	response to external stimulus	4.149E-04	48	1522
109	regulation of transport	4.274E-04	41	1238
110	glycerolipid catabolic process	4.351E-04	5	34
111	positive regulation of lipid metabolic process	4.393E-04	9	118
112	cellular component organization or biogenesis	4.541E-04	110	4304
113	neurological system process	4.756E-04	60	2040
114	regulation of microtubule polymerization	4.965E-04	4	20
115	detection of abiotic stimulus	5.280E-04	9	121
116	glycerophospholipid catabolic process	5.317E-04	3	9
117	regulation of mucus secretion	5.317E-04	3	9
118	synaptic vesicle maturation	5.317E-04	3	9
119	regulation of fatty acid metabolic process	5.394E-04	8	97
120	regulation of lipid catabolic process	5.540E-04	6	54
121	regulation of catabolic process	5.652E-04	25	636
122	response to wounding	6.159E-04	41	1261
123	carboxylic acid transport	6.671E-04	13	237
124	organic acid transport	7.212E-04	13	239
125	negative regulation of lipid catabolic process	7.274E-04	4	22
126	negative regulation of kinase activity	7.397E-04	11	181
127	regulation of prostaglandin biosynthetic process	7.489E-04	3	10
128	positive regulation of prostaglandin biosynthetic process	7.489E-04	3	10
129	detection of temperature stimulus	7.489E-04	3	10
130	system process	7.545E-04	69	2474
131	development of primary female sexual characteristics	7.679E-04	10	154
132	cell-cell adhesion	7.765E-04	18	402
133	regulation of cellular component organization	8.236E-04	42	1321
134	phosphatidylcholine biosynthetic process	8.674E-04	4	23
135	synaptic transmission, GABAergic	8.674E-04	4	23
136	energy reserve metabolic process	8.781E-04	12	214
137	regulation of signaling	9.249E-04	61	2139
138	sensory perception of mechanical stimulus	9.255E-04	11	186
139	ion transport	9.936E-04	35	1049
140	retina vasculature development in camera-type eye	1.015E-03	3	11
141	CDP-choline pathway	1.015E-03	3	11
142	negative regulation of striated muscle contraction	1.015E-03	3	11
143	sensory perception of temperature stimulus	1.015E-03	3	11
144	synaptic vesicle endocytosis	1.025E-03	4	24
145	positive regulation of cell-matrix adhesion	1.025E-03	4	24
146	locomotion	1.035E-03	37	1132
147	wound healing	1.052E-03	28	778
148	cellular response to endogenous stimulus	1.055E-03	27	740
149	clustering of voltage-gated potassium channels	1.076E-03	2	3
150	metanephric glomerulus vasculature morphogenesis	1.076E-03	2	3
151	negative regulation of circadian sleep/wake cycle, non-REM sleep	1.076E-03	2	3
152	negative regulation of neurotrophin production	1.076E-03	2	3
153	negative regulation of mucus secretion	1.076E-03	2	3
154	regulation of neurotrophin production	1.076E-03	2	3
155	cell proliferation in midbrain	1.076E-03	2	3
156	metanephric glomerular capillary formation	1.076E-03	2	3
157	chemokine production	1.076E-03	2	3
158	metanephric glomerulus morphogenesis	1.076E-03	2	3
159	detection of external stimulus	1.099E-03	9	134

160	hemostasis	1.113E-03	24	630
161	protein phosphorylation	1.168E-03	31	900
162	negative regulation of transferase activity	1.198E-03	11	192
163	estrogen metabolic process	1.202E-03	4	25
164	alcohol metabolic process	1.213E-03	23	597
165	brain development	1.228E-03	25	672
166	chemotaxis	1.228E-03	25	672
167	positive regulation of inflammatory response	1.235E-03	8	110
168	female sex differentiation	1.242E-03	10	164
169	regulation of protein phosphorylation	1.252E-03	31	904
170	negative regulation of signaling	1.265E-03	24	636
171	sensory organ development	1.267E-03	21	526
172	taxis	1.280E-03	25	674
173	retina development in camera-type eye	1.284E-03	9	137
174	response to cadmium ion	1.308E-03	5	43
175	neuronal ion channel clustering	1.335E-03	3	12
176	negative regulation of cell communication	1.347E-03	24	639
177	locomotory behavior	1.357E-03	11	195
178	regulation of transmission of nerve impulse	1.414E-03	15	322
179	behavioral fear response	1.453E-03	5	44
180	regulation of body fluid levels	1.465E-03	27	757
181	regulation of cell-substrate adhesion	1.468E-03	8	113
182	regulation of signal transduction	1.494E-03	52	1788
183	protein complex subunit organization	1.532E-03	29	837
184	response to estrogen stimulus	1.543E-03	14	292
185	regulation of microtubule-based process	1.572E-03	7	89
186	innervation	1.619E-03	4	27
187	regulation of neurotransmitter levels	1.625E-03	10	170
188	negative regulation of protein kinase activity	1.625E-03	10	170
189	phospholipid biosynthetic process	1.647E-03	9	142
190	regulation of Ras GTPase activity	1.660E-03	11	200
191	regulation of germinal center formation	1.710E-03	3	13
192	positive regulation of protein dephosphorylation	1.710E-03	3	13
193	amino acid transport	1.729E-03	9	143
194	response to inorganic substance	1.752E-03	22	577
195	behavioral defense response	1.778E-03	5	46
196	glycerophospholipid biosynthetic process	1.788E-03	7	91
197	response to organic nitrogen	1.797E-03	15	330
198	regulation of synaptic transmission	1.807E-03	14	297
199	glycerophospholipid metabolic process	1.850E-03	10	173
200	dendrite morphogenesis	1.860E-03	4	28
201	cGMP-mediated signaling	1.860E-03	4	28
202	amine transport	1.867E-03	11	203
203	response to hydrogen peroxide	1.902E-03	9	145
204	cell cycle arrest	2.013E-03	10	175
205	gonad development	2.026E-03	13	268
206	ovum-producing ovary development	2.039E-03	8	119
207	protein oligomerization	2.070E-03	16	369
208	phospholipid metabolic process	2.093E-03	13	269
209	regulation of multicellular organismal process	2.097E-03	57	2036
210	regulation of protein kinase activity	2.102E-03	24	661
211	regulation of cell projection organization	2.108E-03	14	302
212	lysophospholipid transport	2.124E-03	2	4
213	fractalkine metabolic process	2.124E-03	2	4
214	maintenance of cell polarity	2.124E-03	2	4

215	glomerular capillary formation	2.124E-03	2	4
216	glomerulus vasculature morphogenesis	2.124E-03	2	4
217	cellular response to luteinizing hormone stimulus	2.124E-03	2	4
218	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid transport	2.124E-03	2	4
219	negative regulation of microtubule polymerization or depolymerization	2.126E-03	4	29
220	protein kinase C signaling cascade	2.146E-03	3	14
221	positive regulation of dephosphorylation	2.146E-03	3	14
222	positive regulation of icosanoid secretion	2.146E-03	3	14
223	negative regulation of glutamate secretion	2.146E-03	3	14
224	positive regulation of prostaglandin secretion	2.146E-03	3	14
225	regulation of prostaglandin secretion	2.146E-03	3	14
226	negative regulation of synaptic transmission	2.153E-03	5	48
227	regulation of fatty acid oxidation	2.153E-03	5	48
228	regulation of response to stimulus	2.175E-03	66	2441
229	cellular component assembly at cellular level	2.192E-03	33	1018
230	negative regulation of transport	2.263E-03	15	338
231	positive regulation of cell-substrate adhesion	2.343E-03	6	71
232	positive regulation of fatty acid metabolic process	2.360E-03	5	49
233	fear response	2.360E-03	5	49
234	quaternary ammonium group transport	2.416E-03	4	30
235	neuron maturation	2.416E-03	4	30
236	sensory perception of pain	2.429E-03	7	96
237	regulation of transferase activity	2.479E-03	25	708
238	anion transport	2.483E-03	12	242
239	regulation of protein localization	2.531E-03	15	342
240	cochlea development	2.582E-03	5	50
241	response to oxygen levels	2.630E-03	16	378
242	regulation of circadian sleep/wake cycle, non-REM sleep	2.645E-03	3	15
243	serotonin metabolic process	2.645E-03	3	15
244	positive regulation of microtubule polymerization or depolymerization	2.645E-03	3	15
245	cellular response to hormone stimulus	2.658E-03	22	597
246	response to reactive oxygen species	2.680E-03	10	182
247	phosphate metabolic process	2.748E-03	43	1451
248	phosphorus metabolic process	2.783E-03	43	1452
249	regulation of neurological system process	2.825E-03	15	346
250	regulation of microtubule cytoskeleton organization	2.889E-03	6	74
251	inner ear development	2.899E-03	10	184
252	negative regulation of molecular function	3.122E-03	29	879
253	negative regulation of synaptic transmission, GABAergic	3.210E-03	3	16
254	cellular response to peptide hormone stimulus	3.229E-03	16	386
255	regulation of metal ion transport	3.243E-03	11	218
256	regulation of nervous system development	3.409E-03	20	534
257	regulation of kinase activity	3.435E-03	24	687
258	lipid localization	3.475E-03	11	220
259	facial nucleus development	3.496E-03	2	5
260	regulation of sphingolipid biosynthetic process	3.496E-03	2	5
261	commissural neuron axon guidance	3.496E-03	2	5
262	testosterone biosynthetic process	3.496E-03	2	5
263	insecticide metabolic process	3.496E-03	2	5
264	response to luteinizing hormone stimulus	3.496E-03	2	5
265	regulation of ceramide biosynthetic process	3.496E-03	2	5
266	cellular response to mercury ion	3.496E-03	2	5
267	positive regulation of cell adhesion	3.540E-03	9	159

268	transport	3.618E-03	88	3513
269	regulation of cell-matrix adhesion	3.623E-03	5	54
270	regulation of biological quality	3.629E-03	76	2953
271	response to temperature stimulus	3.645E-03	10	190
272	regulation of phosphorylation	3.649E-03	31	970
273	regulation of Ras protein signal transduction	3.753E-03	14	322
274	negative regulation of MAPKKK cascade	3.760E-03	6	78
275	relaxation of muscle	3.843E-03	3	17
276	regulation of icosanoid secretion	3.843E-03	3	17
277	positive regulation of fatty acid transport	3.843E-03	3	17
278	luteinization	3.843E-03	3	17
279	regulation of synaptic transmission, GABAergic	3.852E-03	4	34
280	ion transmembrane transport	3.859E-03	20	540
281	negative regulation of transmission of nerve impulse	3.924E-03	5	55
282	response to metal ion	3.935E-03	16	394
283	peptidyl-tyrosine dephosphorylation	4.011E-03	7	105
284	regulation of neuron differentiation	4.032E-03	16	395
285	glycerolipid biosynthetic process	4.052E-03	8	133
286	organophosphate metabolic process	4.099E-03	13	291
287	forebrain development	4.188E-03	15	361
288	response to lithium ion	4.242E-03	5	56
289	regulation of activated T cell proliferation	4.284E-03	4	35
290	development of primary sexual characteristics	4.464E-03	13	294
291	coagulation	4.486E-03	22	624
292	blood coagulation	4.486E-03	22	624
293	response to steroid hormone stimulus	4.486E-03	22	624
294	cyclic nucleotide metabolic process	4.530E-03	6	81
295	response to activity	4.530E-03	6	81
296	positive regulation of macrophage derived foam cell differentiation	4.547E-03	3	18
297	positive regulation of receptor activity	4.547E-03	3	18
298	transmembrane receptor protein tyrosine kinase signaling pathway	4.570E-03	22	625

MODEL V – UP

#	GO Processes	pValue	Ratio	
1	cell cycle process	1.581E-38	89	1001
2	mitotic cell cycle	4.771E-37	75	716
3	cell cycle	7.961E-37	97	1262
4	cell cycle phase	3.493E-36	80	851
5	cellular component organization or biogenesis	2.648E-28	168	4304
6	cellular component organization	2.944E-28	165	4177
7	M phase	3.031E-27	55	521
8	cellular component organization or biogenesis at cellular level	1.002E-25	141	3367
9	cellular component organization at cellular level	1.264E-25	138	3253
10	cell division	2.947E-25	48	422
11	M phase of mitotic cell cycle	4.813E-25	44	349
12	regulation of cell cycle process	7.137E-25	49	451
13	regulation of cell cycle	8.817E-24	65	864
14	mitosis	1.547E-23	42	341
15	nuclear division	1.547E-23	42	341
16	cell cycle checkpoint	6.250E-23	37	262
17	organelle fission	7.532E-23	42	355
18	regulation of cell cycle arrest	3.978E-22	37	276
19	interphase of mitotic cell cycle	9.203E-22	44	420
20	interphase	1.780E-21	44	427
21	cellular process	2.570E-21	329	14653
22	organelle organization	4.549E-20	96	2040
23	macromolecular complex subunit organization	7.588E-19	67	1132
24	cellular macromolecule metabolic process	2.534E-18	188	6261
25	DNA conformation change	2.156E-17	28	202
26	organ development	7.591E-17	111	2875
27	DNA metabolic process	9.915E-17	50	728
28	macromolecule metabolic process	1.076E-16	196	6885
29	developmental process	2.032E-16	158	5016
30	nucleic acid metabolic process	3.224E-16	133	3882
31	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	3.566E-16	151	4713
32	regulation of macromolecule metabolic process	3.637E-16	150	4667
33	DNA packaging	4.299E-16	25	173
34	S phase of mitotic cell cycle	5.980E-16	23	143
35	cellular nitrogen compound metabolic process	9.778E-16	160	5196
36	S phase	1.302E-15	23	148
37	G1/S transition of mitotic cell cycle	1.643E-15	27	219
38	multicellular organismal development	1.678E-15	147	4605
39	nitrogen compound metabolic process	1.776E-15	162	5326
40	cellular macromolecular complex subunit organization	2.251E-15	44	618
41	regulation of metabolic process	5.908E-15	168	5690
42	chromosome segregation	6.811E-15	22	143
43	cellular metabolic process	9.084E-15	222	8579
44	positive regulation of biological process	1.067E-14	126	3736
45	primary metabolic process	1.101E-14	222	8592
46	positive regulation of cellular process	1.119E-14	118	3385
47	negative regulation of cellular process	1.220E-14	109	3002
48	positive regulation of cell proliferation	2.183E-14	50	834
49	regulation of cell proliferation	2.369E-14	68	1427
50	anatomical structure development	2.625E-14	138	4329

51	negative regulation of biological process	2.742E-14	115	3296
52	chromosome organization	4.055E-14	46	728
53	anatomical structure morphogenesis	8.361E-14	86	2141
54	system development	8.438E-14	128	3930
55	cellular component disassembly at cellular level	9.208E-14	26	237
56	cellular component disassembly	1.241E-13	26	240
57	regulation of mitotic cell cycle	1.755E-13	31	354
58	microtubule-based process	1.755E-13	31	354
59	protein-DNA complex subunit organization	2.211E-13	21	151
60	metabolic process	3.912E-13	237	9707
61	regulation of cellular metabolic process	4.373E-13	149	5010
62	cell proliferation	6.686E-13	45	757
63	protein-DNA complex assembly	7.473E-13	20	143
64	regulation of primary metabolic process	1.290E-12	147	4978
65	positive regulation of metabolic process	1.796E-12	79	1984
66	biosynthetic process	1.960E-12	136	4475
67	cellular biosynthetic process	3.215E-12	133	4362
68	nucleosome organization	3.297E-12	19	137
69	nucleosome assembly	3.659E-12	18	121
70	biological regulation	6.049E-12	249	10630
71	macromolecule biosynthetic process	6.786E-12	114	3527
72	viral infectious cycle	7.081E-12	20	161
73	chromatin assembly or disassembly	7.170E-12	19	143
74	chromatin assembly	8.494E-12	18	127
75	positive regulation of macromolecule metabolic process	1.046E-11	73	1818
76	macromolecular complex assembly	1.066E-11	50	984
77	response to stress	1.634E-11	106	3216
78	sister chromatid segregation	1.737E-11	13	58
79	protein complex subunit organization	2.020E-11	45	837
80	microtubule cytoskeleton organization	2.092E-11	23	232
81	positive regulation of cellular metabolic process	2.184E-11	74	1886
82	viral reproductive process	3.017E-11	21	194
83	mitotic cell cycle checkpoint	3.032E-11	19	155
84	regulation of cellular process	3.800E-11	228	9537
85	regulation of biological process	3.868E-11	238	10123
86	cellular macromolecule biosynthetic process	4.662E-11	111	3497
87	regulation of gene expression	4.964E-11	117	3775
88	cellular component biogenesis	5.420E-11	66	1611
89	spindle organization	5.847E-11	14	77
90	DNA integrity checkpoint	8.178E-11	18	145
91	mitotic prometaphase	1.148E-10	15	96
92	regulation of interphase of mitotic cell cycle	1.250E-10	19	168
93	regulation of cellular protein metabolic process	1.361E-10	59	1381
94	multi-organism process	1.430E-10	60	1420
95	DNA replication	1.620E-10	22	234
96	cellular response to stress	2.154E-10	52	1142
97	positive regulation of molecular function	2.285E-10	60	1437
98	negative regulation of cell differentiation	2.464E-10	31	469
99	translation	2.940E-10	29	417
100	response to DNA damage stimulus	3.629E-10	36	624
101	regulation of protein kinase activity	4.711E-10	37	661
102	regulation of protein metabolic process	5.589E-10	62	1547
103	regulation of cellular component organization	5.764E-10	56	1321
104	regulation of molecular function	7.720E-10	81	2330

105	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	8.024E-10	14	93
106	cellular component assembly	1.095E-09	59	1458
107	regulation of protein modification process	1.282E-09	49	1093
108	regulation of kinase activity	1.358E-09	37	687
109	viral reproduction	1.497E-09	30	476
110	cellular protein metabolic process	1.804E-09	94	2939
111	protein metabolic process	1.812E-09	107	3529
112	mitotic sister chromatid segregation	1.914E-09	11	54
113	DNA damage checkpoint	2.305E-09	16	137
114	G2/M transition of mitotic cell cycle	2.594E-09	17	158
115	regulation of transferase activity	3.063E-09	37	708
116	regulation of catalytic activity	3.128E-09	70	1939
117	tissue development	3.211E-09	55	1347
118	regulation of cyclin-dependent protein kinase activity	3.618E-09	14	104
119	regulation of developmental process	3.946E-09	60	1548
120	regulation of DNA metabolic process	4.035E-09	20	229
121	cellular protein complex disassembly	6.743E-09	14	109
122	cellular macromolecular complex disassembly	7.797E-09	15	129
123	regulation of protein phosphorylation	7.910E-09	42	904
124	mammary gland development	7.951E-09	17	170
125	negative regulation of developmental process	7.961E-09	32	573
126	cellular macromolecular complex assembly	8.828E-09	29	484
127	negative regulation of macromolecule metabolic process	9.384E-09	55	1389
128	positive regulation of cell cycle process	9.568E-09	16	151
129	protein complex disassembly	9.638E-09	14	112
130	multicellular organismal process	9.836E-09	169	6739
131	macromolecular complex disassembly	1.071E-08	15	132
132	response to abiotic stimulus	1.107E-08	40	845
133	regulation of macromolecule biosynthetic process	1.330E-08	107	3657
134	regulation of phosphorus metabolic process	1.649E-08	44	999
135	regulation of phosphate metabolic process	1.649E-08	44	999
136	chromosome localization	1.818E-08	8	28
137	establishment of chromosome localization	1.818E-08	8	28
138	regulation of organelle organization	1.819E-08	28	470
139	response to drug	1.835E-08	34	658
140	regulation of phosphorylation	2.025E-08	43	970
141	gene expression	2.079E-08	105	3593
142	interspecies interaction between organisms	2.088E-08	30	534
143	regulation of biosynthetic process	2.104E-08	112	3925
144	positive regulation of cell cycle	2.174E-08	15	139
145	embryo development	2.823E-08	46	1091
146	positive regulation of biosynthetic process	2.833E-08	56	1474
147	regulation of cellular macromolecule biosynthetic process	2.878E-08	104	3568
148	positive regulation of catalytic activity	2.960E-08	50	1243
149	organ morphogenesis	3.526E-08	43	989
150	negative regulation of metabolic process	4.381E-08	56	1493
151	regulation of multicellular organismal development	4.770E-08	50	1262
152	reproductive process	5.220E-08	55	1461
153	viral genome expression	5.343E-08	12	90
154	viral transcription	5.343E-08	12	90
155	regulation of cell death	5.489E-08	57	1543
156	neurogenesis	5.665E-08	54	1425
157	embryonic morphogenesis	5.991E-08	30	560
158	positive regulation of organelle organization	6.633E-08	17	196

159	reproduction	6.851E-08	55	1473
160	positive regulation of nitrogen compound metabolic process	7.607E-08	52	1359
161	regulation of cellular biosynthetic process	8.471E-08	109	3881
162	translational termination	8.751E-08	12	94
163	positive regulation of chromosome segregation	9.108E-08	4	4
164	regulation of biological quality	9.567E-08	89	2953
165	regulation of apoptosis	9.785E-08	55	1489
166	DNA recombination	1.106E-07	17	203
167	cytoskeleton organization	1.143E-07	34	710
168	response to mechanical stimulus	1.146E-07	18	228
169	chromatin organization	1.251E-07	29	547
170	regulation of programmed cell death	1.301E-07	55	1502
171	pancreas development	1.345E-07	16	182
172	response to stimulus	1.389E-07	187	7952
173	positive regulation of macromolecule biosynthetic process	1.697E-07	50	1315
174	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.861E-07	50	1319
175	response to external stimulus	1.998E-07	55	1522
176	regulation of protein serine/threonine kinase activity	2.042E-07	25	434
177	positive regulation of cellular biosynthetic process	2.309E-07	53	1448
178	regulation of nitrogen compound metabolic process	2.572E-07	111	4061
179	chordate embryonic development	2.819E-07	32	669
180	M/G1 transition of mitotic cell cycle	3.350E-07	11	87
181	RNA metabolic process	3.787E-07	97	3419
182	embryo development ending in birth or egg hatching	3.913E-07	32	679
183	anti-apoptosis	4.407E-07	20	304
184	anatomical structure formation involved in morphogenesis	4.827E-07	35	791
185	regulation of multicellular organismal process	5.479E-07	66	2036
186	regulation of G2/M transition of mitotic cell cycle	5.580E-07	8	42
187	G1 phase of mitotic cell cycle	6.787E-07	9	58
188	positive regulation of gene expression	6.914E-07	46	1219
189	generation of neurons	7.514E-07	49	1342
190	response to antibiotic	7.887E-07	9	59
191	mitotic spindle organization	8.502E-07	7	31
192	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	9.301E-07	107	3968
193	wound healing	9.386E-07	34	778
194	positive regulation of epithelial cell proliferation	1.009E-06	14	162
195	apoptosis	1.177E-06	39	971
196	response to inorganic substance	1.215E-06	28	577
197	G1 phase	1.216E-06	9	62
198	regeneration	1.279E-06	16	215
199	endocrine pancreas development	1.282E-06	13	142
200	cellular component assembly at cellular level	1.467E-06	40	1018
201	cellular response to fatty acid	1.592E-06	6	22
202	response to organic substance	1.659E-06	72	2368
203	aging	1.741E-06	20	332
204	posttranscriptional regulation of gene expression	1.784E-06	22	393
205	G2 phase	1.802E-06	5	13
206	G2 phase of mitotic cell cycle	1.802E-06	5	13
207	organelle localization	1.819E-06	15	195
208	positive regulation of cellular component organization	1.832E-06	26	522
209	protein complex assembly	1.867E-06	32	730
210	programmed cell death	1.884E-06	39	990
211	skeletal system development	1.993E-06	23	427

212	protein complex biogenesis	2.035E-06	32	733
213	cellular macromolecule catabolic process	2.065E-06	28	593
214	regulation of cell differentiation	2.111E-06	42	1111
215	metaphase plate congression	2.123E-06	6	23
216	chromosome condensation	2.504E-06	7	36
217	G2/M transition checkpoint	2.504E-06	7	36
218	muscle structure development	2.619E-06	25	499
219	negative regulation of cellular metabolic process	2.757E-06	48	1364
220	negative regulation of epithelial cell differentiation	2.789E-06	6	24
221	regulation of epithelial cell proliferation	2.859E-06	17	256
222	organ regeneration	2.979E-06	11	108
223	positive regulation of cellular protein metabolic process	3.280E-06	27	573
224	translational elongation	3.955E-06	13	157
225	cellular response to lipid	4.100E-06	8	54
226	positive regulation of protein metabolic process	4.111E-06	29	650
227	cellular component disassembly involved in apoptosis	4.226E-06	10	91
228	organelle assembly	4.226E-06	10	91
229	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4.226E-06	10	91
230	positive regulation of protein kinase activity	4.275E-06	23	447
231	regulation of RNA metabolic process	4.280E-06	92	3366
232	positive regulation of peptidase activity	4.470E-06	12	135
233	regulation of epidermal cell differentiation	4.632E-06	6	26
234	phosphatidylinositol-mediated signaling	4.669E-06	10	92
235	positive regulation of RNA metabolic process	4.879E-06	43	1189
236	cell differentiation	5.057E-06	82	2905
237	circulatory system development	5.085E-06	33	803
238	cardiovascular system development	5.085E-06	33	803
239	embryonic skeletal system morphogenesis	5.151E-06	10	93
240	inositol lipid-mediated signaling	5.151E-06	10	93
241	positive regulation of attachment of spindle microtubules to kinetochore	5.264E-06	3	3
242	spindle checkpoint	5.267E-06	7	40
243	response to lithium ion	5.430E-06	8	56
244	astrocyte cell migration	6.031E-06	4	8
245	positive regulation of vesicle fusion	6.031E-06	4	8
246	macromolecule catabolic process	6.534E-06	30	702
247	cell death	6.713E-06	42	1164
248	gland development	6.963E-06	20	364
249	positive regulation of kinase activity	7.339E-06	23	462
250	death	7.766E-06	42	1171
251	negative regulation of apoptosis	7.924E-06	30	709
252	negative regulation of cell death	7.982E-06	31	746
253	proteasomal ubiquitin-dependent protein catabolic process	8.400E-06	14	194
254	translational initiation	8.556E-06	9	78
255	gliogenesis	8.864E-06	13	169
256	proteasomal protein catabolic process	8.909E-06	14	195
257	lactation	9.205E-06	8	60
258	response to wounding	9.251E-06	44	1261
259	response to ionizing radiation	9.345E-06	12	145
260	positive regulation of transcription, DNA-dependent	9.617E-06	41	1141
261	embryonic skeletal system development	9.752E-06	11	122
262	negative regulation of programmed cell death	9.842E-06	30	717
263	mitotic cell cycle G1/S transition DNA damage checkpoint	1.055E-05	9	80
264	positive regulation of transferase activity	1.110E-05	23	474

265	regulation of transcription, DNA-dependent	1.113E-05	89	3300
266	mitotic metaphase plate congression	1.116E-05	5	18
267	mitotic chromosome condensation	1.116E-05	5	18
268	DNA replication-independent nucleosome assembly	1.126E-05	6	30
269	DNA replication-independent nucleosome organization	1.126E-05	6	30
270	CenH3-containing nucleosome assembly at centromere	1.126E-05	6	30
271	regulation of epidermis development	1.189E-05	7	45
272	nervous system development	1.263E-05	64	2143
273	endocrine system development	1.324E-05	16	258
274	cellular developmental process	1.345E-05	82	2981
275	response to nutrient	1.386E-05	22	447
276	muscle organ development	1.399E-05	19	350
277	RNA biosynthetic process	1.446E-05	76	2704
278	regulation of chromosome segregation	1.494E-05	5	19
279	regulation of keratinocyte differentiation	1.494E-05	5	19
280	DNA-dependent DNA replication	1.576E-05	9	84
281	regulation of mitosis	1.662E-05	10	106
282	regulation of nuclear division	1.662E-05	10	106
283	chromatin remodeling at centromere	1.669E-05	6	32
284	DNA repair	1.721E-05	21	420
285	negative regulation of epidermal cell differentiation	1.760E-05	4	10
286	regulation of prostaglandin biosynthetic process	1.760E-05	4	10
287	DNA unwinding involved in replication	1.760E-05	4	10
288	positive regulation of prostaglandin biosynthetic process	1.760E-05	4	10
289	negative regulation of gene expression	1.854E-05	37	1012
290	protein import into nucleus	1.918E-05	11	131
291	response to glucocorticoid stimulus	1.931E-05	16	266
292	negative regulation of monocyte differentiation	2.078E-05	3	4
293	regulation of attachment of spindle microtubules to kinetochore	2.078E-05	3	4
294	'de novo' IMP biosynthetic process	2.078E-05	3	4
295	response to vitamin B3	2.078E-05	3	4
296	nuclear import	2.372E-05	11	134
297	tissue morphogenesis	2.666E-05	24	536
298	cellular process involved in reproduction	2.706E-05	22	467
299	embryonic organ morphogenesis	2.723E-05	15	244
300	establishment of organelle localization	2.724E-05	11	136
301	regulation of body fluid levels	2.749E-05	30	757
302	regulation of caspase activity	2.764E-05	13	188
303	positive regulation of protein modification process	2.795E-05	22	468
304	DNA strand elongation involved in DNA replication	2.861E-05	6	35
305	response to biotic stimulus	2.978E-05	32	837
306	intracellular signal transduction	3.310E-05	52	1673
307	muscle cell differentiation	3.341E-05	17	309
308	negative regulation of cellular component organization	3.362E-05	19	373
309	histone exchange	3.383E-05	6	36
310	regulation of ubiquitin-protein ligase activity	3.387E-05	10	115
311	homeostatic process	3.476E-05	45	1374
312	regulation of cell development	3.493E-05	25	581
313	regulation of epithelial cell differentiation	3.591E-05	8	72
314	positive regulation of caspase activity	3.650E-05	10	116
315	regulation of neurogenesis	3.839E-05	22	478
316	DNA strand elongation	3.979E-05	6	37
317	mitotic cell cycle G1/S transition checkpoint	4.252E-05	9	95
318	body fluid secretion	4.252E-05	9	95

319	regulation of ligase activity	4.546E-05	10	119
320	G1/S transition checkpoint	4.620E-05	9	96
321	response to corticosteroid stimulus	4.647E-05	16	286
322	mitotic cell cycle spindle checkpoint	4.656E-05	6	38
323	response to chemical stimulus	4.714E-05	101	4020
324	negative regulation of myeloid cell differentiation	4.837E-05	8	75
325	regulation of cell migration	5.055E-05	20	418
326	T cell migration	5.129E-05	3	5
327	L-serine biosynthetic process	5.129E-05	3	5
328	negative regulation of cell cycle	5.376E-05	17	321
329	activation of caspase activity	5.439E-05	9	98
330	regulation of DNA replication	5.624E-05	10	122
331	regulation of localization	5.779E-05	49	1577
332	positive regulation of protein phosphorylation	5.948E-05	16	292
333	microtubule-based movement	6.312E-05	11	149
334	response to metal ion	7.007E-05	19	394
335	skeletal system morphogenesis	7.118E-05	13	206
336	cellular response to abiotic stimulus	7.124E-05	11	151
337	nuclear transport	7.305E-05	15	266
338	cellular response to external stimulus	7.560E-05	16	298
339	regulation of cell motility	7.950E-05	20	432
340	skeletal muscle organ development	7.973E-05	12	180
341	regulation of G1/S transition of mitotic cell cycle	8.038E-05	9	103
342	ATP-dependent chromatin remodeling	8.342E-05	6	42
343	response to other organism	8.350E-05	28	727
344	response to cAMP	8.441E-05	10	128
345	tube morphogenesis	8.752E-05	17	334
346	neuron differentiation	9.034E-05	36	1050
347	parturition	9.245E-05	5	27
348	protein oligomerization	9.373E-05	18	369
349	negative regulation of cellular macromolecule biosynthetic process	9.400E-05	35	1011
350	regulation of mitotic spindle organization	1.012E-04	3	6
351	IMP biosynthetic process	1.012E-04	3	6
352	protein targeting to plasma membrane	1.012E-04	3	6
353	platelet activating factor biosynthetic process	1.012E-04	3	6
354	small molecule biosynthetic process	1.013E-04	25	621
355	negative regulation of macromolecule biosynthetic process	1.031E-04	36	1057
356	regulation of vesicle fusion	1.067E-04	4	15
357	nucleobase, nucleoside, nucleotide and nucleic acid transport	1.071E-04	11	158
358	response to steroid hormone stimulus	1.092E-04	25	624
359	positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	1.186E-04	8	85
360	response to extracellular stimulus	1.208E-04	26	666
361	striated muscle tissue development	1.242E-04	16	311
362	angiogenesis	1.337E-04	16	313
363	positive regulation of developmental process	1.340E-04	29	787
364	neuron fate commitment	1.354E-04	7	65
365	vasculature development	1.385E-04	22	522
366	positive regulation of fever generation	1.404E-04	4	16
367	glial cell migration	1.404E-04	4	16
368	ribosomal large subunit biogenesis	1.404E-04	4	16
369	cellular protein catabolic process	1.493E-04	18	383
370	blood vessel development	1.515E-04	21	489
371	regulation of microtubule-based process	1.639E-04	8	89

372	protein localization to nucleus	1.658E-04	11	166
373	chemokine-mediated signaling pathway	1.749E-04	3	7
374	regulation of spindle organization	1.749E-04	3	7
375	IMP metabolic process	1.749E-04	3	7
376	platelet activating factor metabolic process	1.749E-04	3	7
377	central nervous system neuron differentiation	1.776E-04	10	140
378	protein import	1.783E-04	12	196
379	response to fatty acid	1.787E-04	6	48
380	cellular response to oxygen levels	1.803E-04	7	68
381	negative regulation of epidermis development	1.810E-04	4	17
382	negative regulation of cellular protein metabolic process	1.880E-04	17	356
383	regulation of response to stimulus	1.886E-04	66	2441
384	regulation of nervous system development	1.907E-04	22	534
385	response to lipopolysaccharide	1.914E-04	16	323
386	striated muscle cell differentiation	1.964E-04	13	228
387	cell migration	1.999E-04	25	649
388	cell development	2.000E-04	45	1482
389	regulation of cellular component movement	2.066E-04	20	464
390	skeletal muscle tissue development	2.149E-04	11	171
391	cellular catabolic process	2.160E-04	47	1576
392	signal transduction involved in mitotic cell cycle checkpoint	2.164E-04	7	70
393	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	2.164E-04	7	70
394	signal transduction involved in DNA damage checkpoint	2.164E-04	7	70
395	signal transduction involved in mitotic cell cycle G1/S checkpoint	2.164E-04	7	70
396	signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint	2.164E-04	7	70
397	signal transduction involved in DNA integrity checkpoint	2.164E-04	7	70
398	positive regulation of phosphorylation	2.199E-04	16	327
399	nucleocytoplasmic transport	2.211E-04	14	262
400	virus-host interaction	2.248E-04	6	50
401	positive regulation of heat generation	2.296E-04	4	18
402	regulation of fever generation	2.296E-04	4	18
403	purine-containing compound transmembrane transport	2.296E-04	4	18
404	embryonic organ development	2.319E-04	18	397
405	cellular response to chemical stimulus	2.325E-04	50	1716
406	muscle tissue development	2.355E-04	16	329
407	positive regulation of cell death	2.364E-04	28	774
408	signal transduction involved in G1/S transition checkpoint	2.365E-04	7	71
409	signal transduction involved in cell cycle checkpoint	2.365E-04	7	71
410	meiosis	2.377E-04	11	173
411	M phase of meiotic cell cycle	2.377E-04	11	173
412	regulation of locomotion	2.443E-04	20	470
413	regulation of endopeptidase activity	2.542E-04	15	298
414	positive regulation of transcription from RNA polymerase II promoter	2.570E-04	28	778
415	negative regulation of cell migration	2.586E-04	9	120
416	negative regulation of biosynthetic process	2.664E-04	36	1110
417	positive regulation of DNA metabolic process	2.751E-04	9	121
418	negative regulation of keratinocyte differentiation	2.762E-04	3	8
419	positive regulation of mammary gland epithelial cell proliferation	2.762E-04	3	8
420	centromere complex assembly	2.762E-04	3	8
421	mitotic metaphase	2.762E-04	3	8
422	pentose biosynthetic process	2.762E-04	3	8

423	luteolysis	2.762E-04	3	8
424	traversing start control point of mitotic cell cycle	2.762E-04	3	8
425	maternal process involved in parturition	2.762E-04	3	8
426	positive regulation of ubiquitin-protein ligase activity	2.770E-04	8	96
427	positive regulation of cytoskeleton organization	2.770E-04	8	96
428	neural tube formation	2.770E-04	8	96
429	icosanoid secretion	2.868E-04	4	19
430	arachidonic acid secretion	2.868E-04	4	19
431	spindle assembly	2.883E-04	5	34
432	appendage development	2.896E-04	11	177
433	meiotic cell cycle	2.896E-04	11	177
434	limb development	2.896E-04	11	177
435	negative regulation of cell motility	2.926E-04	9	122
436	diadenosine tetraphosphate biosynthetic process	3.034E-04	2	2
437	cerebral cortex GABAergic interneuron fate commitment	3.034E-04	2	2
438	positive regulation of retroviral genome replication	3.034E-04	2	2
439	regulation of transcription from RNA polymerase II promoter involved in forebrain neuron fate commitment	3.034E-04	2	2
440	diadenosine tetraphosphate metabolic process	3.034E-04	2	2
441	response to DDT	3.034E-04	2	2
442	bis(5'-nucleosidyl) oligophosphate biosynthetic process	3.034E-04	2	2
443	cellular response to iron(III) ion	3.034E-04	2	2
444	T cell extravasation	3.034E-04	2	2
445	mitotic spindle elongation	3.034E-04	2	2
446	spindle elongation	3.034E-04	2	2
447	regulation of ribonuclease activity	3.034E-04	2	2
448	cellular response to iron ion	3.034E-04	2	2
449	regulation of mitotic anaphase	3.034E-04	2	2
450	mitotic chromosome movement towards spindle pole	3.034E-04	2	2
451	diadenosine polyphosphate biosynthetic process	3.034E-04	2	2
452	helper T cell extravasation	3.034E-04	2	2
453	regulation of chromosome condensation	3.034E-04	2	2
454	regulation of endoribonuclease activity	3.034E-04	2	2
455	regulation of microtubule cytoskeleton organization	3.061E-04	7	74
456	negative regulation of cellular biosynthetic process	3.129E-04	35	1077
457	positive regulation of phosphorus metabolic process	3.181E-04	16	338
458	positive regulation of phosphate metabolic process	3.181E-04	16	338
459	response to bacterium	3.210E-04	21	517
460	positive regulation of apoptosis	3.225E-04	27	749
461	negative regulation of cell development	3.302E-04	9	124
462	regulation of mRNA processing	3.316E-04	5	35
463	maternal placenta development	3.316E-04	5	35
464	positive regulation of bone mineralization	3.316E-04	5	35
465	neural tube closure	3.326E-04	7	75
466	regulation of peptidase activity	3.444E-04	17	375
467	regulation of heat generation	3.536E-04	4	20
468	negative regulation of cell-matrix adhesion	3.536E-04	4	20
469	proteolysis involved in cellular protein catabolic process	3.551E-04	17	376
470	tube closure	3.609E-04	7	76
471	neural tube development	3.639E-04	10	153
472	positive regulation of programmed cell death	3.651E-04	27	755
473	positive regulation of ligase activity	3.660E-04	8	100
474	response to oxygen levels	3.773E-04	17	378
475	cell fate commitment	3.785E-04	13	244
476	positive regulation of ossification	3.811E-04	6	55

477	blood vessel morphogenesis	3.836E-04	18	414
478	negative regulation of cell adhesion	3.915E-04	8	101
479	L-serine metabolic process	4.089E-04	3	9
480	B cell lineage commitment	4.089E-04	3	9
481	negative regulation of myeloid leukocyte differentiation	4.207E-04	6	56
482	cell redox homeostasis	4.234E-04	7	78
483	DNA duplex unwinding	4.308E-04	4	21
484	positive regulation of biomineral tissue development	4.327E-04	5	37
485	negative regulation of cellular component movement	4.420E-04	9	129
486	primary neural tube formation	4.577E-04	7	79
487	regulation of signaling	4.577E-04	58	2139
488	response to molecule of bacterial origin	4.664E-04	16	350
489	negative regulation of neurogenesis	4.770E-04	8	104
490	protein catabolic process	4.809E-04	18	422
491	proximal/distal pattern formation	4.912E-04	5	38
492	positive regulation of cell cycle arrest	4.942E-04	7	80
493	morphogenesis of an epithelium	5.075E-04	17	388
494	regulation of protein stability	5.086E-04	8	105
495	negative regulation of protein modification process	5.111E-04	12	220
496	cellular response to stimulus	5.116E-04	134	6009
497	response to vitamin	5.165E-04	14	285
498	nucleobase, nucleoside and nucleotide interconversion	5.194E-04	4	22
499	protein destabilization	5.194E-04	4	22
500	negative regulation of glial cell differentiation	5.194E-04	4	22
501	cellular response to mechanical stimulus	5.330E-04	7	81
502	protein targeting	5.379E-04	15	320
503	negative regulation of organelle organization	5.523E-04	11	191
504	protein phosphorylation	5.603E-04	30	900
505	regulation of hydrolase activity	5.605E-04	32	984
506	ubiquitin-dependent protein catabolic process	5.606E-04	16	356
507	response to hormone stimulus	5.665E-04	36	1156
508	regulation of gliogenesis	5.742E-04	7	82
509	chorio-allantoic fusion	5.767E-04	3	10
510	cerebellar granular layer development	5.767E-04	3	10
511	mesenchymal cell development	5.770E-04	8	107
512	response to UV	5.770E-04	8	107
513	regulation of transcription from RNA polymerase II promoter	5.892E-04	40	1334
514	regulation of signal transduction	5.981E-04	50	1788
515	cellular response to hypoxia	6.119E-04	6	60
516	cellular component movement	6.127E-04	28	822
517	response to radiation	6.151E-04	18	431
518	icosanoid transport	6.201E-04	4	23
519	protein localization to organelle	6.310E-04	15	325
520	response to nutrient levels	6.428E-04	23	623
521	positive regulation of lymphocyte proliferation	6.492E-04	9	136
522	chemical homeostasis	6.532E-04	32	993
523	coagulation	6.569E-04	23	624
524	blood coagulation	6.569E-04	23	624
525	multicellular organismal metabolic process	6.688E-04	6	61
526	modification-dependent protein catabolic process	6.707E-04	16	362
527	positive regulation of mononuclear cell proliferation	6.844E-04	9	137
528	apoptotic nuclear change	7.027E-04	5	41
529	negative regulation of protein metabolic process	7.133E-04	17	400
530	modification-dependent macromolecule catabolic process	7.323E-04	16	365
531	purine nucleoside monophosphate biosynthetic process	7.340E-04	4	24

532	purine ribonucleoside monophosphate biosynthetic process	7.340E-04	4	24
533	DNA geometric change	7.340E-04	4	24
534	response to organic nitrogen	7.375E-04	15	330
535	epithelium development	7.475E-04	23	630
536	hemostasis	7.475E-04	23	630
537	macromolecule localization	7.503E-04	46	1622
538	positive regulation of leukocyte proliferation	7.595E-04	9	139
539	phosphorylation	7.619E-04	37	1219
540	localization of cell	7.636E-04	25	711
541	cell motility	7.636E-04	25	711
542	ribonucleoside metabolic process	7.648E-04	7	86
543	negative regulation of protein phosphorylation	7.648E-04	7	86
544	interaction with host	7.648E-04	7	86
545	locomotion	7.675E-04	35	1132
546	forebrain neuron fate commitment	7.827E-04	3	11
547	wound healing involved in inflammatory response	7.827E-04	3	11
548	forebrain generation of neurons	7.864E-04	5	42
549	regulation of mitotic metaphase/anaphase transition	7.864E-04	5	42
550	epithelial tube morphogenesis	7.924E-04	13	264
551	cellular homeostasis	8.120E-04	29	879
552	positive regulation of multicellular organismal process	8.221E-04	22	595
553	negative regulation of cell cycle process	8.279E-04	8	113
554	regulation of striated muscle tissue development	8.279E-04	8	113
555	limb morphogenesis	8.300E-04	10	170
556	appendage morphogenesis	8.300E-04	10	170
557	ribosomal small subunit biogenesis	8.619E-04	4	25
558	mammary gland epithelial cell proliferation	8.619E-04	4	25
559	cholesterol homeostasis	8.645E-04	6	64
560	sterol homeostasis	8.645E-04	6	64
561	ribosome biogenesis	8.682E-04	10	171
562	heart development	8.752E-04	19	482
563	mesenchymal cell differentiation	8.771E-04	8	114
564	negative regulation of locomotion	8.845E-04	9	142
565	mitotic cell cycle G2/M transition decatenation checkpoint	8.998E-04	2	3
566	cellular response to prostaglandin D stimulus	8.998E-04	2	3
567	mitotic cell cycle DNA replication checkpoint	8.998E-04	2	3
568	spindle stabilization	8.998E-04	2	3
569	chromosome movement towards spindle pole	8.998E-04	2	3
570	M phase specific microtubule process	8.998E-04	2	3
571	glycine biosynthetic process from serine	8.998E-04	2	3
572	formation of translation preinitiation complex	8.998E-04	2	3
573	ribosomal large subunit export from nucleus	8.998E-04	2	3
574	mitotic spindle stabilization	8.998E-04	2	3
575	response to prostaglandin D stimulus	8.998E-04	2	3
576	regulation of muscle organ development	9.287E-04	8	115
577	regulation of binding	9.512E-04	11	204
578	catabolic process	9.765E-04	51	1875
579	positive regulation of stress fiber assembly	1.005E-03	4	26
580	cell aging	1.018E-03	6	66
581	nucleoside diphosphate phosphorylation	1.030E-03	3	12
582	surfactant homeostasis	1.030E-03	3	12
583	establishment of protein localization in plasma membrane	1.030E-03	3	12
584	chemical homeostasis within a tissue	1.030E-03	3	12
585	positive regulation of penile erection	1.030E-03	3	12
586	response to water deprivation	1.030E-03	3	12

587	protein maturation	1.039E-03	8	117
588	regulation of protein localization	1.057E-03	15	342
589	lipid homeostasis	1.070E-03	7	91
590	placenta development	1.081E-03	10	176
591	regulation of anatomical structure morphogenesis	1.086E-03	22	608
592	embryonic epithelial tube formation	1.098E-03	8	118
593	macromolecule modification	1.129E-03	60	2316
594	embryonic limb morphogenesis	1.130E-03	9	147
595	embryonic appendage morphogenesis	1.130E-03	9	147
596	epithelial tube formation	1.160E-03	8	119
597	positive regulation of fatty acid biosynthetic process	1.163E-03	4	27
598	G2/M transition DNA damage checkpoint	1.163E-03	4	27
599	central nervous system development	1.167E-03	29	900
600	developmental process involved in reproduction	1.172E-03	21	572
601	mammary gland morphogenesis	1.191E-03	6	68
602	regulation of glial cell differentiation	1.191E-03	6	68
603	purine base metabolic process	1.197E-03	5	46
604	collagen metabolic process	1.197E-03	5	46
605	cellular localization	1.224E-03	46	1661
606	response to lipid	1.224E-03	8	120
607	digestive system development	1.242E-03	9	149
608	regulation of ossification	1.281E-03	10	180
609	pallium development	1.302E-03	9	150
610	long-chain fatty acid transport	1.321E-03	5	47
611	establishment of protein localization in membrane	1.322E-03	3	13
612	DNA demethylation	1.322E-03	3	13
613	negative regulation of leukocyte migration	1.322E-03	3	13
614	negative regulation of survival gene product expression	1.322E-03	3	13
615	DNA replication checkpoint	1.322E-03	3	13
616	cellular response to oxidative stress	1.361E-03	8	122
617	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.379E-03	31	996
618	negative regulation of translation	1.385E-03	6	70
619	negative regulation of phosphorylation	1.434E-03	8	123
620	regulation of I-kappaB kinase/NF-kappaB cascade	1.450E-03	10	183
621	nucleobase, nucleoside and nucleotide biosynthetic process	1.497E-03	12	249
622	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	1.497E-03	12	249
623	regulation of muscle cell differentiation	1.511E-03	8	124
624	pattern specification process	1.523E-03	18	467
625	cellular extravasation	1.532E-03	4	29
626	acid secretion	1.532E-03	4	29
627	serine family amino acid metabolic process	1.532E-03	4	29
628	DNA-dependent DNA replication initiation	1.532E-03	4	29
629	negative regulation of gliogenesis	1.532E-03	4	29
630	decidualization	1.532E-03	4	29
631	regulation of intracellular protein kinase cascade	1.540E-03	22	625
632	regulation of cytoskeleton organization	1.548E-03	12	250
633	phosphate metabolic process	1.572E-03	41	1451
634	phosphorus metabolic process	1.592E-03	41	1452
635	response to endogenous stimulus	1.637E-03	39	1363
636	regulation of monocyte differentiation	1.661E-03	3	14
637	purine base biosynthetic process	1.661E-03	3	14
638	metaphase	1.661E-03	3	14
639	serine family amino acid biosynthetic process	1.661E-03	3	14

640	negative regulation of G2/M transition of mitotic cell cycle	1.661E-03	3	14
641	tube formation	1.672E-03	8	126
642	cellular response to organic substance	1.687E-03	38	1320
643	negative regulation of nitrogen compound metabolic process	1.688E-03	31	1009
644	positive regulation of hydrolase activity	1.710E-03	23	671
645	positive regulation of actin filament bundle assembly	1.743E-03	4	30
646	positive regulation of reproductive process	1.758E-03	8	127
647	negative regulation of centrosome duplication	1.779E-03	2	4
648	diadenosine polyphosphate metabolic process	1.779E-03	2	4
649	5-phosphoribose 1-diphosphate metabolic process	1.779E-03	2	4
650	ribosomal small subunit export from nucleus	1.779E-03	2	4
651	positive regulation of centrosome duplication	1.779E-03	2	4
652	negative regulation of nuclear mRNA splicing, via spliceosome	1.779E-03	2	4
653	bis(5'-nucleosidyl) oligophosphate metabolic process	1.779E-03	2	4
654	5-phosphoribose 1-diphosphate biosynthetic process	1.779E-03	2	4
655	apoptotic chromosome condensation	1.779E-03	2	4
656	regulation of immune complex clearance by monocytes and macrophages	1.779E-03	2	4
657	ATP transport	1.779E-03	2	4
658	positive regulation of immune complex clearance by monocytes and macrophages	1.779E-03	2	4
659	establishment of synaptic specificity at neuromuscular junction	1.779E-03	2	4
660	negative regulation of RNA metabolic process	1.816E-03	29	927
661	purine ribonucleotide biosynthetic process	1.848E-03	8	128
662	multicellular organismal macromolecule metabolic process	1.911E-03	5	51
663	positive regulation of sequence-specific DNA binding transcription factor activity	1.916E-03	10	190
664	localization	1.916E-03	97	4235
665	regulation of translation	1.939E-03	11	223
666	response to estrogen stimulus	1.961E-03	13	292
667	regulation of protein ubiquitination	1.991E-03	10	191
668	telencephalon development	2.008E-03	11	224
669	regulation of cellular response to stress	2.015E-03	12	258
670	regionalization	2.033E-03	14	329
671	symbiosis, encompassing mutualism through parasitism	2.037E-03	8	130
672	negative regulation of phosphorus metabolic process	2.037E-03	8	130
673	negative regulation of phosphate metabolic process	2.037E-03	8	130
674	DNA dealkylation	2.049E-03	3	15
675	GTP biosynthetic process	2.049E-03	3	15
676	regulation of penile erection	2.049E-03	3	15
677	UTP biosynthetic process	2.049E-03	3	15
678	UTP metabolic process	2.049E-03	3	15
679	lymphocyte chemotaxis	2.049E-03	3	15
680	heart valve development	2.049E-03	3	15
681	CTP metabolic process	2.049E-03	3	15
682	CTP biosynthetic process	2.049E-03	3	15
683	regulation of estrogen receptor signaling pathway	2.049E-03	3	15
684	positive regulation of lymphocyte activation	2.082E-03	13	294
685	positive regulation of acute inflammatory response	2.084E-03	5	52
686	cytokinesis	2.117E-03	6	76
687	muscle cell development	2.120E-03	9	161
688	purine-containing compound biosynthetic process	2.149E-03	10	193
689	protein processing	2.194E-03	7	103
690	regulation of myeloid cell differentiation	2.211E-03	9	162

691	purine ribonucleoside monophosphate metabolic process	2.226E-03	4	32
692	purine nucleoside monophosphate metabolic process	2.226E-03	4	32
693	tRNA aminoacylation	2.269E-03	5	53
694	amino acid activation	2.269E-03	5	53
695	tRNA aminoacylation for protein translation	2.269E-03	5	53
696	response to estradiol stimulus	2.317E-03	10	195
697	DNA damage response, signal transduction by p53 class mediator	2.447E-03	7	105
698	macrophage chemotaxis	2.490E-03	3	16
699	cellular response to antibiotic	2.490E-03	3	16
700	pyrimidine ribonucleoside triphosphate metabolic process	2.490E-03	3	16
701	glycine metabolic process	2.490E-03	3	16
702	pyrimidine ribonucleoside triphosphate biosynthetic process	2.490E-03	3	16
703	positive regulation of cardiac muscle cell proliferation	2.490E-03	3	16
704	protein localization	2.491E-03	38	1350
705	negative regulation of cell-substrate adhesion	2.498E-03	4	33
706	ribonucleoside monophosphate biosynthetic process	2.498E-03	4	33
707	positive regulation of I-kappaB kinase/NF-kappaB cascade	2.503E-03	9	165
708	lymphocyte proliferation	2.578E-03	6	79
709	nucleoside metabolic process	2.581E-03	7	106
710	heterocycle biosynthetic process	2.627E-03	13	302
711	carbohydrate homeostasis	2.699E-03	8	136
712	glucose homeostasis	2.699E-03	8	136
713	signal transduction in response to DNA damage	2.699E-03	8	136
714	signal transduction by p53 class mediator	2.722E-03	7	107
715	proteolysis	2.783E-03	28	911
716	response to iron ion	2.793E-03	4	34
717	response to hypoxia	2.890E-03	14	342
718	response to iron(III) ion	2.930E-03	2	5
719	positive regulation of mitotic metaphase/anaphase transition	2.930E-03	2	5
720	regulation of endodeoxyribonuclease activity	2.930E-03	2	5
721	anterior neuropore closure	2.930E-03	2	5
722	ribosomal subunit export from nucleus	2.930E-03	2	5
723	purine ribonucleotide transport	2.930E-03	2	5
724	kinetochore assembly	2.930E-03	2	5
725	active induction of host immune response by virus	2.930E-03	2	5
726	rRNA-containing ribonucleoprotein complex export from nucleus	2.930E-03	2	5
727	establishment of ribosome localization	2.930E-03	2	5
728	positive regulation of tooth mineralization	2.930E-03	2	5
729	induction of host immune response by virus	2.930E-03	2	5
730	regulation of retroviral genome replication	2.930E-03	2	5
731	keratinocyte development	2.930E-03	2	5
732	adenine nucleotide transport	2.930E-03	2	5
733	induction by symbiont of host defense response	2.930E-03	2	5
734	ribosome localization	2.930E-03	2	5
735	ribonucleoprotein complex export from nucleus	2.930E-03	2	5
736	neuropore closure	2.930E-03	2	5
737	mammary gland specification	2.930E-03	2	5
738	digestive tract development	2.953E-03	8	138
739	lymphocyte migration	2.985E-03	3	17
740	negative regulation of JAK-STAT cascade	2.985E-03	3	17
741	pentose metabolic process	2.985E-03	3	17
742	ventricular cardiac muscle cell development	2.985E-03	3	17
743	transcription, DNA-dependent	3.035E-03	64	2614

744	ribonucleotide biosynthetic process	3.087E-03	8	139
745	mononuclear cell proliferation	3.109E-03	6	82
746	glucose transport	3.109E-03	6	82
747	positive regulation of calcium ion transport into cytosol	3.111E-03	4	35
748	apoptotic mitochondrial changes	3.129E-03	5	57
749	positive regulation of NF-kappaB transcription factor activity	3.178E-03	7	110
750	positive regulation of protein ubiquitination	3.226E-03	8	140
751	regulation of cell communication	3.236E-03	42	1557
752	regulation of fibroblast proliferation	3.303E-03	6	83
753	hexose transport	3.303E-03	6	83
754	leukocyte proliferation	3.303E-03	6	83
755	regulation of blood coagulation	3.376E-03	5	58
756	regulation of lymphocyte activation	3.394E-03	15	386
757	regulation of S phase	3.452E-03	4	36
758	mitotic cell cycle spindle assembly checkpoint	3.452E-03	4	36
759	multicellular organismal catabolic process	3.452E-03	4	36
760	monosaccharide transport	3.506E-03	6	84
761	pyrimidine nucleoside triphosphate biosynthetic process	3.536E-03	3	18
762	nucleobase biosynthetic process	3.536E-03	3	18
763	protein localization in plasma membrane	3.536E-03	3	18
764	histone phosphorylation	3.536E-03	3	18
765	regulation of cell adhesion	3.563E-03	13	313
766	regulation of bone mineralization	3.637E-03	5	59
767	negative regulation of signal transduction	3.653E-03	20	588
768	regulation of myeloid leukocyte differentiation	3.690E-03	7	113
769	cell cycle arrest	3.704E-03	9	175
770	brain development	3.715E-03	22	672
771	cellular nitrogen compound biosynthetic process	3.815E-03	17	469
772	phospholipid catabolic process	3.818E-03	4	37
773	regulation of stress fiber assembly	3.818E-03	4	37
774	spindle assembly checkpoint	3.818E-03	4	37
775	negative regulation of mitotic metaphase/anaphase transition	3.818E-03	4	37
776	regulation of leukocyte migration	3.940E-03	6	86
777	regulation of leukocyte activation	4.020E-03	16	432
778	multicellular organismal reproductive process	4.042E-03	27	892
779	multicellular organism reproduction	4.042E-03	27	892
780	negative regulation of signaling	4.120E-03	21	636
781	positive regulation of circadian rhythm	4.145E-03	3	19
782	response to water	4.145E-03	3	19
783	cardiac atrium morphogenesis	4.145E-03	3	19
784	protein localization in membrane	4.145E-03	3	19
785	ovulation from ovarian follicle	4.145E-03	3	19
786	hippocampus development	4.171E-03	6	87
787	positive regulation of leukocyte activation	4.178E-03	13	319
788	regulation of neuron differentiation	4.197E-03	15	395
789	tissue regeneration	4.201E-03	5	61
790	protein maturation by peptide bond cleavage	4.201E-03	5	61
791	nucleoside diphosphate metabolic process	4.210E-03	4	38
792	morphogenesis of embryonic epithelium	4.337E-03	8	147
793	commitment of multipotent stem cells to neuronal lineage in forebrain	4.345E-03	2	6
794	response to UV-A	4.345E-03	2	6
795	protein localization to kinetochore	4.345E-03	2	6
796	STAT protein import into nucleus	4.345E-03	2	6

797	ribose phosphate biosynthetic process	4.345E-03	2	6
798	positive regulation of mRNA 3'-end processing	4.345E-03	2	6
799	activation of phospholipase A2 activity	4.345E-03	2	6
800	D-ribose biosynthetic process	4.345E-03	2	6
801	stress-induced premature senescence	4.345E-03	2	6
802	rRNA transport	4.345E-03	2	6
803	positive regulation of mRNA processing	4.345E-03	2	6
804	adenine transport	4.345E-03	2	6
805	negative regulation of mRNA processing	4.345E-03	2	6
806	ribonucleoprotein complex localization	4.345E-03	2	6
807	re-entry into mitotic cell cycle	4.345E-03	2	6
808	induction by organism of defense response of other organism involved in symbiotic interaction	4.345E-03	2	6
809	rRNA export from nucleus	4.345E-03	2	6
810	kinetochore organization	4.345E-03	2	6
811	regulation of deoxyribonuclease activity	4.345E-03	2	6
812	viral genome transport in host cell	4.345E-03	2	6
813	cardiac muscle cell development	4.627E-03	4	39
814	positive regulation of vasoconstriction	4.627E-03	4	39
815	regulation of survival gene product expression	4.627E-03	4	39
816	forebrain development	4.657E-03	14	361
817	positive regulation of response to stimulus	4.659E-03	33	1171
818	I-kappaB kinase/NF-kappaB cascade	4.663E-03	6	89
819	regulation of cell morphogenesis	4.758E-03	12	287
820	regulation of mammary gland epithelial cell proliferation	4.814E-03	3	20
821	cardiac atrium development	4.814E-03	3	20
822	response to methylmercury	4.814E-03	3	20
823	labyrinthine layer morphogenesis	4.814E-03	3	20
824	positive regulation of lipid biosynthetic process	4.826E-03	5	63
825	mesenchyme development	4.895E-03	8	150
826	positive regulation of homeostatic process	4.924E-03	6	90
827	extracellular structure organization	5.024E-03	12	289
828	collagen fibril organization	5.072E-03	4	40
829	embryonic cranial skeleton morphogenesis	5.072E-03	4	40
830	positive regulation of mitotic cell cycle	5.072E-03	4	40
831	negative regulation of protein binding	5.072E-03	4	40
832	establishment of localization in cell	5.075E-03	39	1456
833	positive regulation of cell activation	5.128E-03	13	327
834	regulation of biomineral tissue development	5.161E-03	5	64
835	negative regulation of transcription, DNA-dependent	5.255E-03	27	910
836	neuron projection development	5.405E-03	23	737
837	ribonucleoprotein complex biogenesis	5.523E-03	11	256
838	positive regulation of blood coagulation	5.544E-03	3	21
839	pyrimidine nucleoside triphosphate metabolic process	5.544E-03	3	21
840	cellular response to drug	5.544E-03	3	21
841	retinal ganglion cell axon guidance	5.544E-03	3	21
842	regulation of nuclear mRNA splicing, via spliceosome	5.544E-03	3	21
843	cellular response to monosaccharide stimulus	5.544E-03	4	41
844	cellular response to hexose stimulus	5.544E-03	4	41
845	ribonucleoside monophosphate metabolic process	5.544E-03	4	41
846	cellular response to glucose stimulus	5.544E-03	4	41
847	activation of pro-apoptotic gene products	5.544E-03	4	41
848	response to protein stimulus	5.591E-03	12	293
849	regulation of lymphocyte proliferation	5.696E-03	9	187
850	regulation of intracellular protein transport	5.721E-03	8	154

851	intracellular protein kinase cascade	5.730E-03	19	571
852	cardiac muscle cell differentiation	5.774E-03	6	93
853	negative regulation of transcription from RNA polymerase II promoter	5.835E-03	19	572
854	fatty acid transport	5.882E-03	5	66
855	regulation of coagulation	5.882E-03	5	66
856	regulation of mononuclear cell proliferation	5.893E-03	9	188
857	regulation of response to stress	5.903E-03	24	786
858	protein modification process	5.914E-03	54	2194
859	positive regulation of phospholipase A2 activity	6.013E-03	2	7
860	pathogenesis	6.013E-03	2	7
861	hindbrain radial glia guided cell migration	6.013E-03	2	7
862	positive regulation of nitric-oxide synthase biosynthetic process	6.013E-03	2	7
863	cellular response to cell-matrix adhesion	6.013E-03	2	7
864	positive regulation of keratinocyte differentiation	6.013E-03	2	7
865	connective tissue replacement involved in inflammatory response wound healing	6.013E-03	2	7
866	glycine biosynthetic process	6.013E-03	2	7
867	purine nucleotide transport	6.013E-03	2	7
868	regulation of cell activation	6.028E-03	16	451
869	regulation of actin filament bundle assembly	6.045E-03	4	42
870	purine-containing compound metabolic process	6.132E-03	23	745
871	epithelial cell proliferation	6.267E-03	5	67
872	branching morphogenesis of a tube	6.303E-03	9	190
873	regulation of DNA damage response, signal transduction by p53 class mediator	6.338E-03	3	22
874	protein localization to chromosome	6.338E-03	3	22
875	meiotic chromosome segregation	6.338E-03	3	22
876	osteoblast differentiation	6.396E-03	6	95
877	response to hyperoxia	6.575E-03	4	43
878	regulation of plasma lipoprotein particle levels	6.575E-03	4	43
879	ventricular cardiac muscle cell differentiation	6.575E-03	4	43
880	cardiac cell development	6.575E-03	4	43
881	regulation of leukocyte proliferation	6.735E-03	9	192
882	cardiac muscle tissue development	6.900E-03	8	159
883	morphogenesis of a branching structure	6.944E-03	10	228
884	female gamete generation	6.952E-03	7	127
885	double-strand break repair	7.066E-03	6	97
886	axon guidance	7.086E-03	16	459
887	centrosome organization	7.135E-03	4	44
888	regulation of DNA repair	7.135E-03	4	44
889	cerebellar cortex development	7.135E-03	4	44
890	regulation of leukocyte apoptosis	7.135E-03	4	44
891	somatic stem cell maintenance	7.135E-03	4	44
892	regulation of nucleocytoplasmic transport	7.156E-03	8	160
893	cellular senescence	7.195E-03	3	23
894	positive regulation of cyclin-dependent protein kinase activity	7.195E-03	3	23
895	V(D)J recombination	7.195E-03	3	23
896	regulation of protein import into nucleus	7.248E-03	7	128
897	regulation of cell growth	7.373E-03	14	381
898	regulation of cellular ketone metabolic process	7.426E-03	9	195
899	chemotaxis	7.573E-03	21	672
900	cellular component biogenesis at cellular level	7.692E-03	11	268
901	regulation of fatty acid biosynthetic process	7.725E-03	4	45

902	neutrophil chemotaxis	7.725E-03	4	45
903	taxis	7.819E-03	21	674
904	cellular protein localization	7.905E-03	22	718
905	response to parathyroid hormone stimulus	7.926E-03	2	8
906	resolution of meiotic recombination intermediates	7.926E-03	2	8
907	regulation of stem cell maintenance	7.926E-03	2	8
908	cellular response to prostaglandin stimulus	7.926E-03	2	8
909	axial mesoderm morphogenesis	7.926E-03	2	8
910	cerebellar granule cell differentiation	7.926E-03	2	8
911	ribose phosphate metabolic process	7.926E-03	2	8
912	carbon catabolite regulation of transcription	7.926E-03	2	8
913	cerebellar granular layer formation	7.926E-03	2	8
914	positive regulation of epidermal cell differentiation	7.926E-03	2	8
915	neurotransmitter receptor metabolic process	7.926E-03	2	8
916	collagen biosynthetic process	7.926E-03	2	8
917	regulation of transcription by glucose	7.926E-03	2	8
918	positive regulation of exit from mitosis	7.926E-03	2	8
919	nucleotide transport	7.926E-03	2	8
920	skin development	7.987E-03	5	71
921	anterior/posterior pattern formation	8.033E-03	10	233
922	cellular response to cAMP	8.118E-03	3	24
923	ribosome assembly	8.118E-03	3	24
924	nucleotide phosphorylation	8.118E-03	3	24
925	oocyte maturation	8.118E-03	3	24
926	cellular response to biotic stimulus	8.253E-03	8	164
927	negative regulation of axonogenesis	8.347E-03	4	46
928	response to corticosterone stimulus	8.347E-03	4	46
929	nucleobase, nucleoside and nucleotide metabolic process	8.387E-03	26	899
930	heterocycle metabolic process	8.397E-03	29	1035
931	regulation of growth	8.472E-03	20	636
932	cellular response to extracellular stimulus	8.504E-03	10	235
933	cellular macromolecule localization	8.532E-03	22	723
934	tube development	8.571E-03	17	510
935	response to oxidative stress	8.657E-03	13	349
936	regulation of cell morphogenesis involved in differentiation	8.694E-03	9	200
937	regulation of neuron apoptosis	8.748E-03	10	236
938	positive regulation of protein serine/threonine kinase activity	8.770E-03	11	273
939	rhythmic process	8.798E-03	12	311
940	gland morphogenesis	8.865E-03	7	133
941	negative regulation of cell communication	8.893E-03	20	639
942	second-messenger-mediated signaling	8.914E-03	15	430
943	regulation of wound healing	8.959E-03	5	73
944	histone H4 acetylation	9.001E-03	4	47
945	somatic diversification of immune receptors via germline recombination within a single locus	9.001E-03	4	47
946	negative regulation of nuclear division	9.001E-03	4	47
947	negative regulation of mitosis	9.001E-03	4	47
948	somatic cell DNA recombination	9.001E-03	4	47
949	pyrimidine ribonucleotide biosynthetic process	9.108E-03	3	25
950	positive regulation of cell differentiation	9.160E-03	19	598
951	RNA transport	9.218E-03	7	134
952	establishment of RNA localization	9.218E-03	7	134
953	nucleic acid transport	9.218E-03	7	134
954	ncRNA metabolic process	9.228E-03	12	313
955	regulation of protein binding	9.379E-03	6	103

956	response to organic cyclic compound	9.470E-03	16	474
957	regulation of reproductive process	9.531E-03	9	203
958	intracellular protein transport	9.713E-03	18	559
959	negative regulation of cell proliferation	9.943E-03	20	646
960	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	1.001E-02	5	75
961	regulation of transcription factor import into nucleus	1.001E-02	5	75
962	regulation of nitric-oxide synthase biosynthetic process	1.007E-02	2	9
963	cerebellar granular layer morphogenesis	1.007E-02	2	9
964	regulation of stem cell differentiation	1.007E-02	2	9
965	cell migration in hindbrain	1.007E-02	2	9
966	glycerophospholipid catabolic process	1.007E-02	2	9
967	platelet dense granule organization	1.007E-02	2	9
968	regulation of tooth mineralization	1.007E-02	2	9
969	positive regulation of estrogen receptor signaling pathway	1.007E-02	2	9
970	regulation of phospholipase A2 activity	1.007E-02	2	9
971	positive regulation of histone phosphorylation	1.007E-02	2	9
972	attachment of spindle microtubules to kinetochore	1.007E-02	2	9
973	negative regulation of RNA splicing	1.007E-02	2	9
974	regulation of mRNA 3'-end processing	1.007E-02	2	9
975	immunoglobulin V(D)J recombination	1.007E-02	2	9
976	pyrimidine ribonucleotide metabolic process	1.016E-02	3	26
977	positive regulation of coagulation	1.016E-02	3	26
978	regulation of cardiac muscle cell proliferation	1.016E-02	3	26
979	hydrogen peroxide catabolic process	1.016E-02	3	26
980	cellular response to UV	1.016E-02	3	26
981	limbic system development	1.026E-02	6	105
982	neuron projection morphogenesis	1.026E-02	20	648
983	microtubule organizing center organization	1.041E-02	4	49
984	muscle filament sliding	1.041E-02	4	49
985	positive regulation of fatty acid metabolic process	1.041E-02	4	49
986	response to gamma radiation	1.041E-02	4	49
987	nucleobase metabolic process	1.057E-02	5	76
988	peripheral nervous system development	1.057E-02	5	76
989	odontogenesis of dentine-containing tooth	1.057E-02	5	76
990	negative regulation of Wnt receptor signaling pathway	1.072E-02	6	106
991	maintenance of location	1.073E-02	7	138
992	response to interferon-gamma	1.114E-02	7	139
993	positive regulation of muscle cell differentiation	1.114E-02	5	77
994	actin-myosin filament sliding	1.116E-02	4	50
995	ER-nucleus signaling pathway	1.116E-02	4	50
996	T cell proliferation	1.116E-02	4	50
997	cellular response to carbohydrate stimulus	1.116E-02	4	50
998	neuron migration	1.119E-02	6	107
999	secretion	1.126E-02	20	654
1000	macromolecular complex remodeling	1.129E-02	3	27
1001	plasma lipoprotein particle remodeling	1.129E-02	3	27
1002	centrosome cycle	1.129E-02	3	27
1003	protein-lipid complex remodeling	1.129E-02	3	27
1004	sleep	1.129E-02	3	27
1005	cell projection organization	1.136E-02	26	922
1006	regulation of anatomical structure size	1.150E-02	19	612
1007	RNA localization	1.156E-02	7	140
1008	hindbrain development	1.156E-02	7	140
1009	negative regulation of molecular function	1.171E-02	25	879

1010	regulation of vesicle-mediated transport	1.184E-02	11	285
1011	cellular glucose homeostasis	1.195E-02	4	51
1012	regulation of sequence-specific DNA binding transcription factor activity	1.200E-02	13	364
1013	positive regulation of cell communication	1.203E-02	23	791
1014	cellular response to reactive oxygen species	1.236E-02	5	79
1015	in utero embryonic development	1.238E-02	15	447
1016	regulation of homeostatic process	1.242E-02	11	287
1017	glial cell differentiation	1.242E-02	7	142
1018	chromosome separation	1.245E-02	2	10
1019	positive regulation of transcription during mitosis	1.245E-02	2	10
1020	negative regulation of astrocyte differentiation	1.245E-02	2	10
1021	regulation of transcription during mitosis	1.245E-02	2	10
1022	axial mesoderm development	1.245E-02	2	10
1023	replicative senescence	1.245E-02	2	10
1024	embryonic cleavage	1.245E-02	2	10
1025	thrombin receptor signaling pathway	1.245E-02	2	10
1026	positive regulation of steroid hormone receptor signaling pathway	1.245E-02	2	10
1027	tyrosine phosphorylation of STAT protein	1.245E-02	2	10
1028	meiotic chromosome separation	1.245E-02	2	10
1029	regulation of transcription from RNA polymerase II promoter, mitotic	1.245E-02	2	10
1030	mammary gland formation	1.245E-02	2	10
1031	positive regulation of transcription from RNA polymerase II promoter during mitosis	1.245E-02	2	10
1032	D-ribose metabolic process	1.245E-02	2	10
1033	sequestering of actin monomers	1.245E-02	2	10
1034	regulation of transcription involved in cell fate commitment	1.245E-02	2	10
1035	ephrin receptor signaling pathway	1.248E-02	3	28
1036	collagen catabolic process	1.248E-02	3	28
1037	regulation of viral genome replication	1.248E-02	3	28
1038	transmembrane receptor protein serine/threonine kinase signaling pathway	1.270E-02	8	177
1039	cell chemotaxis	1.271E-02	6	110
1040	regulation of steroid hormone receptor signaling pathway	1.277E-02	4	52
1041	purine ribonucleoside metabolic process	1.277E-02	4	52
1042	purine nucleoside metabolic process	1.277E-02	4	52
1043	positive regulation of B cell proliferation	1.277E-02	4	52
1044	icosanoid biosynthetic process	1.277E-02	4	52
1045	regulation of MAPKKK cascade	1.277E-02	13	367
1046	regulation of muscle contraction	1.287E-02	7	143
1047	regulation of cellular component size	1.305E-02	17	534
1048	establishment of localization	1.330E-02	79	3573
1049	positive regulation of signaling	1.342E-02	23	799
1050	extracellular matrix organization	1.351E-02	8	179
1051	regulation of Wnt receptor signaling pathway	1.351E-02	8	179
1052	response to hydrogen peroxide	1.381E-02	7	145

MODEL V – DOWN

#	GO Processes	pValue	Ratio	
1	multicellular organismal signaling	1.202E-67	175	762
2	transmission of nerve impulse	1.202E-67	175	762
3	synaptic transmission	2.592E-59	154	670
4	cell communication	3.649E-49	213	1416
5	cell-cell signaling	5.980E-49	180	1057
6	regulation of system process	5.588E-46	133	637
7	regulation of transport	1.149E-43	188	1238
8	nervous system development	8.408E-42	258	2143
9	regulation of localization	5.925E-40	210	1577
10	regulation of neurological system process	2.634E-38	89	346
11	regulation of transmission of nerve impulse	7.715E-36	83	322
12	regulation of synaptic transmission	3.386E-35	79	297
13	regulation of multicellular organismal process	7.392E-34	233	2036
14	regulation of biological quality	6.663E-32	293	2953
15	localization	3.131E-31	374	4235
16	regulation of membrane potential	6.176E-31	71	274
17	system process	2.950E-30	256	2474
18	regulation of secretion	1.988E-29	100	549
19	establishment of localization	2.232E-29	327	3573
20	multicellular organismal process	2.367E-29	515	6739
21	transport	5.730E-29	322	3513
22	regulation of ion transport	1.945E-28	81	384
23	behavior	1.013E-27	102	596
24	signaling	1.118E-27	431	5359
25	neurogenesis	3.206E-27	172	1425
26	regulation of neurotransmitter levels	1.084E-26	52	170
27	cellular ion homeostasis	1.096E-26	113	731
28	ion homeostasis	1.533E-26	117	778
29	neurotransmitter transport	2.756E-26	52	173
30	neurological system process	1.097E-25	214	2040
31	regulation of cell communication	2.137E-25	178	1557
32	response to wounding	2.623E-25	155	1261
33	generation of neurons	3.771E-25	161	1342
34	cellular chemical homeostasis	5.481E-25	114	776
35	regulation of nucleotide metabolic process	6.450E-25	95	571
36	regulation of cellular localization	1.761E-24	106	697
37	generation of a signal involved in cell-cell signaling	1.997E-24	56	218
38	signal release	1.997E-24	56	218
39	system development	3.647E-24	334	3930
40	chemical homeostasis	1.083E-23	130	993
41	secretion by cell	1.712E-23	83	472
42	regulation of cyclic nucleotide biosynthetic process	1.790E-23	52	196
43	regulation of nucleotide biosynthetic process	1.790E-23	52	196
44	regulation of signaling	2.188E-23	215	2139
45	neurotransmitter secretion	2.202E-23	41	120
46	neuron differentiation	2.256E-23	134	1050
47	cell development	4.161E-23	167	1482
48	positive regulation of transport	2.579E-22	89	554
49	regulation of cyclic nucleotide metabolic process	2.760E-22	52	207
50	neuron development	5.942E-22	118	891
51	regulation of synaptic plasticity	7.860E-22	43	144
52	wound healing	1.003E-21	108	778

53	ion transport	1.545E-21	130	1049
54	cellular homeostasis	1.840E-21	116	879
55	central nervous system development	4.192E-21	117	900
56	multicellular organismal development	6.482E-21	364	4605
57	metal ion transport	8.578E-21	93	627
58	anatomical structure development	9.265E-21	347	4329
59	regulation of ion transmembrane transport	1.208E-20	55	249
60	regulation of metal ion transport	2.124E-20	51	218
61	cell differentiation	3.048E-20	257	2905
62	membrane depolarization	3.498E-20	33	90
63	secretion	4.790E-20	94	654
64	regulation of transmembrane transport	7.503E-20	69	390
65	regulation of adenylate cyclase activity	1.064E-19	42	154
66	cyclic-nucleotide-mediated signaling	1.734E-19	51	228
67	locomotory behavior	1.817E-19	47	195
68	cellular developmental process	2.411E-19	259	2981
69	cell projection organization	2.542E-19	115	922
70	regulation of cyclase activity	3.051E-19	42	158
71	regulation of neuronal synaptic plasticity	3.134E-19	29	72
72	regulation of lyase activity	5.095E-19	42	160
73	developmental process	5.730E-19	381	5016
74	cAMP-mediated signaling	5.812E-19	45	184
75	platelet activation	5.948E-19	60	316
76	cognition	9.169E-19	54	263
77	regulation of action potential	1.665E-18	39	142
78	neuron projection development	1.837E-18	98	737
79	regulation of exocytosis	1.888E-18	35	114
80	cell activation	2.212E-18	101	775
81	regulation of body fluid levels	3.870E-18	99	757
82	neuron projection morphogenesis	9.661E-18	89	648
83	learning or memory	1.147E-17	51	250
84	regulation of calcium ion transport	1.830E-17	42	175
85	regulation of cAMP biosynthetic process	1.830E-17	42	175
86	exocytosis	2.538E-17	53	273
87	coagulation	2.870E-17	86	624
88	blood coagulation	2.870E-17	86	624
89	negative regulation of adenylate cyclase activity	3.077E-17	29	83
90	negative regulation of lyase activity	3.077E-17	29	83
91	negative regulation of cyclase activity	3.077E-17	29	83
92	regulation of cAMP metabolic process	3.558E-17	42	178
93	homeostatic process	4.307E-17	144	1374
94	cation transport	4.972E-17	96	749
95	hemostasis	5.190E-17	86	630
96	multicellular organismal response to stress	5.622E-17	30	91
97	regulation of calcium ion transport via voltage-gated calcium channel activity	6.642E-17	26	67
98	regulation of heart contraction	1.386E-16	37	144
99	regulation of excitatory postsynaptic membrane potential	2.125E-16	23	53
100	cell morphogenesis involved in neuron differentiation	2.163E-16	85	633
101	regulation of postsynaptic membrane potential	2.184E-16	25	64
102	regulation of synaptic transmission, glutamatergic	2.276E-16	22	48
103	positive regulation of catalytic activity	3.717E-16	132	1243
104	regulation of nervous system development	3.734E-16	76	534
105	synaptic transmission, glutamatergic	3.877E-16	21	44
106	fear response	3.933E-16	22	49

107	regulation of amine transport	4.444E-16	28	84
108	G-protein signaling, coupled to cAMP nucleotide second messenger	4.511E-16	39	165
109	regulation of molecular function	5.756E-16	206	2330
110	G-protein signaling, coupled to cyclic nucleotide second messenger	6.917E-16	43	201
111	ion transmembrane transport	6.954E-16	76	540
112	regulation of action potential in neuron	7.519E-16	32	113
113	regulation of vesicle-mediated transport	7.779E-16	52	285
114	transmembrane transport	8.552E-16	116	1040
115	regulation of peptide secretion	1.010E-15	43	203
116	regulation of peptide transport	1.010E-15	43	203
117	calcium ion transport	1.037E-15	45	221
118	cell morphogenesis involved in differentiation	1.379E-15	91	726
119	cyclic nucleotide metabolic process	1.489E-15	27	81
120	divalent metal ion transport	1.661E-15	49	261
121	positive regulation of molecular function	1.924E-15	144	1437
122	cell projection morphogenesis	2.361E-15	90	720
123	intracellular signal transduction	2.709E-15	160	1673
124	second-messenger-mediated signaling	2.973E-15	65	430
125	divalent inorganic cation transport	3.107E-15	49	265
126	axonogenesis	3.758E-15	80	604
127	calcium ion transmembrane transport	3.846E-15	32	119
128	cell part morphogenesis	6.991E-15	90	733
129	cellular calcium ion homeostasis	9.197E-15	56	343
130	cellular divalent inorganic cation homeostasis	9.833E-15	57	354
131	neuron-neuron synaptic transmission	9.982E-15	26	80
132	regulation of long-term neuronal synaptic plasticity	1.108E-14	20	45
133	regulation of catalytic activity	1.172E-14	176	1939
134	regulation of peptide hormone secretion	1.285E-14	41	199
135	regulation of transmembrane transporter activity	1.522E-14	29	102
136	negative regulation of transport	1.850E-14	55	338
137	synaptic vesicle exocytosis	1.868E-14	20	46
138	behavioral defense response	1.868E-14	20	46
139	response to stimulus	1.869E-14	524	7952
140	positive regulation of hydrolase activity	1.958E-14	84	671
141	regulation of ion transmembrane transporter activity	2.830E-14	28	97
142	positive regulation of secretion	2.859E-14	48	270
143	cell morphogenesis	2.864E-14	100	879
144	regulation of hormone secretion	2.932E-14	45	241
145	regulation of multicellular organismal development	3.589E-14	128	1262
146	calcium ion homeostasis	3.669E-14	56	354
147	divalent inorganic cation homeostasis	4.303E-14	57	366
148	response to external stimulus	4.332E-14	146	1522
149	synapse organization	4.418E-14	31	121
150	learning	4.600E-14	33	137
151	regulation of transporter activity	5.230E-14	30	114
152	regulation of developmental process	7.895E-14	147	1548
153	negative regulation of multicellular organismal process	7.932E-14	60	404
154	vesicle-mediated transport	8.115E-14	105	960
155	positive regulation of phospholipase C activity	8.483E-14	36	165
156	adult behavior	9.508E-14	35	157
157	behavioral fear response	9.851E-14	19	44
158	regulation of sensory perception of pain	9.851E-14	19	44
159	regulation of sensory perception	9.851E-14	19	44

160	muscle system process	1.162E-13	49	290
161	cellular component morphogenesis	1.274E-13	103	940
162	locomotion	1.424E-13	117	1132
163	regulation of blood vessel size	1.645E-13	27	96
164	regulation of insulin secretion	1.895E-13	38	187
165	vasodilation	2.023E-13	20	51
166	regulation of cellular component organization	2.072E-13	130	1321
167	regulation of organic acid transport	2.635E-13	19	46
168	regulation of tube size	2.853E-13	27	98
169	activation of phospholipase C activity	3.748E-13	35	164
170	regulation of hydrolase activity	3.929E-13	105	984
171	biological regulation	4.506E-13	655	10630
172	brain development	4.560E-13	81	672
173	regulation of lipase activity	4.772E-13	40	211
174	inhibition of adenylate cyclase activity by G-protein signaling pathway	5.239E-13	23	72
175	positive regulation of phospholipase activity	5.562E-13	36	175
176	positive regulation of transmission of nerve impulse	5.673E-13	24	79
177	establishment of localization in cell	5.944E-13	138	1456
178	positive regulation of neurological system process	7.617E-13	25	87
179	regulation of cell development	9.047E-13	73	581
180	positive regulation of lipase activity	9.266E-13	37	187
181	cation homeostasis	9.460E-13	70	545
182	metal ion homeostasis	9.862E-13	64	474
183	glutamate signaling pathway	1.034E-12	19	49
184	nucleoside monophosphate metabolic process	1.127E-12	30	127
185	sensory perception of pain	1.216E-12	26	96
186	regulation of synapse structure and activity	1.253E-12	22	68
187	negative regulation of secretion	1.346E-12	34	162
188	synaptic vesicle transport	1.382E-12	23	75
189	regulation of neurotransmitter secretion	1.473E-12	21	62
190	positive regulation of cell communication	1.537E-12	89	791
191	regulation of phospholipase activity	1.600E-12	36	181
192	membrane hyperpolarization	1.723E-12	16	34
193	regulation of vasoconstriction	1.888E-12	23	76
194	signal transduction	2.186E-12	348	4921
195	cellular localization	2.306E-12	150	1661
196	synapse assembly	2.358E-12	20	57
197	cellular metal ion homeostasis	2.435E-12	62	460
198	positive regulation of signaling	2.687E-12	89	799
199	positive regulation of developmental process	2.912E-12	88	787
200	activation of adenylate cyclase activity	3.036E-12	25	92
201	myelination	3.331E-12	24	85
202	regulation of neurotransmitter transport	3.359E-12	22	71
203	vascular process in circulatory system	3.624E-12	28	116
204	cGMP metabolic process	4.443E-12	17	41
205	positive regulation of adenylate cyclase activity	5.129E-12	25	94
206	regulation of cellular process	5.932E-12	594	9537
207	regulation of gamma-aminobutyric acid secretion	6.499E-12	11	15
208	neuron cell-cell adhesion	6.499E-12	11	15
209	positive regulation of protein kinase activity	6.604E-12	60	447
210	regulation of short-term neuronal synaptic plasticity	6.842E-12	10	12
211	cytosolic calcium ion homeostasis	7.241E-12	40	229
212	positive regulation of synaptic transmission	8.509E-12	22	74
213	cellular cation homeostasis	8.968E-12	64	498

214	positive regulation of transferase activity	8.975E-12	62	474
215	ensheathment of neurons	9.878E-12	24	89
216	axon ensheathment	9.878E-12	24	89
217	positive regulation of synaptic transmission, glutamatergic	1.048E-11	12	19
218	positive regulation of cyclase activity	1.095E-11	25	97
219	regulation of synapse organization	1.149E-11	19	55
220	regulation of response to external stimulus	1.257E-11	56	407
221	regulation of glutamate secretion	1.617E-11	15	33
222	positive regulation of lyase activity	1.783E-11	25	99
223	memory	1.813E-11	26	107
224	positive regulation of nucleotide biosynthetic process	2.367E-11	19	57
225	positive regulation of cyclic nucleotide biosynthetic process	2.367E-11	19	57
226	muscle contraction	2.426E-11	41	248
227	positive regulation of kinase activity	2.636E-11	60	462
228	blood circulation	2.741E-11	49	335
229	regulation of muscle contraction	2.833E-11	30	143
230	regulation of neurogenesis	3.739E-11	61	478
231	response to stress	3.775E-11	243	3216
232	circulatory system process	3.788E-11	49	338
233	regulation of muscle system process	3.956E-11	32	163
234	cell adhesion	4.604E-11	92	883
235	biological adhesion	6.239E-11	92	888
236	regulation of catabolic process	6.882E-11	73	636
237	extracellular structure organization	7.531E-11	44	289
238	negative regulation of synaptic transmission	8.864E-11	17	48
239	positive regulation of biological process	9.338E-11	272	3736
240	positive regulation of cellular process	1.099E-10	251	3385
241	negative regulation of transmission of nerve impulse	1.125E-10	18	55
242	regulation of neuron differentiation	1.157E-10	53	395
243	negative regulation of smooth muscle contraction	1.167E-10	12	22
244	negative regulation of neurological system process	1.248E-10	19	62
245	associative learning	1.341E-10	22	84
246	elevation of cytosolic calcium ion concentration	1.404E-10	35	200
247	positive regulation of organic acid transport	1.504E-10	13	27
248	positive regulation of cyclic nucleotide metabolic process	1.702E-10	19	63
249	regulation of purine nucleotide catabolic process	1.762E-10	51	376
250	regulation of nucleotide catabolic process	1.762E-10	51	376
251	regulation of response to stimulus	1.782E-10	193	2441
252	positive regulation of nucleotide metabolic process	2.306E-10	19	64
253	negative regulation of muscle contraction	2.426E-10	14	33
254	regulation of biological process	2.453E-10	615	10123
255	response to ethanol	2.829E-10	35	205
256	regulation of cell projection organization	3.219E-10	44	302
257	anatomical structure morphogenesis	3.755E-10	173	2141
258	regulation of kinase activity	3.860E-10	75	687
259	regulation of the force of heart contraction	3.930E-10	14	34
260	regulation of synaptic transmission, GABAergic	3.930E-10	14	34
261	regulation of catecholamine secretion	4.164E-10	18	59
262	neuromuscular process	4.210E-10	24	105
263	positive regulation of ion transport	5.182E-10	24	106
264	regulation of cellular catabolic process	5.327E-10	65	561
265	positive regulation of locomotion	5.693E-10	42	285
266	positive regulation of cGMP biosynthetic process	6.313E-10	11	20
267	regulation of transferase activity	6.365E-10	76	708
268	positive regulation of cell motility	6.388E-10	41	275

269	regulation of ion homeostasis	6.565E-10	29	152
270	nitric oxide mediated signal transduction	7.779E-10	13	30
271	positive regulation of adenylate cyclase activity by G-protein signaling pathway	8.422E-10	20	76
272	regulation of adenylate cyclase activity involved in G-protein signaling pathway	8.422E-10	20	76
273	activation of adenylate cyclase activity by G-protein signaling pathway	8.422E-10	20	76
274	positive regulation of cellular component movement	8.795E-10	42	289
275	positive regulation of multicellular organismal process	9.577E-10	67	595
276	positive regulation of cell migration	9.991E-10	40	268
277	positive regulation of response to external stimulus	1.013E-09	32	184
278	regulation of amino acid transport	1.264E-09	11	21
279	startle response	1.493E-09	14	37
280	regulation of blood pressure	1.507E-09	33	197
281	purine nucleotide metabolic process	1.754E-09	74	697
282	cyclic nucleotide biosynthetic process	1.779E-09	16	50
283	negative regulation of biological process	1.858E-09	240	3296
284	gliogenesis	2.032E-09	30	169
285	cellular response to stimulus	2.252E-09	393	6009
286	taxis	2.252E-09	72	674
287	regulation of protein kinase activity	2.313E-09	71	661
288	receptor clustering	2.473E-09	12	27
289	gamma-aminobutyric acid signaling pathway	2.544E-09	17	58
290	regulation of phosphorus metabolic process	2.842E-09	95	999
291	regulation of phosphate metabolic process	2.842E-09	95	999
292	response to abiotic stimulus	3.229E-09	84	845
293	energy reserve metabolic process	3.518E-09	34	214
294	axon guidance	3.528E-09	55	459
295	regulation of protein phosphorylation	3.709E-09	88	904
296	response to inorganic substance	4.174E-09	64	577
297	regulation of cGMP biosynthetic process	4.410E-09	11	23
298	chemotaxis	4.647E-09	71	672
299	regulation of cell differentiation	4.673E-09	102	1111
300	positive regulation of amine transport	4.916E-09	14	40
301	positive regulation of protein serine/threonine kinase activity	5.739E-09	39	273
302	regulation of phosphorylation	5.850E-09	92	970
303	positive regulation of amino acid transport	6.395E-09	8	11
304	synaptic vesicle docking involved in exocytosis	6.395E-09	8	11
305	positive regulation of gamma-aminobutyric acid secretion	6.395E-09	8	11
306	positive regulation of cGMP metabolic process	7.767E-09	11	24
307	regulation of inhibitory postsynaptic membrane potential	7.767E-09	11	24
308	negative regulation of catalytic activity	8.053E-09	74	722
309	regulation of locomotion	8.198E-09	55	470
310	visual behavior	8.445E-09	16	55
311	negative regulation of synaptic transmission, glutamatergic	8.526E-09	9	15
312	positive regulation of synaptic transmission, GABAergic	8.526E-09	9	15
313	cGMP biosynthetic process	1.067E-08	12	30
314	response to organic cyclic compound	1.105E-08	55	474
315	response to chemical stimulus	1.135E-08	278	4020
316	visual learning	1.138E-08	15	49
317	telencephalon development	1.159E-08	34	224
318	purine-containing compound metabolic process	1.369E-08	75	745
319	cell-cell adhesion	1.460E-08	49	402
320	negative regulation of ion transport	1.493E-08	16	57
321	response to toxin	1.651E-08	29	174

322	regulated secretory pathway	1.660E-08	12	31
323	response to defense-related nitric oxide production by other organism involved in symbiotic interaction	1.732E-08	6	6
324	response to defense-related host nitric oxide production	1.732E-08	6	6
325	myeloid leukocyte activation	1.761E-08	21	98
326	negative regulation of synaptic transmission, GABAergic	1.860E-08	9	16
327	nucleotide metabolic process	2.074E-08	81	837
328	nucleoside phosphate metabolic process	2.074E-08	81	837
329	activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger	2.129E-08	21	99
330	behavioral response to pain	2.188E-08	11	26
331	response to drug	2.392E-08	68	658
332	developmental maturation	2.436E-08	31	198
333	cellular membrane organization	2.490E-08	67	645
334	calcium ion transport into cytosol	2.803E-08	15	52
335	forebrain development	2.891E-08	45	361
336	membrane organization	2.982E-08	67	648
337	regulation of neuron projection development	3.328E-08	36	256
338	regulation of GTP catabolic process	3.533E-08	43	339
339	positive regulation of response to stimulus	3.592E-08	103	1171
340	regulation of heart rate	3.726E-08	15	53
341	purine nucleotide biosynthetic process	4.070E-08	29	181
342	cytosolic calcium ion transport	4.917E-08	15	54
343	receptor metabolic process	4.967E-08	19	86
344	nucleoside monophosphate biosynthetic process	4.967E-08	19	86
345	glial cell differentiation	5.240E-08	25	142
346	regulation of smooth muscle contraction	5.450E-08	18	78
347	negative regulation of heart contraction	5.533E-08	11	28
348	mast cell activation	5.533E-08	11	28
349	dopamine receptor signaling pathway	5.596E-08	12	34
350	positive regulation of signal transduction	5.817E-08	72	729
351	nitrogen compound transport	5.983E-08	34	239
352	regulation of behavior	6.009E-08	26	153
353	response to pain	6.774E-08	13	41
354	smooth muscle contraction	7.077E-08	16	63
355	glutamate secretion	7.080E-08	10	23
356	regulation of growth	7.436E-08	65	636
357	regulation of GTPase activity	7.714E-08	42	336
358	anion transport	8.148E-08	34	242
359	endocytosis	8.195E-08	43	349
360	membrane invagination	8.195E-08	43	349
361	rhythmic synaptic transmission	9.200E-08	7	10
362	regulation of signal transduction	9.349E-08	141	1788
363	adenosine receptor signaling pathway	1.014E-07	8	14
364	inositol phosphate-mediated signaling	1.048E-07	21	108
365	chloride transport	1.206E-07	23	128
366	regulation of cell migration	1.306E-07	48	418
367	positive regulation of calcium ion transport via voltage-gated calcium channel activity	1.307E-07	9	19
368	regulation of cell motility	1.414E-07	49	432
369	adult locomotory behavior	1.556E-07	19	92
370	positive regulation of nitric oxide biosynthetic process	1.618E-07	14	51
371	myeloid cell activation involved in immune response	1.640E-07	12	37
372	negative regulation of molecular function	1.693E-07	81	879
373	response to carbohydrate stimulus	1.699E-07	30	204

374	activation of protein kinase activity	1.699E-07	30	204
375	purine-containing compound biosynthetic process	1.700E-07	29	193
376	calcium ion-dependent exocytosis	1.730E-07	13	44
377	response to amphetamine	1.730E-07	13	44
378	oligodendrocyte differentiation	1.784E-07	15	59
379	prepulse inhibition	1.842E-07	10	25
380	regulation of cGMP metabolic process	1.894E-07	11	31
381	vesicle docking involved in exocytosis	1.894E-07	11	31
382	positive regulation of MAP kinase activity	1.995E-07	32	228
383	regulation of cellular component movement	2.121E-07	51	464
384	nucleobase, nucleoside and nucleotide metabolic process	2.177E-07	82	899
385	regulation of cell death	2.257E-07	124	1543
386	positive regulation of cellular component biogenesis	2.269E-07	9	20
387	G-protein coupled purinergic receptor signaling pathway	2.286E-07	12	38
388	purinergic receptor signaling pathway	2.320E-07	13	45
389	cell surface receptor linked signaling pathway	2.439E-07	221	3156
390	positive regulation of GTPase activity	2.691E-07	38	302
391	negative regulation of calcium ion transport	2.754E-07	11	32
392	neuromuscular process controlling balance	2.865E-07	15	61
393	response to endogenous stimulus	3.078E-07	112	1363
394	enzyme linked receptor protein signaling pathway	3.134E-07	76	819
395	regulation of MAPKKK cascade	3.373E-07	43	367
396	histone H3-T6 phosphorylation	3.413E-07	5	5
397	positive regulation of behavior	3.730E-07	19	97
398	negative regulation of cellular process	3.788E-07	211	3002
399	glial cell development	3.825E-07	18	88
400	vesicle docking	3.941E-07	11	33
401	negative regulation of ossification	3.941E-07	11	33
402	axon ensheathment in central nervous system	3.965E-07	8	16
403	central nervous system myelination	3.965E-07	8	16
404	response to alkaloid	4.064E-07	26	168
405	positive regulation of the force of heart contraction by epinephrine-norepinephrine	4.438E-07	6	8
406	localization of cell	4.508E-07	68	711
407	cell motility	4.508E-07	68	711
408	phosphorylation	4.697E-07	102	1219
409	amine transport	5.058E-07	29	203
410	regulation of multicellular organism growth	5.197E-07	19	99
411	positive regulation of calcium ion transport	5.454E-07	17	81
412	relaxation of vascular smooth muscle	5.547E-07	7	12
413	regulation of dopamine secretion	5.558E-07	11	34
414	sodium ion transmembrane transport	5.613E-07	15	64
415	cAMP metabolic process	5.787E-07	12	41
416	regulation of homeostatic process	5.952E-07	36	287
417	cellular component organization	6.029E-07	277	4177
418	phasic smooth muscle contraction	6.124E-07	9	22
419	striated muscle contraction	6.557E-07	17	82
420	relaxation of muscle	7.154E-07	8	17
421	ionotropic glutamate receptor signaling pathway	7.154E-07	8	17
422	phosphate metabolic process	7.500E-07	116	1451
423	negative regulation of signaling	7.687E-07	62	636
424	phosphorus metabolic process	7.761E-07	116	1452
425	response to organic substance	7.789E-07	172	2368
426	positive regulation of chemotaxis	7.858E-07	17	83
427	protein phosphorylation	8.657E-07	80	900

428	negative regulation of cell communication	9.011E-07	62	639
429	nucleotide biosynthetic process	9.161E-07	31	232
430	response to metal ion	9.343E-07	44	394
431	positive regulation of MAPKKK cascade	9.351E-07	29	209
432	response to dietary excess	9.606E-07	9	23
433	positive regulation of organ growth	9.606E-07	9	23
434	regulation of anatomical structure size	9.621E-07	60	612
435	positive regulation of exocytosis	1.022E-06	12	43
436	regulation of calcium ion-dependent exocytosis	1.022E-06	12	43
437	regulation of cellular protein metabolic process	1.027E-06	111	1381
438	inorganic anion transport	1.135E-06	25	166
439	response to tropane	1.136E-06	14	59
440	response to cocaine	1.136E-06	14	59
441	MAPKKK cascade	1.189E-06	39	333
442	negative regulation of organic acid transport	1.230E-06	8	18
443	negative regulation of cell death	1.248E-06	69	746
444	neuronal signal transduction	1.274E-06	6	9
445	positive regulation of the force of heart contraction by chemical signal	1.274E-06	6	9
446	regulation of G-protein coupled receptor protein signaling pathway	1.356E-06	20	115
447	regulation of protein modification process	1.382E-06	92	1093
448	response to hormone stimulus	1.452E-06	96	1156
449	nucleobase, nucleoside and nucleotide biosynthetic process	1.462E-06	32	249
450	nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	1.462E-06	32	249
451	regulation of dopamine metabolic process	1.467E-06	9	24
452	inflammatory response	1.561E-06	50	482
453	leukocyte activation	1.617E-06	49	469
454	regulation of potassium ion transport	1.889E-06	10	31
455	transmembrane receptor protein tyrosine kinase signaling pathway	1.909E-06	60	625
456	regulation of sodium ion transport	1.937E-06	11	38
457	positive regulation of heart growth	1.961E-06	5	6
458	vasodilation by norepinephrine-epinephrine involved in regulation of systemic arterial blood pressure	1.961E-06	5	6
459	histone-threonine phosphorylation	1.961E-06	5	6
460	regulation of synaptic vesicle fusion to presynaptic membrane	1.961E-06	5	6
461	positive regulation of nervous system development	2.030E-06	8	19
462	positive regulation of synaptogenesis	2.030E-06	8	19
463	regulation of developmental growth	2.058E-06	20	118
464	elevation of cytosolic calcium ion concentration involved in G-protein signaling coupled to IP3 second messenger	2.189E-06	9	25
465	regulation of synapse maturation	2.196E-06	7	14
466	response to immune response of other organism involved in symbiotic interaction	2.196E-06	7	14
467	negative regulation of glutamate secretion	2.196E-06	7	14
468	response to host immune response	2.196E-06	7	14
469	adult walking behavior	2.251E-06	12	46
470	regulation of blood vessel endothelial cell migration	2.251E-06	12	46
471	regulation of protein serine/threonine kinase activity	2.273E-06	46	434
472	renal system process	2.301E-06	16	80
473	regulation of MAP kinase activity	2.345E-06	36	304
474	regulation of programmed cell death	2.399E-06	117	1502
475	activation of MAPK activity	2.458E-06	25	173
476	positive regulation of vasoconstriction	2.574E-06	11	39

477	oligodendrocyte development	2.574E-06	11	39
478	response to light stimulus	2.617E-06	33	268
479	cellular component movement	2.728E-06	73	822
480	positive regulation of inflammatory response	2.752E-06	19	110
481	negative regulation of blood pressure	2.868E-06	13	55
482	organic substance transport	2.880E-06	53	534
483	negative regulation of response to stimulus	2.884E-06	69	764
484	cell migration	3.112E-06	61	649
485	regulation of fatty acid transport	3.197E-06	9	26
486	nucleoside monophosphate catabolic process	3.197E-06	9	26
487	regulation of nitric oxide biosynthetic process	3.222E-06	14	64
488	response to host defenses	3.232E-06	8	20
489	negative regulation of systemic arterial blood pressure	3.232E-06	8	20
490	response to defenses of other organism involved in symbiotic interaction	3.232E-06	8	20
491	response to host	3.232E-06	8	20
492	regulation of endothelial cell migration	3.327E-06	15	73
493	membrane docking	3.388E-06	11	40
494	regulation of protein metabolic process	3.588E-06	119	1547
495	long-term memory	3.591E-06	10	33
496	positive regulation of sodium ion transport	3.936E-06	7	15
497	regulation of acetylcholine secretion	3.936E-06	7	15
498	negative regulation of calcium ion transport via voltage-gated calcium channel activity	3.936E-06	7	15
499	activation of adenylate cyclase activity by dopamine receptor signaling pathway	3.936E-06	7	15
500	serotonin metabolic process	3.936E-06	7	15
501	regulation of intracellular protein kinase cascade	3.942E-06	59	625
502	regulation of chemotaxis	4.213E-06	18	103
503	regulation of apoptosis	4.406E-06	115	1489
504	regulation of catecholamine metabolic process	4.579E-06	9	27
505	regulation of urine volume	4.579E-06	9	27
506	protein complex assembly	4.581E-06	66	730
507	forebrain cell migration	4.633E-06	12	49
508	monovalent inorganic cation transport	4.835E-06	41	379
509	negative regulation of developmental process	5.127E-06	55	573
510	protein complex biogenesis	5.247E-06	66	733
511	potassium ion transport	5.285E-06	24	169
512	cellular component organization or biogenesis	5.322E-06	278	4304
513	response to hexose stimulus	5.861E-06	24	170
514	negative regulation of urine volume	6.411E-06	6	11
515	gamma-aminobutyric acid transport	6.411E-06	6	11
516	regulation of the force of heart contraction by chemical signal	6.411E-06	6	11
517	cGMP-mediated signaling	6.444E-06	9	28
518	neuron recognition	6.489E-06	10	35
519	neurotransmitter metabolic process	6.489E-06	10	35
520	negative regulation of gamma-aminobutyric acid secretion	6.574E-06	5	7
521	feeding behavior	6.582E-06	20	127
522	negative regulation of hormone secretion	6.668E-06	15	77
523	positive regulation of neurotransmitter transport	6.689E-06	7	16
524	negative regulation of cAMP biosynthetic process	6.689E-06	7	16
525	positive regulation of the force of heart contraction by norepinephrine	6.719E-06	4	4
526	positive regulation of the force of heart contraction by epinephrine	6.719E-06	4	4

527	response to progesterone stimulus	6.859E-06	14	68
528	pallium development	7.612E-06	22	150
529	response to steroid hormone stimulus	7.614E-06	58	624
530	response to monosaccharide stimulus	7.952E-06	24	173
531	positive regulation of intracellular protein kinase cascade	8.229E-06	44	428
532	regulation of inflammatory response	8.430E-06	29	233
533	regulation of positive chemotaxis	8.576E-06	10	36
534	peptidyl-threonine phosphorylation	8.576E-06	10	36
535	positive regulation of ion transmembrane transporter activity	8.576E-06	10	36
536	positive regulation of cell death	8.602E-06	68	774
537	positive regulation of cell differentiation	8.770E-06	56	598
538	negative regulation of response to external stimulus	9.555E-06	21	141
539	G-protein coupled receptor protein signaling pathway	9.875E-06	117	1548
540	rhythmic process	1.003E-05	35	311
541	negative regulation of nucleotide biosynthetic process	1.087E-05	7	17
542	negative regulation of cyclic nucleotide biosynthetic process	1.087E-05	7	17
543	negative regulation of cAMP metabolic process	1.087E-05	7	17
544	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway	1.109E-05	12	53
545	positive regulation of phosphatidylinositol 3-kinase cascade	1.122E-05	10	37
546	nerve growth factor receptor signaling pathway	1.206E-05	32	275
547	regulation of macrophage cytokine production	1.227E-05	6	12
548	positive regulation of odontogenesis	1.227E-05	6	12
549	positive regulation of neurotransmitter secretion	1.227E-05	6	12
550	positive regulation of blood pressure by epinephrine-norepinephrine	1.227E-05	6	12
551	cellular component assembly	1.239E-05	111	1458
552	negative regulation of apoptosis	1.299E-05	63	709
553	hormone secretion	1.313E-05	16	91
554	calcium-mediated signaling	1.416E-05	13	63
555	positive regulation of cellular component organization	1.446E-05	50	522
556	hormone transport	1.485E-05	17	102
557	glycerolipid metabolic process	1.506E-05	32	278
558	positive regulation of hormone secretion	1.515E-05	16	92
559	heterocycle metabolic process	1.595E-05	84	1035
560	regulation of small GTPase mediated signal transduction	1.608E-05	42	412
561	positive regulation of excitatory postsynaptic membrane potential	1.679E-05	5	8
562	positive regulation of peptide secretion	1.695E-05	13	64
563	cyclic nucleotide catabolic process	1.701E-05	7	18
564	negative regulation of cyclic nucleotide metabolic process	1.701E-05	7	18
565	positive regulation of muscle organ development	1.701E-05	7	18
566	positive regulation of G-protein coupled receptor protein signaling pathway	1.701E-05	7	18
567	positive regulation of striated muscle tissue development	1.701E-05	7	18
568	sodium ion transport	1.834E-05	21	147
569	negative regulation of programmed cell death	1.834E-05	63	717
570	release of sequestered calcium ion into cytosol	1.866E-05	10	39
571	positive regulation of transporter activity	1.866E-05	10	39
572	negative regulation of sequestering of calcium ion	1.866E-05	10	39
573	peptidyl-threonine modification	1.866E-05	10	39
574	response to mineralocorticoid stimulus	2.016E-05	12	56
575	L-amino acid import	2.180E-05	6	13
576	negative regulation of heart rate	2.180E-05	6	13
577	adrenergic receptor signaling pathway	2.180E-05	6	13

578	regulation of systemic arterial blood pressure by norepinephrine-epinephrine	2.180E-05	6	13
579	leukocyte degranulation	2.208E-05	8	25
580	negative regulation of peptide secretion	2.436E-05	12	57
581	positive regulation of programmed cell death	2.554E-05	65	755
582	positive regulation of renal sodium excretion	2.574E-05	7	19
583	regulation of smooth muscle cell proliferation	2.627E-05	19	128
584	response to corticosteroid stimulus	2.664E-05	32	286
585	positive regulation of developmental growth	2.801E-05	11	49
586	nucleobase, nucleoside, nucleotide and nucleic acid catabolic process	2.836E-05	53	579
587	nucleobase, nucleoside and nucleotide catabolic process	2.836E-05	53	579
588	positive regulation of heart contraction	2.857E-05	9	33
589	regulation of sequestering of calcium ion	2.998E-05	10	41
590	cellular component organization at cellular level	3.034E-05	214	3253
591	regulation of establishment of protein localization	3.035E-05	33	301
592	phenol-containing compound metabolic process	3.088E-05	15	87
593	hippocampus development	3.088E-05	15	87
594	carboxylic acid transport	3.147E-05	28	237
595	phosphatidylinositol metabolic process	3.198E-05	17	108
596	protein oligomerization	3.215E-05	38	369
597	musculoskeletal movement, spinal reflex action	3.223E-05	4	5
598	positive regulation of skeletal muscle tissue growth	3.223E-05	4	5
599	positive regulation of cell growth involved in cardiac muscle cell development	3.223E-05	4	5
600	regulation of cell growth involved in cardiac muscle cell development	3.223E-05	4	5
601	positive regulation of cardiac muscle tissue growth	3.223E-05	4	5
602	heterocycle biosynthetic process	3.245E-05	33	302
603	nucleotide catabolic process	3.286E-05	51	553
604	defense response	3.468E-05	93	1201
605	diet induced thermogenesis	3.619E-05	5	9
606	positive regulation of heart rate by epinephrine-norepinephrine	3.619E-05	5	9
607	regulation of somatostatin secretion	3.619E-05	5	9
608	gamma-aminobutyric acid secretion	3.619E-05	5	9
609	organ development	3.639E-05	192	2875
610	amino acid import	3.650E-05	6	14
611	protein heterotetramerization	3.650E-05	6	14
612	organic acid transport	3.665E-05	28	239
613	response to dexamethasone stimulus	3.711E-05	9	34
614	dopamine metabolic process	3.711E-05	9	34
615	grooming behavior	3.786E-05	7	20
616	metabotropic glutamate receptor signaling pathway	3.786E-05	7	20
617	negative regulation of nucleotide metabolic process	3.786E-05	7	20
618	intracellular protein kinase cascade	3.856E-05	52	571
619	aging	4.022E-05	35	332
620	negative regulation of cellular component organization	4.069E-05	38	373
621	response to calcium ion	4.522E-05	19	133
622	regulation of protein secretion	4.610E-05	18	122
623	regulation of synaptogenesis	4.771E-05	9	35
624	positive regulation of positive chemotaxis	4.771E-05	9	35
625	regulation of dephosphorylation	4.972E-05	12	61
626	positive regulation of peptide hormone secretion	4.972E-05	12	61
627	response to extracellular stimulus	5.029E-05	58	666
628	response to nutrient	5.117E-05	43	447

629	regulation of hormone levels	5.230E-05	32	296
630	regulation of anatomical structure morphogenesis	5.408E-05	54	608
631	response to oxygen levels	5.425E-05	38	378
632	desensitization of G-protein coupled receptor protein signaling pathway	5.536E-05	8	28
633	regulation of renal sodium excretion	5.536E-05	8	28
634	negative adaptation of signaling pathway	5.536E-05	8	28
635	adaptation of signaling pathway	5.536E-05	8	28
636	negative regulation of amine transport	5.536E-05	8	28
637	regulation of endocytosis	5.540E-05	22	170
638	regulation of dendritic spine development	5.820E-05	6	15
639	regulation of vesicle fusion	5.820E-05	6	15
640	mast cell degranulation	5.820E-05	6	15
641	positive regulation of membrane potential	5.820E-05	6	15
642	mast cell activation involved in immune response	5.820E-05	6	15
643	response to estradiol stimulus	5.889E-05	24	195
644	positive regulation of immune effector process	6.011E-05	21	159
645	purine-containing compound catabolic process	6.093E-05	49	537
646	cellular nitrogen compound catabolic process	6.161E-05	54	611
647	response to growth factor stimulus	6.593E-05	21	160
648	negative regulation of amino acid transport	6.933E-05	5	10
649	positive regulation of synapse maturation	6.933E-05	5	10
650	neural precursor cell proliferation	6.934E-05	12	63
651	neutrophil chemotaxis	7.086E-05	10	45
652	positive regulation of endothelial cell migration	7.086E-05	10	45
653	immune response-activating cell surface receptor signaling pathway	7.225E-05	21	161
654	glycerophospholipid metabolic process	7.225E-05	22	173
655	regulation of glucose import	7.286E-05	11	54
656	regulation of lipid catabolic process	7.286E-05	11	54
657	regulation of protein localization	7.370E-05	35	342
658	negative regulation of ion transmembrane transporter activity	7.614E-05	7	22
659	negative regulation of lipid catabolic process	7.614E-05	7	22
660	cellular component assembly at cellular level	7.619E-05	80	1018
661	purinergic nucleotide receptor signaling pathway	7.668E-05	9	37
662	positive regulation of multicellular organismal metabolic process	7.668E-05	9	37
663	negative regulation of catabolic process	7.816E-05	15	94
664	response to glucose stimulus	7.910E-05	21	162
665	negative regulation of growth	8.123E-05	27	237
666	response to organic nitrogen	8.136E-05	34	330
667	telencephalon cell migration	8.645E-05	10	46
668	regulation of phosphatidylinositol 3-kinase cascade	8.645E-05	10	46
669	response to morphine	8.645E-05	10	46
670	purine nucleotide catabolic process	8.664E-05	48	530
671	regulation of calcium ion transport into cytosol	8.692E-05	11	55
672	cAMP catabolic process	8.911E-05	6	16
673	mast cell mediated immunity	8.911E-05	6	16
674	calcium ion-dependent exocytosis of neurotransmitter	9.276E-05	4	6
675	positive regulation of saliva secretion	9.276E-05	4	6
676	positive regulation of cardiac muscle tissue development	9.276E-05	4	6
677	regulation of skeletal muscle tissue growth	9.276E-05	4	6
678	regulation of neuron maturation	9.276E-05	4	6
679	synaptic vesicle priming	9.276E-05	4	6

680	positive regulation of odontogenesis of dentine-containing tooth	9.276E-05	4	6
681	small molecule biosynthetic process	9.422E-05	54	621
682	negative regulation of transporter activity	9.519E-05	8	30
683	G-protein coupled purinergic nucleotide receptor signaling pathway	9.519E-05	8	30
684	peptide hormone secretion	9.529E-05	12	65
685	response to estrogen stimulus	9.537E-05	31	292
686	regulation of phosphatase activity	9.596E-05	9	38
687	response to radiation	9.703E-05	41	431
688	protein localization	9.808E-05	100	1350
689	tissue remodeling	1.005E-04	17	118
690	regulation of cellular component biogenesis	1.011E-04	33	320
691	response to nutrient levels	1.024E-04	54	623
692	negative regulation of peptide hormone secretion	1.032E-04	11	56
693	synaptic transmission, GABAergic	1.047E-04	7	23
694	response to isoquinoline alkaloid	1.048E-04	10	47
695	response to temperature stimulus	1.074E-04	23	190
696	regulation of lipid metabolic process	1.074E-04	28	254
697	cellular process	1.105E-04	800	14653
698	regulation of organ growth	1.119E-04	13	76
699	leukocyte migration	1.157E-04	27	242
700	positive regulation of smooth muscle cell migration	1.192E-04	9	39
701	lipid phosphorylation	1.192E-04	9	39
702	phospholipid metabolic process	1.210E-04	29	269
703	L-glutamate import	1.218E-04	5	11
704	activation of phospholipase C activity by dopamine receptor signaling pathway	1.218E-04	5	11
705	elastic fiber assembly	1.218E-04	5	11
706	amino acid transport	1.224E-04	19	143
707	vasoconstriction	1.226E-04	8	31
708	immune response-regulating cell surface receptor signaling pathway	1.228E-04	21	167
709	response to lipid	1.242E-04	17	120
710	regulation of multicellular organismal metabolic process	1.264E-04	10	48
711	positive regulation of cardiac muscle hypertrophy	1.318E-04	6	17
712	positive regulation of muscle hypertrophy	1.318E-04	6	17
713	positive regulation of fatty acid transport	1.318E-04	6	17
714	positive regulation of plasma membrane long-chain fatty acid transport	1.321E-04	3	3
715	cerebellum maturation	1.321E-04	3	3
716	vestibular nucleus development	1.321E-04	3	3
717	negative regulation of neuron maturation	1.321E-04	3	3
718	cellular response to histamine	1.321E-04	3	3
719	spinal cord oligodendrocyte cell fate specification	1.321E-04	3	3
720	cerebellar molecular layer development	1.321E-04	3	3
721	positive regulation of smooth muscle cell chemotaxis	1.321E-04	3	3
722	spinal cord oligodendrocyte cell differentiation	1.321E-04	3	3
723	detection of abiotic stimulus	1.377E-04	17	121
724	positive regulation of cAMP biosynthetic process	1.469E-04	9	40
725	regulation of calcium-mediated signaling	1.469E-04	9	40
726	positive regulation of ERK1 and ERK2 cascade	1.470E-04	13	78
727	peptide secretion	1.497E-04	12	68
728	regulation of cell adhesion	1.502E-04	32	313
729	regulation of systemic arterial blood pressure mediated by a chemical signal	1.517E-04	10	49

730	response to electrical stimulus	1.517E-04	10	49
731	regulation of vasodilation	1.517E-04	10	49
732	negative regulation of neuron apoptosis	1.526E-04	17	122
733	microspike assembly	1.562E-04	8	32
734	regulation of excretion	1.562E-04	8	32
735	detection of external stimulus	1.589E-04	18	134
736	leukocyte activation involved in immune response	1.602E-04	15	100
737	cell activation involved in immune response	1.602E-04	15	100
738	regulation of cell morphogenesis	1.618E-04	30	287
739	regulation of bone mineralization	1.687E-04	11	59
740	small molecule metabolic process	1.734E-04	162	2428
741	macromolecule localization	1.753E-04	115	1622
742	heterocycle catabolic process	1.754E-04	52	606
743	negative regulation of cell adhesion	1.794E-04	15	101
744	positive regulation of catecholamine secretion	1.876E-04	7	25
745	regulation of norepinephrine secretion	1.876E-04	7	25
746	regulation of neuron apoptosis	1.883E-04	26	236
747	actin filament-based process	1.884E-04	40	430
748	neurotransmitter uptake	1.892E-04	6	18
749	phosphatidylinositol 3-kinase cascade	1.892E-04	6	18
750	carbohydrate homeostasis	1.920E-04	18	136
751	glucose homeostasis	1.920E-04	18	136
752	regulation of striated muscle tissue development	1.956E-04	16	113
753	positive regulation of vasodilation	1.971E-04	8	33
754	response to yeast	2.000E-04	5	12
755	regulation of synaptic vesicle exocytosis	2.000E-04	5	12
756	positive regulation of penile erection	2.000E-04	5	12
757	cellular response to lipoteichoic acid	2.077E-04	4	7
758	regulation of cardiac muscle cell differentiation	2.077E-04	4	7
759	involuntary skeletal muscle contraction	2.077E-04	4	7
760	regulation of melanocyte differentiation	2.077E-04	4	7
761	diaphragm contraction	2.077E-04	4	7
762	regulation of saliva secretion	2.077E-04	4	7
763	positive regulation of mucus secretion	2.077E-04	4	7
764	desensitization of G-protein coupled receptor protein signaling pathway by arrestin	2.077E-04	4	7
765	response to lipoteichoic acid	2.077E-04	4	7
766	regulation of pigment cell differentiation	2.077E-04	4	7
767	response to histamine	2.077E-04	4	7
768	positive regulation of apoptosis	2.111E-04	61	749
769	cellular protein localization	2.115E-04	59	718
770	negative regulation of G-protein coupled receptor protein signaling pathway	2.185E-04	9	42
771	positive regulation of cAMP metabolic process	2.185E-04	9	42
772	positive regulation of growth	2.270E-04	22	187
773	regulation of dendrite development	2.287E-04	12	71
774	response to glucocorticoid stimulus	2.347E-04	28	266
775	regulation of immune response	2.354E-04	57	690
776	regulation of muscle organ development	2.403E-04	16	115
777	cellular component organization or biogenesis at cellular level	2.412E-04	214	3367
778	positive regulation of blood vessel endothelial cell migration	2.455E-04	7	26
779	phosphatidylinositol phosphorylation	2.463E-04	8	34
780	positive regulation of lipid transport	2.463E-04	8	34
781	mononuclear cell proliferation	2.463E-04	13	82
782	small GTPase mediated signal transduction	2.482E-04	42	465

783	negative regulation of neurogenesis	2.496E-04	15	104
784	regulation of Ras protein signal transduction	2.516E-04	32	322
785	cellular macromolecule localization	2.534E-04	59	723
786	negative regulation of blood vessel endothelial cell migration	2.646E-04	6	19
787	G-protein signaling, coupled to cGMP nucleotide second messenger	2.646E-04	6	19
788	response to fungicide	2.646E-04	6	19
789	vesicle organization	2.658E-04	16	116
790	hindbrain development	2.768E-04	18	140
791	actin filament organization	2.768E-04	18	140
792	limbic system development	2.777E-04	15	105
793	leukocyte proliferation	2.787E-04	13	83
794	positive regulation of phosphorus metabolic process	2.809E-04	33	338
795	positive regulation of phosphate metabolic process	2.809E-04	33	338
796	negative regulation of signal transduction	2.872E-04	50	588
797	positive regulation of I-kappaB kinase/NF-kappaB cascade	2.895E-04	20	165
798	multicellular organismal homeostasis	2.895E-04	20	165
799	protein complex subunit organization	2.922E-04	66	837
800	catechol metabolic process	2.992E-04	10	53
801	catecholamine metabolic process	2.992E-04	10	53
802	diol metabolic process	2.992E-04	10	53
803	positive regulation of bone mineralization	3.051E-04	8	35
804	regulation of heart growth	3.051E-04	8	35
805	benzene-containing compound metabolic process	3.085E-04	15	106
806	regulation of axon regeneration	3.113E-04	5	13
807	peristalsis	3.113E-04	5	13
808	regulation of neuron projection regeneration	3.113E-04	5	13
809	positive regulation of skeletal muscle tissue development	3.113E-04	5	13
810	positive regulation of potassium ion transport	3.113E-04	5	13
811	negative regulation of myeloid cell apoptosis	3.113E-04	5	13
812	positive regulation of protein secretion	3.146E-04	13	84
813	negative regulation of endothelial cell migration	3.170E-04	7	27
814	positive regulation of systemic arterial blood pressure	3.170E-04	7	27
815	sleep	3.170E-04	7	27
816	acidic amino acid transport	3.170E-04	7	27
817	tissue homeostasis	3.239E-04	16	118
818	homophilic cell adhesion	3.241E-04	19	154
819	cell death	3.297E-04	86	1164
820	negative regulation of locomotion	3.302E-04	18	142
821	digestion	3.306E-04	17	130
822	actin cytoskeleton organization	3.335E-04	36	384
823	negative regulation of lipid metabolic process	3.406E-04	12	74
824	response to hypoxia	3.474E-04	33	342
825	regulation of ossification	3.499E-04	21	180
826	negative regulation of insulin secretion	3.506E-04	10	54
827	organ growth	3.506E-04	10	54
828	regulation of acute inflammatory response	3.543E-04	13	85
829	regulation of biomineral tissue development	3.553E-04	11	64
830	positive regulation of nitric-oxide synthase activity	3.618E-04	6	20
831	regulation of ATPase activity	3.749E-04	8	36
832	response to peptide hormone stimulus	3.776E-04	50	595
833	temperature homeostasis	3.785E-04	9	45
834	regulation of protein transport	3.815E-04	28	274
835	cell maturation	3.924E-04	18	144
836	receptor-mediated endocytosis	3.941E-04	14	97

837	positive regulation of phosphoprotein phosphatase activity	3.986E-04	4	8
838	striated muscle myosin thick filament assembly	3.986E-04	4	8
839	skeletal muscle myosin thick filament assembly	3.986E-04	4	8
840	regulation of plasma membrane long-chain fatty acid transport	3.986E-04	4	8
841	death	3.988E-04	86	1171
842	ribonucleotide metabolic process	4.027E-04	51	612
843	regulation of lipid kinase activity	4.042E-04	7	28
844	purine ribonucleotide metabolic process	4.078E-04	50	597
845	positive regulation of blood pressure	4.083E-04	11	65
846	positive regulation of ossification	4.092E-04	10	55
847	regulation of systemic arterial blood pressure	4.386E-04	12	76
848	positive regulation of cell proliferation	4.433E-04	65	834
849	positive regulation of biomineral tissue development	4.572E-04	8	37
850	organophosphate metabolic process	4.586E-04	29	291
851	protein kinase C signaling cascade	4.640E-04	5	14
852	skeletal myofibril assembly	4.640E-04	5	14
853	pons development	4.640E-04	5	14
854	response to folic acid	4.640E-04	5	14
855	glycosphingolipid biosynthetic process	4.640E-04	5	14
856	regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity	4.640E-04	5	14
857	extracellular matrix assembly	4.640E-04	5	14
858	regulation of growth hormone secretion	4.640E-04	5	14
859	axonal fasciculation	4.640E-04	5	14
860	positive regulation of glutamate secretion	4.640E-04	5	14
861	positive regulation of tumor necrosis factor biosynthetic process	4.640E-04	5	14
862	protein targeting	4.838E-04	31	320
863	response to fluid shear stress	4.848E-04	6	21
864	regulation of lipid transport	4.958E-04	12	77
865	positive regulation of muscle cell differentiation	4.958E-04	12	77
866	protein heterooligomerization	5.045E-04	18	147
867	negative regulation of synapse maturation	5.084E-04	3	4
868	regulation of smooth muscle cell chemotaxis	5.084E-04	3	4
869	regulation of digestive system process	5.096E-04	7	29
870	positive regulation of Ras protein signal transduction	5.096E-04	7	29
871	insulin secretion	5.312E-04	9	47
872	energy derivation by oxidation of organic compounds	5.397E-04	36	394
873	regulation of immune effector process	5.420E-04	29	294
874	germ cell development	5.437E-04	21	186
875	positive regulation of protein transport	5.476E-04	18	148
876	negative regulation of neuron projection development	5.535E-04	8	38
877	musculoskeletal movement	5.535E-04	8	38
878	positive regulation of glucose import	5.535E-04	8	38
879	multicellular organismal movement	5.535E-04	8	38
880	positive regulation of chemokine production	5.535E-04	8	38
881	cellular nitrogen compound biosynthetic process	5.679E-04	41	469
882	regulation of cell morphogenesis involved in differentiation	5.808E-04	22	200
883	regulation of cell growth	5.811E-04	35	381
884	positive regulation of cell development	6.216E-04	22	201
885	lymphocyte proliferation	6.294E-04	12	79
886	neuron maturation	6.357E-04	7	30
887	indolalkylamine metabolic process	6.357E-04	7	30
888	indole-containing compound metabolic process	6.357E-04	7	30
889	regulation of cell size	6.362E-04	38	427

890	regulation of phosphatidylinositol 3-kinase activity	6.381E-04	6	22
891	cellular component biogenesis	6.544E-04	111	1611
892	plasma membrane organization	6.656E-04	8	39
893	negative regulation of multicellular organism growth	6.669E-04	5	15
894	macrophage activation involved in immune response	6.669E-04	5	15
895	respiratory system process	6.669E-04	5	15
896	histamine secretion	6.669E-04	5	15
897	neurotransmitter biosynthetic process	6.669E-04	5	15
898	vascular smooth muscle contraction	6.669E-04	5	15
899	tolerance induction	6.669E-04	5	15
900	regulation of penile erection	6.669E-04	5	15
901	purine ribonucleoside triphosphate metabolic process	6.687E-04	47	564
902	regulation of axonogenesis	6.792E-04	15	114
903	cGMP catabolic process	6.885E-04	4	9
904	plasma membrane repair	6.885E-04	4	9
905	regulation of mucus secretion	6.885E-04	4	9
906	artery smooth muscle contraction	6.885E-04	4	9
907	tonic smooth muscle contraction	6.885E-04	4	9
908	short-term memory	6.885E-04	4	9
909	bleb assembly	6.885E-04	4	9
910	positive regulation of protein maturation by peptide bond cleavage	6.885E-04	4	9
911	synaptic vesicle maturation	6.885E-04	4	9
912	sperm ejaculation	6.885E-04	4	9
913	potassium ion transmembrane transport	6.939E-04	13	91
914	cellular potassium ion transport	6.939E-04	13	91
915	cell junction organization	6.955E-04	23	216
916	positive regulation of phosphorylation	6.960E-04	31	327
917	regulation of cell proliferation	6.973E-04	100	1427
918	phagocytosis	7.309E-04	14	103
919	regulation of neural precursor cell proliferation	7.310E-04	9	49
920	blood vessel remodeling	7.310E-04	9	49
921	regulation of cellular response to stress	7.469E-04	26	258
922	ribonucleoside triphosphate metabolic process	7.487E-04	47	567
923	regulation of cardiac muscle tissue growth	7.853E-04	7	31
924	ERK1 and ERK2 cascade	7.853E-04	7	31
925	regulation of myeloid leukocyte mediated immunity	7.953E-04	8	40
926	regulation of nitric-oxide synthase activity	7.953E-04	8	40
927	purine nucleoside triphosphate metabolic process	8.066E-04	47	569
928	regulation of cardiac muscle contraction	8.263E-04	6	23
929	T cell proliferation	8.518E-04	9	50
930	cellular response to carbohydrate stimulus	8.518E-04	9	50
931	leukocyte chemotaxis	8.553E-04	13	93
932	positive T cell selection	9.296E-04	5	16
933	reduction of cytosolic calcium ion concentration	9.296E-04	5	16
934	regulation of membrane depolarization	9.296E-04	5	16
935	regulation of feeding behavior	9.296E-04	5	16
936	positive regulation of establishment of protein localization in plasma membrane	9.296E-04	5	16
937	eating behavior	9.445E-04	8	41
938	positive regulation of calcium-mediated signaling	9.615E-04	7	32
939	positive regulation of small GTPase mediated signal transduction	9.615E-04	7	32
940	metencephalon development	1.047E-03	13	95
941	cerebellar Purkinje cell layer development	1.055E-03	6	24
942	positive regulation of heart rate	1.055E-03	6	24

943	positive regulation of striated muscle cell differentiation	1.055E-03	6	24
944	regulation of cardiac muscle hypertrophy	1.055E-03	6	24
945	establishment of protein localization	1.094E-03	78	1077
946	regulation of I-kappaB kinase/NF-kappaB cascade	1.095E-03	20	183
947	muscle fiber development	1.100E-03	12	84
948	response to aluminum ion	1.101E-03	4	10
949	inhibition of adenylate cyclase activity by metabotropic glutamate receptor signaling pathway	1.101E-03	4	10
950	positive regulation of dendritic spine development	1.101E-03	4	10
951	negative regulation of neuroblast proliferation	1.101E-03	4	10
952	positive regulation of inositol phosphate biosynthetic process	1.101E-03	4	10
953	microglial cell activation involved in immune response	1.101E-03	4	10
954	L-amino acid transport	1.115E-03	8	42
955	regulation of production of molecular mediator of immune response	1.120E-03	11	73
956	cellular response to molecule of bacterial origin	1.161E-03	15	120
957	regulation of muscle adaptation	1.167E-03	7	33
958	negative regulation of cell adhesion mediated by integrin	1.223E-03	3	5
959	intestine smooth muscle contraction	1.223E-03	3	5
960	gastro-intestinal system smooth muscle contraction	1.223E-03	3	5
961	oligodendrocyte cell fate specification	1.223E-03	3	5
962	glial cell fate specification	1.223E-03	3	5
963	peptidyl-cysteine methylation	1.223E-03	3	5
964	hindbrain maturation	1.223E-03	3	5
965	negative regulation of serotonin secretion	1.223E-03	3	5
966	NFAT protein import into nucleus	1.223E-03	3	5
967	exploration behavior	1.223E-03	3	5
968	negative regulation of macrophage cytokine production	1.223E-03	3	5
969	negative regulation of axon regeneration	1.223E-03	3	5
970	central nervous system maturation	1.223E-03	3	5
971	negative regulation of inclusion body assembly	1.223E-03	3	5
972	regulation of phagocytosis	1.238E-03	10	63
973	positive regulation of lipid biosynthetic process	1.238E-03	10	63
974	glycolipid biosynthetic process	1.262E-03	5	17
975	histamine transport	1.262E-03	5	17
976	positive regulation of phosphatase activity	1.262E-03	5	17
977	regulation of icosanoid secretion	1.262E-03	5	17
978	regulation of ERK1 and ERK2 cascade	1.274E-03	13	97
979	protein localization to organelle	1.286E-03	30	325
980	myeloid leukocyte mediated immunity	1.310E-03	8	43
981	positive regulation of glucose transport	1.310E-03	8	43
982	regulation of smooth muscle cell migration	1.314E-03	9	53
983	positive regulation of phagocytosis	1.314E-03	9	53
984	circadian rhythm	1.324E-03	16	134
985	positive regulation of monooxygenase activity	1.328E-03	6	25
986	regulation of establishment of protein localization in plasma membrane	1.328E-03	6	25
987	regulation of muscle hypertrophy	1.328E-03	6	25
988	sensory perception of mechanical stimulus	1.338E-03	20	186
989	negative regulation of cell proliferation	1.343E-03	51	646
990	nucleoside triphosphate metabolic process	1.383E-03	47	584
991	cell chemotaxis	1.404E-03	14	110
992	regulation of striated muscle cell differentiation	1.406E-03	11	75
993	regulation of meiotic cell cycle	1.406E-03	7	34
994	B cell receptor signaling pathway	1.406E-03	7	34

995	sodium ion export	1.406E-03	7	34
996	immune effector process	1.409E-03	28	298
997	small molecule catabolic process	1.480E-03	64	858
998	response to cold	1.507E-03	9	54
999	regeneration	1.512E-03	22	215
1000	anatomical structure maturation	1.531E-03	8	44
1001	cerebellar cortex development	1.531E-03	8	44
1002	multicellular organismal reproductive process	1.536E-03	66	892
1003	multicellular organism reproduction	1.536E-03	66	892
1004	cell recognition	1.540E-03	13	99
1005	peripheral nervous system development	1.569E-03	11	76
1006	growth	1.583E-03	39	464
1007	negative regulation of cell development	1.622E-03	15	124
1008	positive regulation of ATPase activity	1.653E-03	6	26
1009	myosin filament assembly	1.661E-03	4	11
1010	regulation of epinephrine secretion	1.661E-03	4	11
1011	detection of mechanical stimulus involved in sensory perception of pain	1.661E-03	4	11
1012	cardiac muscle hypertrophy	1.661E-03	4	11
1013	cerebral cortex GABAergic interneuron differentiation	1.661E-03	4	11
1014	myosin filament organization	1.661E-03	4	11
1015	striated muscle hypertrophy	1.661E-03	4	11
1016	regulation of inositol phosphate biosynthetic process	1.661E-03	4	11
1017	cardiac muscle fiber development	1.661E-03	4	11
1018	cellular response to growth factor stimulus	1.672E-03	14	112
1019	positive regulation of urine volume	1.675E-03	5	18
1020	reflex	1.675E-03	5	18
1021	histone phosphorylation	1.675E-03	5	18
1022	astrocyte differentiation	1.681E-03	7	35
1023	regulation of cardiac muscle tissue development	1.681E-03	7	35
1024	positive regulation of calcium ion transport into cytosol	1.681E-03	7	35
1025	regulation of humoral immune response	1.681E-03	7	35
1026	intracellular protein transport	1.721E-03	45	559
1027	mating	1.722E-03	9	55
1028	bone remodeling	1.780E-03	8	45
1029	regulation of striated muscle contraction	1.780E-03	8	45
1030	positive regulation of cellular metabolic process	1.822E-03	124	1886
1031	peptide transport	1.832E-03	12	89
1032	leukocyte mediated immunity	1.843E-03	20	191
1033	purine ribonucleotide catabolic process	1.861E-03	41	499
1034	regulation of response to stress	1.932E-03	59	786
1035	regulation of cell adhesion mediated by integrin	1.997E-03	7	36
1036	response to vitamin D	1.999E-03	10	67
1037	peptidyl-serine modification	2.018E-03	12	90
1038	detection of mechanical stimulus involved in sensory perception	2.035E-03	6	27
1039	response to gravity	2.035E-03	6	27
1040	regulation of phosphoprotein phosphatase activity	2.035E-03	6	27
1041	response to corticosterone stimulus	2.060E-03	8	46
1042	response to fungus	2.060E-03	8	46
1043	protein localization to nucleus	2.071E-03	18	166
1044	central nervous system neuron differentiation	2.095E-03	16	140
1045	positive regulation of protein phosphorylation	2.135E-03	27	292
1046	cell proliferation	2.135E-03	57	757
1047	regulation of cellular component size	2.142E-03	43	534

1048	ribonucleotide catabolic process	2.153E-03	41	503
1049	ameboidal cell migration	2.156E-03	11	79
1050	cellular lipid metabolic process	2.168E-03	62	839
1051	positive regulation of neutrophil chemotaxis	2.178E-03	5	19
1052	response to herbicide	2.178E-03	5	19
1053	glutamate metabolic process	2.178E-03	5	19
1054	positive regulation of humoral immune response	2.178E-03	5	19
1055	negative regulation of neural precursor cell proliferation	2.178E-03	5	19
1056	positive regulation of metabolic process	2.202E-03	129	1984
1057	respiratory gaseous exchange	2.225E-03	9	57
1058	response to protein stimulus	2.241E-03	27	293
1059	positive regulation of defense response	2.337E-03	25	265
1060	cellular response to temperature stimulus	2.353E-03	3	6
1061	complement receptor mediated signaling pathway	2.353E-03	3	6
1062	positive regulation of acetylcholine secretion	2.353E-03	3	6
1063	renal control of peripheral vascular resistance involved in regulation of systemic arterial blood pressure	2.353E-03	3	6
1064	frontal suture morphogenesis	2.353E-03	3	6
1065	regulation of NAD(P)H oxidase activity	2.353E-03	3	6
1066	transcription factor import into nucleus	2.353E-03	3	6
1067	renin-angiotensin regulation of aldosterone production	2.353E-03	3	6
1068	negative regulation of neuron projection regeneration	2.353E-03	3	6
1069	regulation of alkaline phosphatase activity	2.353E-03	3	6
1070	regulation of blood vessel size by renin-angiotensin	2.353E-03	3	6
1071	astrocyte activation	2.353E-03	3	6
1072	regulation of interleukin-1 production	2.373E-03	8	47
1073	positive regulation of digestive system process	2.391E-03	4	12
1074	negative regulation of glucose import	2.391E-03	4	12
1075	regulation of nerve growth factor receptor signaling pathway	2.391E-03	4	12
1076	induction of programmed cell death in response to chemical stimulus	2.391E-03	4	12
1077	N-glycan processing	2.391E-03	4	12
1078	neuronal ion channel clustering	2.391E-03	4	12
1079	regulation of cAMP-mediated signaling	2.391E-03	4	12
1080	blood vessel morphogenesis	2.433E-03	35	414
1081	response to ATP	2.480E-03	6	28
1082	cellular response to dexamethasone stimulus	2.480E-03	6	28
1083	positive regulation of lipid catabolic process	2.480E-03	6	28
1084	multicellular organismal reproductive behavior	2.480E-03	6	28
1085	cellular protein complex assembly	2.525E-03	23	238
1086	lymphocyte activation	2.566E-03	33	385
1087	regulation of sprouting of injured axon	2.597E-03	2	2
1088	tolerance induction to nonself antigen	2.597E-03	2	2
1089	enteric smooth muscle cell differentiation	2.597E-03	2	2
1090	regulation of collateral sprouting of intact axon in response to injury	2.597E-03	2	2
1091	tolerance induction dependent upon immune response	2.597E-03	2	2
1092	glutamate decarboxylation to succinate	2.597E-03	2	2
1093	cell surface pattern recognition receptor signaling pathway	2.597E-03	2	2
1094	regulation of axon extension involved in regeneration	2.597E-03	2	2
1095	negative regulation of growth hormone secretion	2.597E-03	2	2
1096	substantia nigra development	2.597E-03	2	2
1097	lung connective tissue development	2.597E-03	2	2
1098	cytotoxic T cell differentiation	2.597E-03	2	2
1099	synaptonemal complex disassembly	2.597E-03	2	2
1100	negative regulation of alkaline phosphatase activity	2.597E-03	2	2

1101	axonogenesis involved in innervation	2.597E-03	2	2
1102	phenylethylamine metabolic process	2.597E-03	2	2
1103	negative regulation of cortisol secretion	2.597E-03	2	2
1104	immune response-activating signal transduction	2.630E-03	24	253
1105	positive regulation of immune response	2.669E-03	37	447
1106	response to fatty acid	2.723E-03	8	48
1107	positive regulation of lipid metabolic process	2.740E-03	14	118
1108	response to amine stimulus	2.768E-03	24	254
1109	negative regulation of steroid biosynthetic process	2.784E-03	5	20
1110	regulation of tumor necrosis factor biosynthetic process	2.784E-03	5	20
1111	serotonin receptor signaling pathway	2.784E-03	5	20
1112	regulation of receptor activity	2.787E-03	10	70
1113	protein import into nucleus	2.792E-03	15	131
1114	defense response to Gram-positive bacterium	2.838E-03	9	59
1115	activation of MAPKK activity	2.838E-03	9	59
1116	protein transport	2.936E-03	74	1050
1117	neurological system process involved in regulation of systemic arterial blood pressure	2.994E-03	6	29
1118	regulation of leukocyte degranulation	2.994E-03	6	29
1119	response to purine-containing compound	2.994E-03	6	29
1120	macromolecular complex assembly	3.010E-03	70	984
1121	positive regulation of leukocyte migration	3.099E-03	10	71
1122	behavioral interaction between organisms	3.099E-03	10	71
1123	neuron migration	3.104E-03	13	107
1124	positive regulation of cellular catabolic process	3.104E-03	13	107
1125	positive regulation of nitrogen compound metabolic process	3.144E-03	92	1359
1126	response to mechanical stimulus	3.151E-03	22	228
1127	regulation of Ras GTPase activity	3.160E-03	20	200
1128	membrane lipid metabolic process	3.202E-03	14	120
1129	response to biotic stimulus	3.202E-03	61	837
1130	generation of precursor metabolites and energy	3.309E-03	42	531
1131	cerebellar Purkinje cell differentiation	3.316E-03	4	13
1132	activation of transmembrane receptor protein tyrosine kinase activity	3.316E-03	4	13
1133	cerebellar Purkinje cell layer formation	3.316E-03	4	13
1134	cerebellar Purkinje cell layer morphogenesis	3.316E-03	4	13
1135	positive regulation of fatty acid beta-oxidation	3.316E-03	4	13
1136	positive thymic T cell selection	3.316E-03	4	13
1137	positive regulation of protein dephosphorylation	3.316E-03	4	13
1138	negative regulation of potassium ion transport	3.316E-03	4	13
1139	negative regulation of glucose transport	3.316E-03	4	13
1140	antigen receptor-mediated signaling pathway	3.436E-03	16	147
1141	regulation of cytokine secretion	3.438E-03	10	72
1142	nuclear import	3.473E-03	15	134
1143	striated muscle cell development	3.473E-03	15	134
1144	epidermal growth factor receptor signaling pathway	3.484E-03	12	96
1145	cerebral cortex neuron differentiation	3.502E-03	5	21
1146	lipoprotein transport	3.502E-03	5	21
1147	negative regulation of exocytosis	3.502E-03	5	21
1148	insemination	3.502E-03	5	21
1149	heat generation	3.502E-03	5	21
1150	cellular aromatic compound metabolic process	3.528E-03	26	288
1151	regulation of chemokine production	3.542E-03	8	50
1152	tissue regeneration	3.577E-03	9	61
1153	negative regulation of angiogenesis	3.577E-03	9	61

1154	muscle cell development	3.582E-03	17	161
1155	filopodium assembly	3.584E-03	6	30
1156	regulation of odontogenesis	3.584E-03	6	30
1157	T cell selection	3.584E-03	6	30
1158	response to other organism	3.655E-03	54	727
1159	lipid metabolic process	3.659E-03	80	1161
1160	neuron death	3.736E-03	7	40
1161	positive regulation of leukocyte activation	3.757E-03	28	319
1162	positive regulation of adaptive immune response	3.796E-03	12	97
1163	negative regulation of cell projection organization	3.796E-03	12	97
1164	protein tetramerization	3.862E-03	11	85
1165	cerebellum development	3.862E-03	11	85
1166	positive regulation of proteolysis	3.862E-03	11	85
1167	negative regulation of cell size	3.952E-03	19	190
1168	cerebral cortex GABAergic interneuron migration	3.961E-03	3	7
1169	cellular response to manganese ion	3.961E-03	3	7
1170	negative regulation of nerve growth factor receptor signaling pathway	3.961E-03	3	7
1171	oligodendrocyte cell fate commitment	3.961E-03	3	7
1172	regulation of retinal cell programmed cell death	3.961E-03	3	7
1173	smooth muscle contraction involved in micturition	3.961E-03	3	7
1174	positive regulation of macrophage cytokine production	3.961E-03	3	7
1175	interneuron migration from the subpallium to the cortex	3.961E-03	3	7
1176	embryonic neurocranium morphogenesis	3.961E-03	3	7
1177	inhibition of adenylate cyclase activity by dopamine receptor signaling pathway	3.961E-03	3	7
1178	regulation of serotonin secretion	3.961E-03	3	7
1179	regulation of Rap GTPase activity	3.961E-03	3	7
1180	cerebral cortex GABAergic interneuron development	3.961E-03	3	7
1181	central nervous system neuron development	3.999E-03	9	62
1182	neuromuscular junction development	4.017E-03	8	51
1183	regulation of monooxygenase activity	4.017E-03	8	51
1184	fluid transport	4.017E-03	8	51
1185	immune response-regulating signaling pathway	4.112E-03	24	262
1186	spinal cord development	4.130E-03	12	98
1187	intracellular transport	4.131E-03	71	1014
1188	cell junction assembly	4.185E-03	19	191
1189	purine ribonucleoside triphosphate catabolic process	4.227E-03	39	491
1190	regulation of leukocyte migration	4.229E-03	11	86
1191	positive regulation of smooth muscle cell proliferation	4.229E-03	11	86
1192	interaction with host	4.229E-03	11	86
1193	regulation of circadian sleep/wake cycle	4.255E-03	6	31
1194	regulation of circadian sleep/wake cycle, sleep	4.255E-03	6	31
1195	neuromuscular synaptic transmission	4.255E-03	6	31
1196	retina development in camera-type eye	4.283E-03	15	137
1197	cardiac muscle contraction	4.311E-03	7	41
1198	regulation of muscle cell differentiation	4.316E-03	14	124
1199	cellular response to biotic stimulus	4.326E-03	17	164
1200	protein kinase B signaling cascade	4.344E-03	5	22
1201	positive regulation of epithelial cell migration	4.344E-03	5	22
1202	regulation of interleukin-1 beta secretion	4.344E-03	5	22
1203	positive regulation of T-helper cell differentiation	4.344E-03	5	22
1204	regulation of filopodium assembly	4.344E-03	5	22
1205	ribonucleoside triphosphate catabolic process	4.373E-03	39	492
1206	positive regulation of cytokine production	4.375E-03	21	220

1207	negative regulation of cell growth	4.401E-03	18	178
1208	positive regulation of dephosphorylation	4.457E-03	4	14
1209	negative regulation of production of molecular mediator of immune response	4.457E-03	4	14
1210	peptidyl-cysteine modification	4.457E-03	4	14
1211	regulation of cholesterol esterification	4.457E-03	4	14
1212	platelet degranulation	4.488E-03	12	99
1213	purine nucleoside triphosphate catabolic process	4.523E-03	39	493
1214	positive regulation of endocytosis	4.614E-03	13	112
1215	regulation of oxidoreductase activity	4.635E-03	10	75
1216	muscle cell differentiation	4.650E-03	27	309
1217	positive regulation of Ras GTPase activity	4.772E-03	16	152
1218	regulation of leukocyte activation	4.796E-03	35	432
1219	regulation of cytokine production involved in immune response	4.950E-03	7	42
1220	regulation of interleukin-1 beta production	4.950E-03	7	42
1221	glycolipid metabolic process	4.950E-03	7	42
1222	positive regulation of oxidoreductase activity	4.950E-03	7	42
1223	cellular response to lipopolysaccharide	4.977E-03	13	113
1224	sphingolipid metabolic process	4.977E-03	13	113
1225	detection of mechanical stimulus	5.015E-03	6	32
1226	regulation of type 2 immune response	5.015E-03	6	32
1227	regulation of release of sequestered calcium ion into cytosol	5.015E-03	6	32
1228	positive regulation of immune system process	5.018E-03	50	673
1229	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	5.047E-03	11	88
1230	striated muscle tissue development	5.066E-03	27	311
1231	cellular response to chemical stimulus	5.211E-03	111	1716
1232	positive regulation of cell activation	5.270E-03	28	327
1233	regulation of cellular metabolic process	5.274E-03	291	5010
1234	regulation of neutrophil chemotaxis	5.322E-03	5	23
1235	regulation of interleukin-1 secretion	5.322E-03	5	23
1236	astrocyte development	5.322E-03	5	23
1237	regulation of insulin secretion involved in cellular response to glucose stimulus	5.322E-03	5	23
1238	L-glutamate transport	5.322E-03	5	23
1239	positive regulation of cyclin-dependent protein kinase activity	5.322E-03	5	23
1240	positive regulation of cell size	5.342E-03	14	127
1241	T cell activation	5.375E-03	21	224
1242	regulation of cell activation	5.399E-03	36	451
1243	cerebral cortex development	5.501E-03	11	89
1244	angiogenesis	5.513E-03	27	313
1245	nucleoside triphosphate catabolic process	5.518E-03	39	499
1246	protein import	5.526E-03	19	196
1247	response to reactive oxygen species	5.544E-03	18	182
1248	monovalent inorganic cation homeostasis	5.600E-03	10	77
1249	peptidyl-serine phosphorylation	5.600E-03	10	77
1250	positive regulation of interleukin-6 production	5.658E-03	7	43
1251	transition metal ion transport	5.725E-03	14	128
1252	digestive system process	5.741E-03	8	54
1253	negative regulation of cell differentiation	5.830E-03	37	469
1254	low-density lipoprotein particle remodeling	5.835E-03	4	15
1255	receptor guanylyl cyclase signaling pathway	5.835E-03	4	15
1256	estrous cycle phase	5.835E-03	4	15

1257	regulation of developmental pigmentation	5.835E-03	4	15
1258	regulation of odontogenesis of dentine-containing tooth	5.835E-03	4	15
1259	negative regulation of catecholamine secretion	5.835E-03	4	15
1260	regulation of lipoprotein lipase activity	5.870E-03	6	33
1261	regulation of oligodendrocyte differentiation	5.870E-03	6	33
1262	phospholipid biosynthetic process	5.972E-03	15	142
1263	positive regulation of homeostatic process	5.986E-03	11	90
1264	cellular response to metal ion	5.986E-03	11	90
1265	response to vitamin	5.998E-03	25	285
1266	regulation of kidney size	6.099E-03	3	8
1267	regulation of inclusion body assembly	6.099E-03	3	8
1268	Rab protein signal transduction	6.099E-03	3	8
1269	positive regulation of Rho protein signal transduction	6.099E-03	3	8
1270	negative regulation of calcium ion transport into cytosol	6.099E-03	3	8
1271	negative regulation of hormone metabolic process	6.099E-03	3	8
1272	positive regulation of T-helper 1 cell differentiation	6.099E-03	3	8
1273	negative regulation of fatty acid transport	6.099E-03	3	8
1274	positive regulation of long-term neuronal synaptic plasticity	6.099E-03	3	8
1275	negative regulation of hormone biosynthetic process	6.099E-03	3	8
1276	negative regulation of cAMP-mediated signaling	6.099E-03	3	8
1277	gap junction assembly	6.099E-03	3	8
1278	menstrual cycle phase	6.099E-03	3	8
1279	manganese ion transmembrane transport	6.099E-03	3	8
1280	histamine production involved in inflammatory response	6.099E-03	3	8
1281	response to iron(II) ion	6.099E-03	3	8
1282	positive regulation of norepinephrine secretion	6.099E-03	3	8
1283	histamine secretion by mast cell	6.099E-03	3	8
1284	regulation of Rap protein signal transduction	6.099E-03	3	8
1285	neuronal action potential propagation	6.099E-03	3	8
1286	histamine secretion involved in inflammatory response	6.099E-03	3	8
1287	negative regulation of cellular component movement	6.129E-03	14	129
1288	cell growth	6.129E-03	14	129
1289	brown fat cell differentiation	6.439E-03	7	44
1290	sphingolipid biosynthetic process	6.439E-03	7	44
1291	synaptic vesicle endocytosis	6.444E-03	5	24
1292	negative regulation of osteoclast differentiation	6.444E-03	5	24
1293	regulation of respiratory gaseous exchange	6.444E-03	5	24
1294	regulation of myeloid cell apoptosis	6.444E-03	5	24
1295	negative regulation of steroid metabolic process	6.444E-03	5	24
1296	spinal cord motor neuron differentiation	6.444E-03	5	24
1297	thymic T cell selection	6.444E-03	5	24
1298	regulation of stress-activated MAPK cascade	6.444E-03	5	24
1299	regulation of immune system process	6.493E-03	72	1051
1300	regulation of lipid biosynthetic process	6.556E-03	14	130
1301	skeletal muscle tissue development	6.562E-03	17	171
1302	positive regulation of protein metabolic process	6.578E-03	48	650
1303	blood vessel development	6.681E-03	38	489
1304	activation of immune response	6.714E-03	28	333
1305	response to iron ion	6.827E-03	6	34
1306	neural retina development	6.827E-03	6	34
1307	macrophage activation	6.827E-03	6	34
1308	circadian sleep/wake cycle process	6.827E-03	6	34
1309	glycosphingolipid metabolic process	6.827E-03	6	34
1310	response to cortisol stimulus	6.827E-03	6	34
1311	positive regulation of smooth muscle contraction	6.827E-03	6	34

1312	response to oxidative stress	6.897E-03	29	349
1313	organic anion transport	7.056E-03	11	92
1314	peptidyl-tyrosine dephosphorylation	7.183E-03	12	105
1315	water transport	7.297E-03	7	45
1316	regulation of receptor-mediated endocytosis	7.297E-03	7	45
1317	regulation of intracellular transport	7.302E-03	18	187
1318	circulatory system development	7.325E-03	57	803
1319	cardiovascular system development	7.325E-03	57	803
1320	regulation of angiogenesis	7.349E-03	17	173
1321	positive regulation of transmembrane transport	7.411E-03	9	68
1322	regulation of glial cell differentiation	7.411E-03	9	68
1323	cytokine secretion	7.470E-03	4	16
1324	glial cell migration	7.470E-03	4	16
1325	regulation of endothelial cell differentiation	7.470E-03	4	16
1326	positive regulation of stress-activated MAPK cascade	7.470E-03	4	16
1327	macrophage chemotaxis	7.470E-03	4	16
1328	negative regulation of meiotic cell cycle	7.526E-03	2	3
1329	detection of hypoxia	7.526E-03	2	3
1330	germ-line stem cell division	7.526E-03	2	3
1331	male germ-line stem cell division	7.526E-03	2	3
1332	ossification involved in bone remodeling	7.526E-03	2	3
1333	T-helper 17 cell chemotaxis	7.526E-03	2	3
1334	negative regulation of eosinophil degranulation	7.526E-03	2	3
1335	nipple morphogenesis	7.526E-03	2	3
1336	negative regulation of release of sequestered calcium ion into cytosol	7.526E-03	2	3
1337	detection of fungus	7.526E-03	2	3
1338	regulation of eosinophil degranulation	7.526E-03	2	3
1339	nipple development	7.526E-03	2	3
1340	T cell chemotaxis	7.526E-03	2	3
1341	helper T cell chemotaxis	7.526E-03	2	3
1342	negative regulation of acetylcholine secretion	7.526E-03	2	3
1343	D-aspartate transport	7.526E-03	2	3
1344	regulation of catagen	7.526E-03	2	3
1345	monocyte extravasation	7.526E-03	2	3
1346	protein localization to juxtaparanode region of axon	7.526E-03	2	3
1347	activation of phospholipase A2 activity by calcium-mediated signaling	7.526E-03	2	3
1348	positive regulation of T cell extravasation	7.526E-03	2	3
1349	negative regulation of icosanoid secretion	7.526E-03	2	3
1350	regulation of atrial cardiomyocyte membrane depolarization	7.526E-03	2	3
1351	activation of adenylate cyclase activity by serotonin receptor signaling pathway	7.526E-03	2	3
1352	positive regulation of catagen	7.526E-03	2	3
1353	regulation of T cell extravasation	7.526E-03	2	3
1354	glutamine biosynthetic process	7.526E-03	2	3
1355	ammonia assimilation cycle	7.526E-03	2	3
1356	thymine catabolic process	7.526E-03	2	3
1357	posterior midgut development	7.526E-03	2	3
1358	positive regulation of mismatch repair	7.526E-03	2	3
1359	cellular response to magnesium starvation	7.526E-03	2	3
1360	negative regulation of gastric acid secretion	7.526E-03	2	3
1361	positive regulation of NAD(P)H oxidase activity	7.526E-03	2	3
1362	thymine metabolic process	7.526E-03	2	3
1363	D-aspartate import	7.526E-03	2	3
1364	AMP catabolic process	7.526E-03	2	3

1365	positive regulation of cell growth	7.665E-03	13	119
1366	production of molecular mediator involved in inflammatory response	7.724E-03	5	25
1367	skeletal muscle contraction	7.724E-03	5	25
1368	positive regulation of neurogenesis	7.768E-03	16	160
1369	cerebellum morphogenesis	7.891E-03	6	35
1370	positive regulation of epidermal growth factor receptor signaling pathway	7.891E-03	6	35
1371	positive regulation of tumor necrosis factor production	7.891E-03	6	35
1372	receptor internalization	7.891E-03	6	35
1373	defense response to virus	7.976E-03	8	57
1374	regulation of skeletal muscle tissue development	8.147E-03	9	69
1375	cellular biogenic amine metabolic process	8.161E-03	15	147
1376	regulation of cytokine production	8.197E-03	33	416
1377	negative regulation of cell migration	8.207E-03	13	120
1378	membrane lipid biosynthetic process	8.237E-03	7	46
1379	regulation of adaptive immune response	8.667E-03	15	148
1380	regulation of gliogenesis	8.701E-03	10	82
1381	fibroblast migration	8.804E-03	3	9
1382	negative regulation of circadian rhythm	8.804E-03	3	9
1383	urinary bladder smooth muscle contraction	8.804E-03	3	9
1384	aspartate transport	8.804E-03	3	9
1385	activation of phospholipase D activity	8.804E-03	3	9
1386	regulation of uterine smooth muscle contraction	8.804E-03	3	9
1387	negative regulation of phosphatase activity	8.804E-03	3	9
1388	positive regulation of uterine smooth muscle contraction	8.804E-03	3	9
1389	negative regulation of circadian sleep/wake cycle, sleep	8.804E-03	3	9
1390	regulation of defense response	8.842E-03	39	514
1391	cytokine production	8.935E-03	11	95
1392	regulation of glucose transport	8.935E-03	11	95
1393	actin filament-based movement	8.938E-03	9	70
1394	cell-cell junction organization	9.060E-03	14	135
1395	regulation of protein maturation by peptide bond cleavage	9.169E-03	5	26
1396	positive regulation of branching involved in ureteric bud morphogenesis	9.169E-03	5	26
1397	cerebellar cortex morphogenesis	9.169E-03	5	26
1398	copulation	9.169E-03	5	26
1399	cell differentiation in spinal cord	9.263E-03	7	47
1400	two-component signal transduction system (phosphorelay)	9.380E-03	4	17
1401	dentate gyrus development	9.380E-03	4	17
1402	suckling behavior	9.380E-03	4	17
1403	catecholamine transport	9.380E-03	4	17
1404	regulation of respiratory gaseous exchange by neurological system process	9.380E-03	4	17
1405	glial cell fate commitment	9.380E-03	4	17
1406	drinking behavior	9.380E-03	4	17
1407	positive regulation of filopodium assembly	9.380E-03	4	17
1408	negative regulation of cell motility	9.382E-03	13	122
1409	regulation of metabolic process	9.545E-03	324	5690
1410	positive regulation of angiogenesis	9.641E-03	11	96
1411	response to nicotine	9.793E-03	8	59
1412	hormone metabolic process	1.022E-02	19	208
1413	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	1.025E-02	14	137
1414	nerve development	1.026E-02	10	84

1415	positive regulation of NF-kappaB transcription factor activity	1.028E-02	12	110
1416	circadian sleep/wake cycle	1.037E-02	6	37
1417	positive regulation of biosynthetic process	1.038E-02	95	1474
1418	positive regulation of insulin secretion	1.038E-02	7	48
1419	muscle tissue development	1.040E-02	27	329
1420	detection of light stimulus	1.069E-02	9	72
1421	anatomical structure homeostasis	1.072E-02	19	209
1422	skeletal muscle organ development	1.072E-02	17	180
1423	negative regulation of cell-cell adhesion	1.079E-02	5	27
1424	positive regulation of Rac GTPase activity	1.079E-02	5	27
1425	regulation of protein processing	1.079E-02	5	27
1426	parturition	1.079E-02	5	27
1427	response to magnesium ion	1.079E-02	5	27
1428	digestive tract development	1.089E-02	14	138
1429	programmed cell death	1.094E-02	67	990
1430	acylglycerol metabolic process	1.101E-02	12	111
1431	positive regulation of T cell differentiation	1.111E-02	10	85
1432	triglyceride metabolic process	1.118E-02	11	98
1433	ribonucleotide biosynthetic process	1.156E-02	14	139
1434	acute inflammatory response to antigenic stimulus	1.158E-02	4	18
1435	regulation of respiratory system process	1.158E-02	4	18
1436	chemosensory behavior	1.158E-02	4	18
1437	muscle hypertrophy	1.158E-02	4	18
1438	neural nucleus development	1.158E-02	4	18
1439	positive regulation of cell division	1.159E-02	7	49
1440	muscle filament sliding	1.159E-02	7	49
1441	positive regulation of fatty acid metabolic process	1.159E-02	7	49
1442	response to osmotic stress	1.166E-02	9	73
1443	excretion	1.166E-02	9	73
1444	regulation of systemic arterial blood pressure by hormone	1.180E-02	6	38
1445	retina morphogenesis in camera-type eye	1.180E-02	6	38
1446	positive regulation of cellular protein metabolic process	1.185E-02	42	573
1447	response to testosterone stimulus	1.190E-02	8	61
1448	post-Golgi vesicle-mediated transport	1.201E-02	10	86
1449	atrial cardiac muscle tissue morphogenesis	1.211E-02	3	10
1450	positive regulation of triglyceride biosynthetic process	1.211E-02	3	10
1451	parental behavior	1.211E-02	3	10
1452	calcium ion import	1.211E-02	3	10
1453	urinary tract smooth muscle contraction	1.211E-02	3	10
1454	brain renin-angiotensin system	1.211E-02	3	10
1455	epithelial structure maintenance	1.211E-02	3	10
1456	protein-cofactor linkage	1.211E-02	3	10
1457	negative regulation of astrocyte differentiation	1.211E-02	3	10
1458	maternal behavior	1.211E-02	3	10
1459	negative regulation of epinephrine secretion	1.211E-02	3	10
1460	atrial cardiac muscle tissue development	1.211E-02	3	10
1461	regulation of mitochondrial depolarization	1.211E-02	3	10
1462	detection of calcium ion	1.211E-02	3	10
1463	positive regulation of cellular biosynthetic process	1.216E-02	93	1448
1464	GTP metabolic process	1.221E-02	24	287
1465	regulation of primary metabolic process	1.229E-02	285	4978
1466	GTP catabolic process	1.234E-02	23	272
1467	negative regulation of immune system process	1.235E-02	19	212
1468	neutral lipid metabolic process	1.259E-02	12	113
1469	regulation of mast cell activation	1.260E-02	5	28

1470	dendrite morphogenesis	1.260E-02	5	28
1471	bone resorption	1.260E-02	5	28
1472	regulation of branching involved in ureteric bud morphogenesis	1.260E-02	5	28
1473	negative regulation of homeostatic process	1.260E-02	5	28
1474	positive regulation vascular endothelial growth factor production	1.260E-02	5	28
1475	thyroid hormone metabolic process	1.260E-02	5	28
1476	response to insulin stimulus	1.280E-02	29	366
1477	acute inflammatory response	1.290E-02	11	100
1478	actin-myosin filament sliding	1.290E-02	7	50
1479	heart contraction	1.290E-02	7	50
1480	positive regulation of alpha-beta T cell differentiation	1.290E-02	7	50
1481	anti-apoptosis	1.300E-02	25	304
1482	striated muscle cell differentiation	1.301E-02	20	228
1483	cellular response to glucagon stimulus	1.307E-02	8	62
1484	cytoskeleton organization	1.320E-02	50	710
1485	hindbrain morphogenesis	1.336E-02	6	39
1486	purine ribonucleotide biosynthetic process	1.371E-02	13	128
1487	regulation of cellular amine metabolic process	1.399E-02	10	88
1488	inositol phosphate metabolic process	1.409E-02	4	19
1489	synaptonemal complex organization	1.409E-02	4	19
1490	regulation of appetite	1.409E-02	4	19
1491	dicarboxylic acid transport	1.409E-02	4	19
1492	insulin-like growth factor receptor signaling pathway	1.409E-02	4	19
1493	long-chain fatty-acyl-CoA metabolic process	1.409E-02	4	19
1494	cerebellar cortex formation	1.409E-02	4	19
1495	SMAD protein import into nucleus	1.409E-02	4	19
1496	positive regulation of triglyceride metabolic process	1.409E-02	4	19
1497	long-chain fatty-acyl-CoA biosynthetic process	1.409E-02	4	19
1498	cellular response to hormone stimulus	1.449E-02	43	597
1499	regulation of synapse structural plasticity	1.454E-02	2	4
1500	positive regulation of chemokine (C-X-C motif) ligand 2 production	1.454E-02	2	4
1501	smooth muscle cell proliferation	1.454E-02	2	4
1502	activation of phospholipase D activity by G-protein coupled receptor protein signaling pathway	1.454E-02	2	4
1503	positive regulation of melanocyte differentiation	1.454E-02	2	4
1504	positive regulation of catecholamine metabolic process	1.454E-02	2	4
1505	subthalamus development	1.454E-02	2	4
1506	regulation of phosphatidylinositol dephosphorylation	1.454E-02	2	4
1507	regulation of immune complex clearance by monocytes and macrophages	1.454E-02	2	4
1508	Tie receptor signaling pathway	1.454E-02	2	4
1509	cellular response to peptidoglycan	1.454E-02	2	4
1510	regulation of cyclin-dependent protein kinase activity involved in G2/M	1.454E-02	2	4
1511	vasodilation by angiotensin involved in regulation of systemic arterial blood pressure	1.454E-02	2	4
1512	endothelial cell activation	1.454E-02	2	4
1513	paranodal junction assembly	1.454E-02	2	4
1514	positive regulation of complement activation	1.454E-02	2	4
1515	positive regulation of dopamine receptor signaling pathway	1.454E-02	2	4
1516	cell proliferation in hindbrain	1.454E-02	2	4
1517	protein targeting to Golgi	1.454E-02	2	4
1518	positive regulation of dopamine metabolic process	1.454E-02	2	4

1519	positive regulation of protein activation cascade	1.454E-02	2	4
1520	regulation of metanephros size	1.454E-02	2	4
1521	establishment of meiotic spindle localization	1.454E-02	2	4
1522	regulation of gastric acid secretion	1.454E-02	2	4
1523	catagen	1.454E-02	2	4
1524	positive regulation of cyclin-dependent protein kinase activity involved in G2/M	1.454E-02	2	4
1525	inhibition of adenylate cyclase activity by serotonin receptor signaling pathway	1.454E-02	2	4
1526	locomotory exploration behavior	1.454E-02	2	4
1527	cellular response to purine-containing compound	1.454E-02	2	4
1528	regulation of cortisol secretion	1.454E-02	2	4
1529	positive regulation of oocyte development	1.454E-02	2	4
1530	response to blue light	1.454E-02	2	4
1531	positive regulation of pigment cell differentiation	1.454E-02	2	4
1532	regulation of chemokine (C-X-C motif) ligand 2 production	1.454E-02	2	4
1533	establishment of protein localization in Golgi	1.454E-02	2	4
1534	deoxyribonucleoside diphosphate biosynthetic process	1.454E-02	2	4
1535	minus-end-directed organelle transport along microtubule	1.454E-02	2	4
1536	positive regulation of immune complex clearance by monocytes and macrophages	1.454E-02	2	4
1537	positive regulation of catabolic process	1.457E-02	14	143
1538	neuroblast proliferation	1.460E-02	5	29
1539	monoamine transport	1.460E-02	5	29
1540	regulation of epithelial cell migration	1.460E-02	5	29
1541	cellular response to peptide hormone stimulus	1.471E-02	30	386
1542	regulation of lymphocyte activation	1.471E-02	30	386
1543	response to lipopolysaccharide	1.477E-02	26	323